

# Bonnie Ann Wallace

## List of Publications by Year in descending order

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267  
papers

19,653  
citations

17429

63  
h-index

12585

132  
g-index

273  
all docs

273  
docs citations

273  
times ranked

17860  
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>DichroWeb</scp>, a website for calculating protein secondary structure from circular dichroism spectroscopic data. <i>Protein Science</i> , 2022, 31, 37-46.	3.1	208
2	The PCDDDB (Protein Circular Dichroism Data Bank): A Bioinformatics Resource for Protein Characterisations and Methods Development. <i>Journal of Molecular Biology</i> , 2022, 434, 167441.	2.0	14
3	The T1â€tetramerization Domain of Kv1.2 Rescues Expression and Preserves Function of a Truncated NaChBac Sodium Channel. <i>FEBS Letters</i> , 2022, , .	1.3	0
4	Tools and methods for circular dichroism spectroscopy of proteins: a tutorial review. <i>Chemical Society Reviews</i> , 2021, 50, 8400-8413.	18.7	107
5	A tamoxifen receptor within a voltage-gated sodium channel. <i>Molecular Cell</i> , 2021, 81, 1160-1169.e5.	4.5	19
6	Reference Protocol to Assess Analytical Performance of Higher Order Structural Analysis Measurements: Results from an Interlaboratory Comparison. <i>Analytical Chemistry</i> , 2021, 93, 9041-9048.	3.2	4
7	Interactions of amphipathic Î±-helical MEG proteins from <i>Schistosoma mansoni</i> with membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183173.	1.4	8
8	Biopharmaceutical applications of protein characterisation by circular dichroism spectroscopy. , 2020, , 123-152.		3
9	Cannabidiol interactions with voltage-gated sodium channels. <i>ELife</i> , 2020, 9, .	2.8	40
10	Unveiling the binding and orientation of the antimicrobial peptide Plantaricin 149 in zwitterionic and negatively charged membranes. <i>European Biophysics Journal</i> , 2019, 48, 621-633.	1.2	9
11	The role of circular dichroism spectroscopy in the era of integrative structural biology. <i>Current Opinion in Structural Biology</i> , 2019, 58, 191-196.	2.6	33
12	Valproic acid interactions with the NavMs voltage-gated sodium channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26549-26554.	3.3	20
13	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
14	The intrinsically disordered Tarp protein from chlamydia binds actin with a partially preformed helix. <i>Scientific Reports</i> , 2018, 8, 1960.	1.6	18
15	Thermal Melt Circular Dichroism Spectroscopy of Membrane Proteins as a Tool for Cryo-EM Preparations. <i>Biophysical Journal</i> , 2018, 114, 634a.	0.2	0
16	DichroMatch at the protein circular dichroism data bank (DM@PCDDDB): A webâ€based tool for identifying protein nearest neighbors using circular dichroism spectroscopy. <i>Protein Science</i> , 2018, 27, 10-13.	3.1	10
17	Thermal melt circular dichroism spectroscopic studies for identifying stabilising amphipathic molecules for the voltageâ€gated sodium channel NavMs. <i>Biopolymers</i> , 2018, 109, e23067.	1.2	12
18	Comparisons of voltage-gated sodium channel structures with open and closed gates and implications for state-dependent drug design. <i>Biochemical Society Transactions</i> , 2018, 46, 1567-1575.	1.6	9

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19	Role of the Interaction Motif in Maintaining the Open Gate of an Open Sodium Channel. <i>Biophysical Journal</i> , 2018, 115, 1920-1930.	0.2	13
20	Fenestration Mutants of a Voltage-Gated Sodium Channel that Modify Channel Blocker Ingress. <i>Biophysical Journal</i> , 2018, 114, 38a.	0.2	0
21	CDtoolX, a downloadable software package for processing and analyses of circular dichroism spectroscopic data. <i>Protein Science</i> , 2018, 27, 1717-1722.	3.1	89
22	Characterization of esterase activity from an <i>Acetomicrobium hydrogeniformans</i> enzyme with high structural stability in extreme conditions. <i>Extremophiles</i> , 2018, 22, 781-793.	0.9	10
23	Lipid binding attenuates channel closure of the outer membrane protein OmpF. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6691-6696.	3.3	39
24	Differential dehydration effects on globular proteins and intrinsically disordered proteins during film formation. <i>Protein Science</i> , 2017, 26, 718-726.	3.1	21
25	Structure and function of PspA and Vipp1 N-terminal peptides: Insights into the membrane stress sensing and mitigation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017, 1859, 28-39.	1.4	35
26	Voltage-gated sodium channels as targets for pyrethroid insecticides. <i>European Biophysics Journal</i> , 2017, 46, 675-679.	1.2	116
27	The complete structure of an activated open sodium channel. <i>Nature Communications</i> , 2017, 8, 14205.	5.8	118
28	The Complete Crystal Structure of an Open Activated Sodium Channel. <i>Biophysical Journal</i> , 2017, 112, 18a-19a.	0.2	0
29	Interpreting the functional role of a novel interaction motif in prokaryotic sodium channels. <i>Journal of General Physiology</i> , 2017, 149, 613-622.	0.9	17
30	Oriented Circular Dichroism Spectroscopy as a Tool for Studying the Gating of Sodium Channels. <i>Biophysical Journal</i> , 2017, 112, 241a.	0.2	0
31	How C-Terminal Domain Stabilize the Gate of Voltage-Gated Sodium Channels. <i>Biophysical Journal</i> , 2017, 112, 106a.	0.2	0
32	Attenuation of Phosphorylation-dependent Activation of Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) by Disease-causing Mutations at the Transmission Interface. <i>Journal of Biological Chemistry</i> , 2017, 292, 1988-1999.	1.6	7
33	PCDDb: new developments at the Protein Circular Dichroism Data Bank. <i>Nucleic Acids Research</i> , 2017, 45, D303-D307.	6.5	52
34	Mutagenesis of the NaChBac sodium channel discloses a functional role for a conserved S6 asparagine. <i>European Biophysics Journal</i> , 2017, 46, 665-674.	1.2	12
35	Interaction of an esophageal MEG protein from schistosomes with a human S100 protein involved in inflammatory response. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3490-3497.	1.1	13
36	Environmental Factors Modulating the Stability and Enzymatic Activity of the <i>Petrotoga mobilis</i> Esterase (PmEst). <i>PLoS ONE</i> , 2016, 11, e0158146.	1.1	8

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37	AnglerFish: a webserver for defining the geometry of $\alpha$ -helices in membrane proteins. <i>Bioinformatics</i> , 2016, 33, btw781.	1.8	1
38	Molecular basis of ion permeability in a voltage-gated sodium channel. <i>EMBO Journal</i> , 2016, 35, 820-830.	3.5	95
39	Isolated pores dissected from human two-pore channel 2 are functional. <i>Scientific Reports</i> , 2016, 6, 38426.	1.6	9
40	Sodium Channel/Ligand Complex Structures as a Guide for Rational Drug Design. <i>Biophysical Journal</i> , 2016, 110, 33a.	0.2	0
41	Protein Design for Decreased Disorder: SHERP as an Exemplar Protein. <i>Biophysical Journal</i> , 2016, 110, 555a.	0.2	0
42	Structure of the C-terminal domain of the prokaryotic sodium channel orthologue NsvBa. <i>European Biophysics Journal</i> , 2016, 45, 807-814.	1.2	2
43	Circular dichroism spectroscopy of membrane proteins. <i>Chemical Society Reviews</i> , 2016, 45, 4859-4872.	18.7	234
44	Spectral Properties of $\alpha$ -Disordered and Polyproline II Structures Defined by Circular Dichroism Spectroscopy. <i>Biophysical Journal</i> , 2016, 110, 559a-560a.	0.2	0
45	Sodium Ion Coordination in the Selectivity Filter of a Voltage-Gated Sodium Channel. <i>Biophysical Journal</i> , 2015, 108, 490a.	0.2	0
46	Deconstructing the DGAT1 Enzyme: Membrane Interactions at Substrate Binding Sites. <i>PLoS ONE</i> , 2015, 10, e0118407.	1.1	8
47	Screening ion-channel ligand interactions with passive pumping in a microfluidic bilayer lipid membrane chip. <i>Biomicrofluidics</i> , 2015, 9, 014103.	1.2	4
48	Voltage-Gated Sodium Channels: Structure and Function of Complexes with Sodium Channel Blockers. <i>Biophysical Journal</i> , 2015, 108, 10a.	0.2	0
49	An evolutionarily unique heterodimeric voltage-gated cation channel found in aphids. <i>FEBS Letters</i> , 2015, 589, 598-607.	1.3	21
50	X-ray, spectroscopic and normal-mode dynamics of calyculin: structure-function studies of a neuronal calcium-signalling protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 615-631.	2.5	7
51	Third International Synchrotron Radiation Circular Dichroism Spectroscopy Meeting. <i>Synchrotron Radiation News</i> , 2015, 28, 58-59.	0.2	2
52	Structural model of the open-closed-inactivated cycle of prokaryotic voltage-gated sodium channels. <i>Journal of General Physiology</i> , 2015, 145, 5-16.	0.9	47
53	Circular Dichroism Spectroscopy for Protein Characterization. , 2015, , 109-137.		7
54	Characterization of the Prokaryotic Sodium Channel NavSp Pore with a Microfluidic Bilayer Platform. <i>PLoS ONE</i> , 2015, 10, e0131286.	1.1	8

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55	Shaped Apertures in Photoresist Films Enhance the Lifetime and Mechanical Stability of Suspended Lipid Bilayers. <i>Biophysical Journal</i> , 2014, 106, 1650-1659.	0.2	34
56	Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. <i>Nature Communications</i> , 2014, 5, 4863.	5.8	91
57	Deconstructing the DGAT1 enzyme: Binding sites and substrate interactions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 3145-3152.	1.4	21
58	Prokaryotic NavMs channel as a structural and functional model for eukaryotic sodium channel antagonism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8428-8433.	3.3	120
59	Lipid interactions of LAH4, a peptide with antimicrobial and nucleic acid transfection activities. <i>European Biophysics Journal</i> , 2014, 43, 499-507.	1.2	29
60	Distinct circular dichroism spectroscopic signatures of polyproline II and unordered secondary structures: Applications in secondary structure analyses. <i>Protein Science</i> , 2014, 23, 1765-1772.	3.1	151
61	Chaperone-mediated native folding of a Î²-scorpion toxin in the periplasm of <i>Escherichia coli</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 10-15.	1.1	10
62	Predictive 3D modelling of the interactions of pyrethroids with the voltage-gated sodium channels of ticks and mites. <i>Pest Management Science</i> , 2014, 70, 369-377.	1.7	41
63	Folding Factors and Partners for the Intrinsically Disordered Protein Micro-Exon Gene 14 (MEG-14). <i>Biophysical Journal</i> , 2013, 104, 2512-2520.	0.2	21
64	Molecular dynamics of ion transport through the open conformation of a bacterial voltage-gated sodium channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6364-6369.	3.3	149
65	Stabilisation of Na,K-ATPase structure by the cardiotonic steroid ouabain. <i>Biochemical and Biophysical Research Communications</i> , 2013, 435, 300-305.	1.0	10
66	Membrane defects enhance the interaction of antimicrobial peptides, aurein 1.2 versus caerin 1.1. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 1863-1872.	1.4	37
67	Peptaibols. , 2013, , 150-156.		6
68	ValiDichro: a website for validating and quality control of protein circular dichroism spectra. <i>Nucleic Acids Research</i> , 2013, 41, W417-W421.	6.5	13
69	Role of the C-terminal domain in the structure and function of tetrameric sodium channels. <i>Nature Communications</i> , 2013, 4, 2465.	5.8	71
70	Differential Lipid Dependence of the Function of Bacterial Sodium Channels. <i>PLoS ONE</i> , 2013, 8, e61216.	1.1	18
71	Membrane Interactions of S100A12 (Calgranulin C). <i>PLoS ONE</i> , 2013, 8, e82555.	1.1	10
72	DichroMatch: a website for similarity searching of circular dichroism spectra. <i>Nucleic Acids Research</i> , 2012, 40, W547-W552.	6.5	12

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73	Structure of a bacterial voltage-gated sodium channel pore reveals mechanisms of opening and closing. <i>Nature Communications</i> , 2012, 3, 1102.	5.8	255
74	Association of Neonicotinoid Insensitivity with a Conserved Residue in the Loop D Binding Region of the Tick Nicotinic Acetylcholine Receptor. <i>Biochemistry</i> , 2012, 51, 4627-4629.	1.2	24
75	Transmembrane and extramembrane contributions to membrane protein thermal stability: Studies with the NaChBac sodium channel. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 889-895.	1.4	12
76	Bisphenol A Binds to the Local Anesthetic Receptor Site to Block the Human Cardiac Sodium Channel. <i>PLoS ONE</i> , 2012, 7, e41667.	1.1	63
77	Circular Dichroism Spectral Data and Metadata in the Protein Circular Dichroism Data Bank (PCDDDB): A Tutorial Guide to Accession and Deposition. <i>Chirality</i> , 2012, 24, 751-763.	1.3	3
78	JCAMP-DX for circular dichroism spectra and metadata (IUPAC Recommendations 2012). <i>Pure and Applied Chemistry</i> , 2012, 84, 2171-2182.	0.9	4
79	The Metastasis-Associated Extracellular Matrix Protein Osteopontin Forms Transient Structure in Ligand Interaction Sites. <i>Biochemistry</i> , 2011, 50, 6113-6124.	1.2	64
80	NaChBac: The Long Lost Sodium Channel Ancestor. <i>Biochemistry</i> , 2011, 50, 6742-6752.	1.2	60
81	Molecular Dynamics Simulation of the Antiamoebin Ion Channel: Linking Structure and Conductance. <i>Biophysical Journal</i> , 2011, 100, 2394-2402.	0.2	39
82	The influence of different lipid environments on the structure and function of the hepatitis C virus p7 ion channel protein. <i>Molecular Membrane Biology</i> , 2011, 28, 254-264.	2.0	18
83	A reference dataset for the analyses of membrane protein secondary structures and transmembrane residues using circular dichroism spectroscopy. <i>Bioinformatics</i> , 2011, 27, 1630-1636.	1.8	135
84	Validichro, a Software Tool for Validation of Circular Dichroism (CD) Spectroscopic Data. <i>Biophysical Journal</i> , 2011, 100, 320a.	0.2	1
85	Correlation of structural and functional thermal stability of the integral membrane protein Na,K-ATPase. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 2573-2580.	1.4	16
86	AcrB contamination in 2-D crystallization of membrane proteins: Lessons from a sodium channel and a putative monovalent cation/proton antiporter. <i>Journal of Structural Biology</i> , 2011, 176, 419-424.	1.3	20
87	Synchrotron radiation circular dichroism (SRCD) spectroscopy: An emerging method in structural biology for examining protein conformations and protein interactions. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2011, 649, 177-178.	0.7	24
88	Surface architecture of endospores of the <i>Bacillus cereus/anthracis/thuringiensis</i> family at the subnanometer scale. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16014-16019.	3.3	67
89	PCDDDB: the protein circular dichroism data bank, a repository for circular dichroism spectral and metadata. <i>Nucleic Acids Research</i> , 2011, 39, D480-D486.	6.5	79
90	Structural insights into the dynamics and function of the C-terminus of the E. coli RNA chaperone Hfq. <i>Nucleic Acids Research</i> , 2011, 39, 4900-4915.	6.5	74

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91	Simplified Bacterial "Pore" Channel Provides Insight into the Assembly, Stability, and Structure of Sodium Channels. <i>Journal of Biological Chemistry</i> , 2011, 286, 16386-16391.	1.6	31
92	Structural Basis of Molecular Recognition of the Leishmania Small Hydrophilic Endoplasmic Reticulum-associated Protein (SHERP) at Membrane Surfaces. <i>Journal of Biological Chemistry</i> , 2011, 286, 9246-9256.	1.6	7
93	Synchrotron radiation circular dichroism (SRCD) spectroscopy: an enhanced method for examining protein conformations and protein interactions. <i>Biochemical Society Transactions</i> , 2010, 38, 861-873.	1.6	44
94	The Protein Circular Dichroism Data Bank, A Web-Based Site for Access to Circular Dichroism Spectroscopic Data. <i>Structure</i> , 2010, 18, 1267-1269.	1.6	40
95	Synchrotron radiation circular dichroism spectroscopy-defined structure of the C-terminal domain of NaChBac and its role in channel assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14064-14069.	3.3	41
96	2Struc: the secondary structure server. <i>Bioinformatics</i> , 2010, 26, 2624-2625.	1.8	110
97	Consistent Picture of the Reversible Thermal Unfolding of Hen Egg-White Lysozyme from Experiment and Molecular Dynamics. <i>Biophysical Journal</i> , 2010, 99, 2255-2263.	0.2	48
98	Role of the Protective Antigen Octamer in the Molecular Mechanism of Anthrax Lethal Toxin Stabilization in Plasma. <i>Journal of Molecular Biology</i> , 2010, 399, 741-758.	2.0	58
99	Changes in $\beta$ -Lactoglobulin Conformation at the Oil/Water Interface of Emulsions Studied by Synchrotron Radiation Circular Dichroism Spectroscopy. <i>Biomacromolecules</i> , 2010, 11, 2136-2142.	2.6	66
100	SRCD2009. <i>Synchrotron Radiation News</i> , 2009, 22, 2-4.	0.2	1
101	Effect of lipid on the conformation of the N-terminal region of equinatoxin II: a synchrotron radiation circular dichroism spectroscopic study. <i>European Biophysics Journal</i> , 2009, 39, 121-127.	1.2	12
102	Thermal and chemical unfolding and refolding of a eukaryotic sodium channel. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009, 1788, 1279-1286.	1.4	24
103	Protein characterisation by synchrotron radiation circular dichroism spectroscopy. <i>Quarterly Reviews of Biophysics</i> , 2009, 42, 317-370.	2.4	99
104	Oriented Synchrotron Radiation Circular Dichroism and Linear Dichroism Spectroscopy of Peptides in Model Membranes. <i>Biophysical Journal</i> , 2009, 96, 337a.	0.2	1
105	Evaluating protein:protein complex formation using synchrotron radiation circular dichroism spectroscopy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1142-1146.	1.5	28
106	Light flux density threshold at which protein denaturation is induced by synchrotron radiation circular dichroism beamlines. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 420-422.	1.0	91
107	Knockdown resistance to DDT and pyrethroids: from target site mutations to molecular modelling. <i>Pest Management Science</i> , 2008, 64, 1126-1130.	1.7	65
108	Protein secondary structure analyses from circular dichroism spectroscopy: Methods and reference databases. <i>Biopolymers</i> , 2008, 89, 392-400.	1.2	1,969

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109	Crystal Structure of a vFlip-IKK $\beta$ Complex: Insights into Viral Activation of the IKK Signalingosome. <i>Molecular Cell</i> , 2008, 30, 620-631.	4.5	108
110	The effects of lipids on the structure of the eukaryotic cytolysin equinatoxin II: A synchrotron radiation circular dichroism spectroscopic study. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2008, 1778, 2091-2096.	1.4	26
111	G219S mutagenesis as a means of stabilizing conformational flexibility in the bacterial sodium channel NaChBac. <i>Molecular Membrane Biology</i> , 2008, 25, 670-676.	2.0	14
112	Tetrameric Bacterial Sodium Channels: Characterization of Structure, Stability, and Drug Binding. <i>Biochemistry</i> , 2008, 47, 8114-8121.	1.2	22
113	Charge-Transfer Transitions in the Vacuum-Ultraviolet of Protein Circular Dichroism Spectra. <i>Journal of Physical Chemistry B</i> , 2008, 112, 1866-1874.	1.2	53
114	A Pore-blocking Hydrophobic Motif at the Cytoplasmic Aperture of the Closed-state Nav1.7 Channel Is Disrupted by the Erythromelalgia-associated F1449V Mutation. <i>Journal of Biological Chemistry</i> , 2008, 283, 24118-24127.	1.6	40
115	Association of partially folded lens $\beta$ 2-crystallins with the $\beta$ -crystallin molecular chaperone. <i>Biochemical Journal</i> , 2008, 409, 691-699.	1.7	22
116	A reference dataset for circular dichroism spectroscopy tailored for the $\beta$ -crystallin lens proteins. <i>Experimental Eye Research</i> , 2007, 84, 1001-1008.	1.2	16
117	Opsin Stability and Folding: Modulation by Phospholipid Bicelles. <i>Journal of Molecular Biology</i> , 2007, 374, 1319-1332.	2.0	73
118	Synchrotron Radiation Circular Dichroism (SRCD) spectroscopy: New beamlines and new applications in biology. <i>Spectroscopy</i> , 2007, 21, 245-255.	0.8	85
119	Peptaibols. , 2006, , 83-88.		2
120	A reference database for circular dichroism spectroscopy covering fold and secondary structure space. <i>Bioinformatics</i> , 2006, 22, 1955-1962.	1.8	395
121	Synchrotron radiation circular dichroism spectroscopy of proteins and applications in structural and functional genomics. <i>Chemical Society Reviews</i> , 2006, 35, 39-51.	18.7	218
122	Novel methods for secondary structure determination using low wavelength (VUV) circular dichroism spectroscopic data. <i>BMC Bioinformatics</i> , 2006, 7, 507.	1.2	26
123	Protein circular dichroism data bank (PCDDDB): Data bank and website design. <i>Chirality</i> , 2006, 18, 426-429.	1.3	10
124	Modelling insecticide-binding sites in the voltage-gated sodium channel. <i>Biochemical Journal</i> , 2006, 396, 255-263.	1.7	248
125	VUV irradiation effects on proteins in high-flux synchrotron radiation circular dichroism spectroscopy. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 517-523.	1.0	41
126	The Protein Circular Dichroism Data Bank (PCDDDB): A bioinformatics and spectroscopic resource. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 1-3.	1.5	29

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127	Calibration and standardisation of synchrotron radiation and conventional circular dichroism spectrometers. Part 2: Factors affecting magnitude and wavelength. <i>Spectroscopy</i> , 2005, 19, 43-51.	0.8	54
128	Meeting Reports: International Workshop on the Protein Circular Dichroism Data Bank. <i>Synchrotron Radiation News</i> , 2005, 18, 20-21.	0.2	1
129	Effects of Deglycosylation of Sodium Channels on Their Structure and Function. <i>Biochemistry</i> , 2005, 44, 441-449.	1.2	44
130	Calcium Fluoride Micro Cells for Synchrotron Radiation Circular Dichroism Spectroscopy. <i>Applied Spectroscopy</i> , 2005, 59, 1109-1113.	1.2	65
131	Spectral magnitude effects on the analyses of secondary structure from circular dichroism spectroscopic data. <i>Protein Science</i> , 2005, 14, 368-374.	3.1	53
132	Redetermination of the extinction coefficient of camphor-10-sulfonic acid, a calibration standard for circular dichroism spectroscopy. <i>Analytical Biochemistry</i> , 2004, 335, 338-339.	1.1	43
133	Analysis of peptaibol sequence composition: implications for in vivo synthesis and channel formation. <i>European Biophysics Journal</i> , 2004, 33, 233-7.	1.2	39
134	CDtool—an integrated software package for circular dichroism spectroscopic data processing, analysis, and archiving. <i>Analytical Biochemistry</i> , 2004, 332, 285-289.	1.1	233
135	Biomedical applications of synchrotron radiation circular dichroism spectroscopy: Identification of mutant proteins associated with disease and development of a reference database for fold motifs. <i>Faraday Discussions</i> , 2004, 126, 237.	1.6	33
136	The Peptaibol Database: a database for sequences and structures of naturally occurring peptaibols. <i>Nucleic Acids Research</i> , 2004, 32, 593D-594.	6.5	154
137	DICHROWEB, an online server for protein secondary structure analyses from circular dichroism spectroscopic data. <i>Nucleic Acids Research</i> , 2004, 32, W668-W673.	6.5	2,106
138	Conductance Studies on Trichotoxin_A50E and Implications for Channel Structure. <i>Biophysical Journal</i> , 2004, 87, 1705-1710.	0.2	25
139	The P23T Cataract Mutation Causes Loss of Solubility of Folded $^{13}\text{D}$ -Crystallin. <i>Journal of Molecular Biology</i> , 2004, 343, 435-444.	2.0	93
140	The peptaibol antiamoebin as a model ion channel: similarities to bacterial potassium channels. <i>Journal of Peptide Science</i> , 2003, 9, 769-775.	0.8	17
141	The peptaibol database: a sequence and structure resource. <i>Journal of Peptide Science</i> , 2003, 9, 663-665.	0.8	45
142	Analyses of circular dichroism spectra of membrane proteins. <i>Protein Science</i> , 2003, 12, 875-884.	3.1	149
143	Solution NMR Studies of Antiamoebin, a Membrane Channel-Forming Polypeptide. <i>Biophysical Journal</i> , 2003, 84, 185-194.	0.2	24
144	Binding of the Anticonvulsant Drug Lamotrigine and the Neurotoxin Batrachotoxin to Voltage-gated Sodium Channels Induces Conformational Changes Associated with Block and Steady-state Activation. <i>Journal of Biological Chemistry</i> , 2003, 278, 10675-10682.	1.6	40

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145	Circular dichroism and synchrotron radiation circular dichroism spectroscopy: tools for drug discovery. <i>Biochemical Society Transactions</i> , 2003, 31, 631-633.	1.6	21
146	Calibration and Standardisation of Synchrotron Radiation Circular Dichroism and Conventional Circular Dichroism Spectrophotometers. <i>Spectroscopy</i> , 2003, 17, 653-661.	0.8	86
147	The Temperature Dependence of Gramicidin Conformational States in Octanol. <i>Protein and Peptide Letters</i> , 2003, 10, 9-17.	0.4	13
148	Interactions of the Type III Secretion Pathway Proteins LcrV and LcrG from <i>Yersinia pestis</i> Are Mediated by Coiled-Coil Domains. <i>Journal of Biological Chemistry</i> , 2002, 277, 38714-38722.	1.6	44
149	DICHROWEB: an interactive website for the analysis of protein secondary structure from circular dichroism spectra. <i>Bioinformatics</i> , 2002, 18, 211-212.	1.8	677
150	Model for a Helical Bundle Channel Based on the High-Resolution Crystal Structure of Trichotoxin_A50E. <i>Biochemistry</i> , 2002, 41, 12934-12941.	1.2	62
151	Characterization and Membrane Assembly of the TatA Component of the <i>Escherichia coli</i> Twin-Arginine Protein Transport System. <i>Biochemistry</i> , 2002, 41, 13690-13697.	1.2	108
152	Structure and Function of Voltage-Dependent Ion Channel Regulatory $\hat{I}^2$ Subunits. <i>Biochemistry</i> , 2002, 41, 2886-2894.	1.2	95
153	Synchrotron radiation circular dichroism and conventional circular dichroism spectroscopy: A comparison. <i>Spectroscopy</i> , 2002, 16, 121-125.	0.8	24
154	Antiamoebin: A polypeptide ion carrier and channel. , 2002, , 733-735.		2
155	Endothelin precursor isoforms: Structural basis for rational drug design of ECE inhibitors. , 2002, , 511-512.		0
156	Peptaibols: models for ion channels. <i>Biochemical Society Transactions</i> , 2001, 29, 565-570.	1.6	194
157	Synchrotron radiation circular dichroism spectroscopy: vacuum ultraviolet irradiation does not damage protein integrity. <i>Journal of Synchrotron Radiation</i> , 2001, 8, 1027-1029.	1.0	9
158	Synchrotron radiation circular dichroism spectroscopy of proteins: secondary structure, fold recognition and structural genomics. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 567-571.	2.8	129
159	Expression and Characterization of the Human Endothelin-A-Receptor in <i>Pichia pastoris</i> . <i>Journal of Cardiovascular Pharmacology</i> , 2000, 36, S55-S57.	0.8	0
160	Common structural features in gramicidin and other ion channels. <i>BioEssays</i> , 2000, 22, 227-234.	1.2	76
161	Synchrotron radiation circular-dichroism spectroscopy as a tool for investigating protein structures. <i>Journal of Synchrotron Radiation</i> , 2000, 7, 289-295.	1.0	74
162	Conformational changes by synchrotron radiation circular dichroism spectroscopy. , 2000, 7, 708-709.		51

#	ARTICLE	IF	CITATIONS
163	Modeling and Docking the Endothelin G-Protein-Coupled Receptor. <i>Biophysical Journal</i> , 2000, 79, 3083-3094.	0.2	48
164	Transmembrane Peptide NB of Influenza B: A Simulation, Structure, and Conductance Study. <i>Biochemistry</i> , 2000, 39, 12708-12716.	1.2	36
165	In vitro membrane-inserted conformation of the cytochrome b5 tail. <i>Biochemical Journal</i> , 2000, 352, 117.	1.7	10
166	In vitro membrane-inserted conformation of the cytochrome b(5) tail. <i>Biochemical Journal</i> , 2000, 352 Pt 1, 117-24.	1.7	2
167	The molecular-replacement solution of an intermediate-sized helical polypeptide, anti amoebic I. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1539-1545.	2.5	5
168	Gramicidin channel controversy--revisited. <i>Nature Structural Biology</i> , 1999, 6, 610-611.	9.7	58
169	Phospholipid chain length alters the equilibrium between pore and channel forms of gramicidin. <i>Faraday Discussions</i> , 1999, 111, 159-164.	1.6	36
170	Modelling of a voltage-dependent Ca <sup>2+</sup> channel $\hat{I}^2$ subunit as a basis for understanding its functional properties. <i>FEBS Letters</i> , 1999, 445, 366-370.	1.3	114
171	Do the Structures of Big ET-1 and Big ET-3 Adopt a Similar Overall Fold? Consequences for Endothelin Converting Enzyme Specificity. <i>Biochemistry</i> , 1999, 38, 1721-1726.	1.2	3
172	Screening of a library of phage-displayed peptides identifies human Bcl-2 as a taxol-binding protein 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1999, 285, 197-203.	2.0	231
173	Tryptophans in Membrane Proteins. <i>Advances in Experimental Medicine and Biology</i> , 1999, 467, 789-799.	0.8	36
174	The structure and function of anti amoebic I, a proline-rich membrane-active polypeptide. <i>Structure</i> , 1998, 6, 783-792.	1.6	68
175	Anti amoebic I can function as a carrier or as a pore-forming peptide. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1998, 1415, 255-260.	1.4	32
176	Recent Advances in the High Resolution Structures of Bacterial Channels: Gramicidin A. <i>Journal of Structural Biology</i> , 1998, 121, 123-141.	1.3	162
177	Shifting the Equilibrium Mixture of Gramicidin Double Helices Toward a Single Conformation with Multivalent Cationic Salts. <i>Biophysical Journal</i> , 1998, 75, 635-640.	0.2	22
178	Structure of the CLN3 Gene and Predicted Structure, Location and Function of CLN3 Protein. <i>Neuropediatrics</i> , 1997, 28, 12-14.	0.3	18
179	The dynamic nature of gramicidin. <i>Biomembranes: A Multi-Volume Treatise</i> , 1997, , 327-359.	0.1	1
180	Slow $\hat{I}^2$ Helix Formation during Folding of a Membrane Protein. <i>Biochemistry</i> , 1997, 36, 192-196.	1.2	122

#	ARTICLE	IF	CITATIONS
181	Crystal structure of the Gramicidin/Potassium thiocyanate complex. <i>Journal of Molecular Biology</i> , 1997, 266, 963-977.	2.0	54
182	Endothelin (ET), its Precursor BigET, and its Receptor, ETA. <i>Expert Opinion on Therapeutic Targets</i> , 1997, 1, 121-123.	1.0	0
183	The effects of calcium ions on double helical forms of gramicidin. <i>European Biophysics Journal</i> , 1997, 26, 299-306.	1.2	14
184	Secondary solvent effects on the circular dichroism spectra of polypeptides in non-aqueous environments: influence of polarisation effects on the far ultraviolet spectra of alamethicin. <i>Biophysical Chemistry</i> , 1997, 65, 65-74.	1.5	34
185	Solvent effects on the conformation and far UV CD spectra of gramicidin. , 1997, 42, 771-781.		36
186	Circular dichroism studies of human bigâ€œendothelinâ€œ1 (Big ETâ€œ1). <i>Chemical Biology and Drug Design</i> , 1997, 49, 331-335.	1.2	5
187	Binding of alkaline cations to the double-helical form of gramicidin. <i>Biophysical Journal</i> , 1996, 71, 163-170.	0.2	17
188	A molecular model for human Big-Endothelin-1 (Big ET-1). <i>FEBS Letters</i> , 1996, 394, 191-195.	1.3	16
189	Solution Structure of a Parallel Left-handed Double-helical Gramicidin-A Determined by 2D1H NMR. <i>Journal of Molecular Biology</i> , 1996, 264, 757-769.	2.0	35
190	A model for Batten disease protein CLN3: Functional implications from homology and mutations. <i>FEBS Letters</i> , 1996, 399, 75-77.	1.3	71
191	HOLE: A program for the analysis of the pore dimensions of ion channel structural models. <i>Journal of Molecular Graphics</i> , 1996, 14, 354-360.	1.7	1,425
192	The Roles of Tryptophan Residues in the Structure, Function, and Folding of the Gramicidin Transmembrane Ion Channel. <i>Advances in Experimental Medicine and Biology</i> , 1996, 398, 607-614.	0.8	12
193	The Crystal Structure of Human Endothelin-1 and How It Relates to Receptor Binding. <i>Journal of Cardiovascular Pharmacology</i> , 1995, 26, S250-253.	0.8	14
194	Effects of Local Environment on the Circular Dichroism Spectra of Polypeptides. <i>Analytical Biochemistry</i> , 1995, 227, 90-100.	1.1	31
195	A comparison of Xâ€œray and NMR structures for human endothelinâ€œ1. <i>Protein Science</i> , 1995, 4, 75-83.	3.1	33
196	Cystine nooses and protein specificity. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 266-268.	3.6	22
197	Comparison of the structures of the endothelin A receptor antagonists BQ123 and N -methyl leucine BQ123 with the crystal structure of the C-terminal tail of endothelin-1. <i>FEBS Letters</i> , 1995, 374, 379-383.	1.3	11
198	The crystal structure of human endothelin-1 and how it relates to receptor binding. <i>Journal of Cardiovascular Pharmacology</i> , 1995, 26 Suppl 3, S250-3.	0.8	4

#	ARTICLE	IF	CITATIONS
199	The crystal structure of human endothelin. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 311-319.	3.6	90
200	Alamethicin Pyromellitate: An Ion-Activated Channel-Forming Peptide. <i>Biochemistry</i> , 1994, 33, 6850-6858.	1.2	37
201	Modelling the structures of the isoforms of human endothelins based on the crystal structure of human endothelin-I. <i>Biochemical Society Transactions</i> , 1994, 22, 1037-1043.	1.6	6
202	Caesium-binding sites in the gramicidin pore. <i>Biochemical Society Transactions</i> , 1994, 22, 1043-1045.	1.6	11
203	Preliminary analysis of the pore dimensions of human annexin V. <i>Biochemical Society Transactions</i> , 1994, 22, 146S-146S.	1.6	3
204	Membrane Protein Structure: Lessons from Gramicidin. , 1994, , 314-334.		3
205	Red- and Blue-Shifting in the Circular Dichroism Spectra of Polypeptides due to Dipole Effects. <i>Protein and Peptide Letters</i> , 1994, 1, 136-140.	0.4	9
206	Preliminary Crystallization and X-ray Analysis of Orthorhombic Human Endothelin. <i>Journal of Molecular Biology</i> , 1993, 234, 1250-1252.	2.0	3
207	Temperature dependence of the interaction of alamethicin helices in membranes. <i>Biochemistry</i> , 1993, 32, 9819-9825.	1.2	57
208	Analyses of ligand binding in five endothiapepsin crystal complexes and their use in the design and evaluation of novel renin inhibitors. <i>Journal of Medicinal Chemistry</i> , 1993, 36, 3809-3820.	2.9	21
209	The pore dimensions of gramicidin A. <i>Biophysical Journal</i> , 1993, 65, 2455-2460.	0.2	595
210	Circular-dichroism analyses of membrane proteins: examination of environmental effects on bacteriorhodopsin spectra. <i>Biochemical Journal</i> , 1993, 289, 215-219.	1.7	35
211	Gramicidinâ€™lipid interactions induce specific tryptophan side-chain conformations. <i>Biochemical Society Transactions</i> , 1992, 20, 864-867.	1.6	14
212	Crystallographic studies of a transmembrane ion channel, gramicidin A. <i>Progress in Biophysics and Molecular Biology</i> , 1992, 57, 59-69.	1.4	26
213	Model ion channels: Gramicidin and alamethicin. <i>Journal of Membrane Biology</i> , 1992, 129, 109-36.	1.0	261
214	Effects of pH on conformational properties related to the toxicity of <i>Bacillus thuringiensis</i> Îˆ-endotoxin. <i>BBA - Proteins and Proteomics</i> , 1992, 1159, 185-192.	2.1	17
215	Circular dichroism studies of tryptophan residues in gramicidin. , 1992, , 247-249.		1
216	Protein-chromophore interactions in bacteriorhodopsin: the effects of a change in surface potential. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1991, 1070, 313-320.	1.4	0

#	ARTICLE	IF	CITATIONS
217	Co-crystals of gramicidin A and phospholipid. <i>Journal of Molecular Biology</i> , 1991, 217, 625-627.	2.0	30
218	The use of single-wavelength anomalous scattering to solve the crystal structure of a gramicidin A/caesium chloride complex. <i>Acta Crystallographica Section B: Structural Science</i> , 1990, 46, 440-446.	1.8	18
219	Gramicidin Channels and Pores. <i>Annual Review of Biophysics and Biophysical Chemistry</i> , 1990, 19, 127-157.	12.2	185
220	The secondary structure of gap junctions. Influence of isolation methods and proteolysis.. <i>Journal of Biological Chemistry</i> , 1990, 265, 2358-2364.	1.6	35
221	The secondary structure of gap junctions. Influence of isolation methods and proteolysis. <i>Journal of Biological Chemistry</i> , 1990, 265, 2358-64.	1.6	30
222	The secondary structure of human amyloid deposits as determined by circular dichroism spectroscopy. <i>Biochemical and Biophysical Research Communications</i> , 1989, 162, 1162-1166.	1.0	10
223	Conformation of alamethicin in phospholipid vesicles: Implications for insertion models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 89-98.	1.5	60
224	The gramicidin pore: crystal structure of a cesium complex. <i>Science</i> , 1988, 241, 182-187.	6.0	257
225	Chapter 3 Gramicidin, a Simple Ion Channel. <i>Current Topics in Membranes and Transport</i> , 1988, 33, 35-50.	0.6	8
226	The Gramicidin Pore: Crystal Structure of a Gramicidin/Cesium Chloride Complex. <i>Jerusalem Symposia on Quantum Chemistry and Biochemistry</i> , 1988, , 103-113.	0.2	2
227	Secondary structural analyses of the nicotinic acetylcholine receptor as a test of molecular models.. <i>Journal of Biological Chemistry</i> , 1988, 263, 3177-3182.	1.6	47
228	Structural studies of Na,K-ATPase subunits. <i>Progress in Clinical and Biological Research</i> , 1988, 268A, 121-8.	0.2	0
229	Secondary structural analyses of the nicotinic acetylcholine receptor as a test of molecular models. <i>Journal of Biological Chemistry</i> , 1988, 263, 3177-82.	1.6	39
230	Membrane protein folding: motifs and predictions. <i>Progress in Clinical and Biological Research</i> , 1988, 273, 133-8.	0.2	2
231	The E1 $\rightarrow$ E2 transition of Ca <sup>2+</sup> -transporting ATPase in sarcoplasmic reticulum occurs without major changes in secondary structure. A circular-dichroism study. <i>Biochemical Journal</i> , 1987, 241, 663-669.	1.7	49
232	A theoretical analysis of the effects of sonication on differential absorption flattening in suspensions of membrane sheets. <i>Biophysical Journal</i> , 1987, 51, 527-532.	0.2	13
233	Comparison of lipid/gramicidin dispersions and cocrystals by Raman scattering. <i>Biochemistry</i> , 1987, 26, 557-562.	1.2	21
234	Differential absorption flattening optical effects are significant in the circular dichroism spectra of large membrane fragments. <i>Biochemistry</i> , 1987, 26, 65-70.	1.2	131

#	ARTICLE	IF	CITATIONS
235	Structure of gramicidin A. <i>Biophysical Journal</i> , 1986, 49, 295-306.	0.2	157
236	Structure/Function Relationships in Detergent-Solubilized Na/K-ATPase. <i>Annals of the New York Academy of Sciences</i> , 1986, 463, 375-380.	1.8	0
237	Folding Pathways for the Glycophorin Transmembrane Fragment. <i>Annals of the New York Academy of Sciences</i> , 1986, 463, 384-388.	1.8	0
238	Nicotinic Acetylcholine Receptor: Secondary Structure Determined by Circular Dichroism Spectroscopy. <i>Annals of the New York Academy of Sciences</i> , 1986, 463, 392-395.	1.8	7
239	Transferrin and Apotransferrin: pH-dependent Conformational Changes Associated with Receptor-mediated Uptake. <i>Annals of the New York Academy of Sciences</i> , 1986, 463, 403-407.	1.8	3
240	Evaluation of methods for the prediction of membrane protein secondary structures.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986, 83, 9423-9427.	3.3	78
241	Secondary structure and assembly mechanism of an oligomeric channel protein. <i>Biochemistry</i> , 1985, 24, 1915-1920.	1.2	185
242	Circular dichroism analyses of membrane proteins: An examination of differential light scattering and absorption flattening effects in large membrane vesicles and membrane sheets. <i>Analytical Biochemistry</i> , 1984, 142, 317-328.	1.1	104
243	Ion-Bond Forms of the Gramicidin a Transmembrane Channel. <i>Biophysical Journal</i> , 1984, 45, 114-116.	0.2	42
244	The Effects of Environment on the Conformation of the Alamethicin Membrane Channel. <i>Annals of the New York Academy of Sciences</i> , 1984, 435, 527-529.	1.8	11
245	Crystalline Ion Complexes of Gramicidin A. <i>Annals of the New York Academy of Sciences</i> , 1984, 435, 551-554.	1.8	15
246	Differential light scattering and absorption flattening optical effects are minimal in the circular dichroism spectra of small unilamellar vesicles. <i>Biochemistry</i> , 1984, 23, 2667-2673.	1.2	230
247	The C-terminus of bacteriorhodopsin is a random coil. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1984, 777, 93-98.	1.4	8
248	Crambin in phospholipid vesicles: Circular dichroism analysis of crystal structure relevance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1984, 81, 1406-1410.	3.3	24
249	Secondary structural composition of the Na/K-ATPase E1 and E2 conformers.. <i>Journal of Biological Chemistry</i> , 1984, 259, 2622-2628.	1.6	58
250	Structure of a gramicidin A/cesium complex. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1984, 40, C49-C49.	0.3	3
251	Secondary structural composition of the Na/K-ATPase E1 and E2 conformers. <i>Journal of Biological Chemistry</i> , 1984, 259, 2622-8.	1.6	49
252	Gramicidin a adopts distinctly different conformations in membranes and in organic solvents. <i>Biopolymers</i> , 1983, 22, 397-402.	1.2	67

#	ARTICLE	IF	CITATIONS
253	Binding of fibronectin to phospholipid vesicles.. Journal of Biological Chemistry, 1983, 258, 3327-3331.	1.6	41
254	Binding of fibronectin to phospholipid vesicles. Journal of Biological Chemistry, 1983, 258, 3327-31.	1.6	35
255	[60] Comparison of bacteriorhodopsin and rhodopsin molecular structure. Methods in Enzymology, 1982, 88, 447-462.	0.4	10
256	Folding of the mitochondrial proton adenosine triphosphatase proteolipid channel in phospholipid vesicles. Biochemistry, 1982, 21, 4960-4968.	1.2	174
257	Location of the carboxyl terminus of bacteriorhodopsin in purple membrane. Biophysical Journal, 1982, 39, 233-239.	0.2	58
258	The Effects of Lipid Environment, Ion-Binding and Chemical Modifications on the Structure of the Gramicidin Transmembrane Channel. Biophysical Journal, 1982, 37, 197-199.	0.2	4
259	Hydrophobic oligopeptides in solution and in phospholipid vesicles: synthetic fragments of bacteriorhodopsin. Biochemistry, 1982, 21, 3444-3452.	1.2	14
260	Conformation of gramicidin A in phospholipid vesicles: circular dichroism studies of effects of ion binding, chemical modification, and lipid structure. Biochemistry, 1981, 20, 5754-5760.	1.2	161
261	Path of the polypeptide in bacteriorhodopsin.. Proceedings of the National Academy of Sciences of the United States of America, 1980, 77, 2023-2027.	3.3	393
262	Conformation of the gramicidin A transmembrane channel: A <sup>13</sup> C nuclear magnetic resonance study of <sup>13</sup> C-enriched gramicidin in phosphatidylcholine vesicles. Journal of Molecular Biology, 1980, 143, 1-19.	2.0	126
263	Diffraction Studies of Modified Purple Membrane. Proceedings in Life Sciences, 1980, , 57-60.	0.5	1
264	Conformation of gramicidin A channel in phospholipid vesicles: a <sup>13</sup> C and <sup>19</sup> F nuclear magnetic resonance study.. Proceedings of the National Academy of Sciences of the United States of America, 1979, 76, 4230-4234.	3.3	166
265	Conformation of an oligopeptide in phospholipid vesicles.. Proceedings of the National Academy of Sciences of the United States of America, 1979, 76, 1775-1779.	3.3	24
266	The planar distributions of surface proteins and intramembrane particles in <i>Acholeplasma laidlawii</i> are differentially affected by the physical state of membrane lipids. Biochimica Et Biophysica Acta - Biomembranes, 1978, 508, 431-449.	1.4	33
267	The influence of lipid state on the planar distribution of membrane proteins in <i>Acholeplasma laidlawii</i> . Journal of Molecular Biology, 1976, 107, 255-269.	2.0	36