

# 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	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
2	Protein secondary structure analyses from circular dichroism spectroscopy: Methods and reference databases. <i>Biopolymers</i> , 2008, 89, 392-400.	1.2	1,969
3	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
4	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
5	The pore dimensions of gramicidin A. <i>Biophysical Journal</i> , 1993, 65, 2455-2460.	0.2	595
6	A reference database for circular dichroism spectroscopy covering fold and secondary structure space. <i>Bioinformatics</i> , 2006, 22, 1955-1962.	1.8	395
7	Path of the polypeptide in bacteriorhodopsin.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1980, 77, 2023-2027.	3.3	393
8	Model ion channels: Gramicidin and alamethicin. <i>Journal of Membrane Biology</i> , 1992, 129, 109-36.	1.0	261
9	The gramicidin pore: crystal structure of a cesium complex. <i>Science</i> , 1988, 241, 182-187.	6.0	257
10	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
11	Modelling insecticide-binding sites in the voltage-gated sodium channel. <i>Biochemical Journal</i> , 2006, 396, 255-263.	1.7	248
12	Circular dichroism spectroscopy of membrane proteins. <i>Chemical Society Reviews</i> , 2016, 45, 4859-4872.	18.7	234
13	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
14	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
15	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
16	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
17	<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
18	Peptaibols: models for ion channels. <i>Biochemical Society Transactions</i> , 2001, 29, 565-570.	1.6	194

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19	Secondary structure and assembly mechanism of an oligomeric channel protein. <i>Biochemistry</i> , 1985, 24, 1915-1920.	1.2	185
20	Gramicidin Channels and Pores. <i>Annual Review of Biophysics and Biophysical Chemistry</i> , 1990, 19, 127-157.	12.2	185
21	Folding of the mitochondrial proton adenosine triphosphatase proteolipid channel in phospholipid vesicles. <i>Biochemistry</i> , 1982, 21, 4960-4968.	1.2	174
22	Conformation of gramicidin A channel in phospholipid vesicles: a <sup>13</sup> C and <sup>19</sup> F nuclear magnetic resonance study.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1979, 76, 4230-4234.	3.3	166
23	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
24	Conformation of gramicidin A in phospholipid vesicles: circular dichroism studies of effects of ion binding, chemical modification, and lipid structure. <i>Biochemistry</i> , 1981, 20, 5754-5760.	1.2	161
25	Structure of gramicidin A. <i>Biophysical Journal</i> , 1986, 49, 295-306.	0.2	157
26	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
27	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
28	Analyses of circular dichroism spectra of membrane proteins. <i>Protein Science</i> , 2003, 12, 875-884.	3.1	149
29	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
30	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
31	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
32	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
33	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. <i>Journal of Molecular Biology</i> , 1980, 143, 1-19.	2.0	126
34	Slow $\pm$ Helix Formation during Folding of a Membrane Protein. <i>Biochemistry</i> , 1997, 36, 192-196.	1.2	122
35	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
36	The complete structure of an activated open sodium channel. <i>Nature Communications</i> , 2017, 8, 14205.	5.8	118

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37	Voltage-gated sodium channels as targets for pyrethroid insecticides. <i>European Biophysics Journal</i> , 2017, 46, 675-679.	1.2	116
38	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
39	2Struc: the secondary structure server. <i>Bioinformatics</i> , 2010, 26, 2624-2625.	1.8	110
40	Characterization and Membrane Assembly of the TatA Component of the Escherichia coli Twin-Arginine Protein Transport System. <i>Biochemistry</i> , 2002, 41, 13690-13697.	1.2	108
41	Crystal Structure of a vFlip-IKK $\hat{I}^3$ Complex: Insights into Viral Activation of the IKK Signalingosome. <i>Molecular Cell</i> , 2008, 30, 620-631.	4.5	108
42	Tools and methods for circular dichroism spectroscopy of proteins: a tutorial review. <i>Chemical Society Reviews</i> , 2021, 50, 8400-8413.	18.7	107
43	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
44	Protein characterisation by synchrotron radiation circular dichroism spectroscopy. <i>Quarterly Reviews of Biophysics</i> , 2009, 42, 317-370.	2.4	99
45	Structure and Function of Voltage-Dependent Ion Channel Regulatory $\hat{I}^2$ Subunits. <i>Biochemistry</i> , 2002, 41, 2886-2894.	1.2	95
46	Molecular basis of ion permeability in a voltage-gated sodium channel. <i>EMBO Journal</i> , 2016, 35, 820-830.	3.5	95
47	The P23T Cataract Mutation Causes Loss of Solubility of Folded $\hat{I}^3$ D-Crystallin. <i>Journal of Molecular Biology</i> , 2004, 343, 435-444.	2.0	93
48	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
49	Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. <i>Nature Communications</i> , 2014, 5, 4863.	5.8	91
50	The crystal structure of human endothelin. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 311-319.	3.6	90
51	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
52	Calibration and Standardisation of Synchrotron Radiation Circular Dichroism and Conventional Circular Dichroism Spectrophotometers. <i>Spectroscopy</i> , 2003, 17, 653-661.	0.8	86
53	Synchrotron Radiation Circular Dichroism (SRCD) spectroscopy: New beamlines and new applications in biology. <i>Spectroscopy</i> , 2007, 21, 245-255.	0.8	85
54	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

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55	Evaluation of methods for the prediction of membrane protein secondary structures.. Proceedings of the National Academy of Sciences of the United States of America, 1986, 83, 9423-9427.	3.3	78
56	Common structural features in gramicidin and other ion channels. BioEssays, 2000, 22, 227-234.	1.2	76
57	Synchrotron radiation circular-dichroism spectroscopy as a tool for investigating protein structures. Journal of Synchrotron Radiation, 2000, 7, 289-295.	1.0	74
58	Structural insights into the dynamics and function of the C-terminus of the E. coli RNA chaperone Hfq. Nucleic Acids Research, 2011, 39, 4900-4915.	6.5	74
59	Opsin Stability and Folding: Modulation by Phospholipid Bicelles. Journal of Molecular Biology, 2007, 374, 1319-1332.	2.0	73
60	A model for Batten disease protein CLN3: Functional implications from homology and mutations. FEBS Letters, 1996, 399, 75-77.	1.3	71
61	Role of the C-terminal domain in the structure and function of tetrameric sodium channels. Nature Communications, 2013, 4, 2465.	5.8	71
62	The structure and function of antiameobin I, a proline-rich membrane-active polypeptide. Structure, 1998, 6, 783-792.	1.6	68
63	Gramicidin a adopts distinctly different conformations in membranes and in organic solvents. Biopolymers, 1983, 22, 397-402.	1.2	67
64	Surface architecture of endospores of the <i>Bacillus cereus/anthracis/thuringiensis</i> family at the subnanometer scale. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16014-16019.	3.3	67
65	Changes in $\hat{2}$ -Lactoglobulin Conformation at the Oil/Water Interface of Emulsions Studied by Synchrotron Radiation Circular Dichroism Spectroscopy. Biomacromolecules, 2010, 11, 2136-2142.	2.6	66
66	Calcium Fluoride Micro Cells for Synchrotron Radiation Circular Dichroism Spectroscopy. Applied Spectroscopy, 2005, 59, 1109-1113.	1.2	65
67	Knockdown resistance to DDT and pyrethroids: from target site mutations to molecular modelling. Pest Management Science, 2008, 64, 1126-1130.	1.7	65
68	The Metastasis-Associated Extracellular Matrix Protein Osteopontin Forms Transient Structure in Ligand Interaction Sites. Biochemistry, 2011, 50, 6113-6124.	1.2	64
69	Bisphenol A Binds to the Local Anesthetic Receptor Site to Block the Human Cardiac Sodium Channel. PLoS ONE, 2012, 7, e41667.	1.1	63
70	Model for a Helical Bundle Channel Based on the High-Resolution Crystal Structure of Trichotoxin_A50E. Biochemistry, 2002, 41, 12934-12941.	1.2	62
71	Conformation of alamethicin in phospholipid vesicles: Implications for insertion models. Proteins: Structure, Function and Bioinformatics, 1988, 4, 89-98.	1.5	60
72	NaChBac: The Long Lost Sodium Channel Ancestor. Biochemistry, 2011, 50, 6742-6752.	1.2	60

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73	Location of the carboxyl terminus of bacteriorhodopsin in purple membrane. <i>Biophysical Journal</i> , 1982, 39, 233-239.	0.2	58
74	Gramicidin channel controversy--revisited. <i>Nature Structural Biology</i> , 1999, 6, 610-611.	9.7	58
75	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
76	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
77	Temperature dependence of the interaction of alamethicin helices in membranes. <i>Biochemistry</i> , 1993, 32, 9819-9825.	1.2	57
78	Crystal structure of the Gramicidin/Potassium thiocyanate complex. <i>Journal of Molecular Biology</i> , 1997, 266, 963-977.	2.0	54
79	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
80	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
81	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
82	PCDDDB: new developments at the Protein Circular Dichroism Data Bank. <i>Nucleic Acids Research</i> , 2017, 45, D303-D307.	6.5	52
83	Conformational changes by synchrotron radiation circular dichroism spectroscopy. , 2000, 7, 708-709.		51
84	The E1 to 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
85	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
86	Modeling and Docking the Endothelin G-Protein-Coupled Receptor. <i>Biophysical Journal</i> , 2000, 79, 3083-3094.	0.2	48
87	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
88	Structural model of the open to closed inactivated cycle of prokaryotic voltage-gated sodium channels. <i>Journal of General Physiology</i> , 2015, 145, 5-16.	0.9	47
89	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
90	The peptaibol database: a sequence and structure resource. <i>Journal of Peptide Science</i> , 2003, 9, 663-665.	0.8	45

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91	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
92	Effects of Deglycosylation of Sodium Channels on Their Structure and Function. <i>Biochemistry</i> , 2005, 44, 441-449.	1.2	44
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	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
95	Ion-Bond Forms of the Gramicidin a Transmembrane Channel. <i>Biophysical Journal</i> , 1984, 45, 114-116.	0.2	42
96	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
97	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
98	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
99	Binding of fibronectin to phospholipid vesicles.. <i>Journal of Biological Chemistry</i> , 1983, 258, 3327-3331.	1.6	41
100	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
101	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
102	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
103	Cannabidiol interactions with voltage-gated sodium channels. <i>ELife</i> , 2020, 9, .	2.8	40
104	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
105	Molecular Dynamics Simulation of the Antiamoebic Ion Channel: Linking Structure and Conductance. <i>Biophysical Journal</i> , 2011, 100, 2394-2402.	0.2	39
106	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
107	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
108	Alamethicin Pyromellitate: An Ion-Activated Channel-Forming Peptide. <i>Biochemistry</i> , 1994, 33, 6850-6858.	1.2	37

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109	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
110	The influence of lipid state on the planar distribution of membrane proteins in <i>Acholeplasma laidlawii</i> . <i>Journal of Molecular Biology</i> , 1976, 107, 255-269.	2.0	36
111	Solvent effects on the conformation and far UV CD spectra of gramicidin. , 1997, 42, 771-781.		36
112	Phospholipid chain length alters the equilibrium between pore and channel forms of gramicidin. <i>Faraday Discussions</i> , 1999, 111, 159-164.	1.6	36
113	Transmembrane Peptide NB of Influenza B: A Simulation, Structure, and Conductance Study. <i>Biochemistry</i> , 2000, 39, 12708-12716.	1.2	36
114	Tryptophans in Membrane Proteins. <i>Advances in Experimental Medicine and Biology</i> , 1999, 467, 789-799.	0.8	36
115	Circular-dichroism analyses of membrane proteins: examination of environmental effects on bacteriorhodopsin spectra. <i>Biochemical Journal</i> , 1993, 289, 215-219.	1.7	35
116	Solution Structure of a Parallel Left-handed Double-helical Gramicidin-A Determined by 2D <sup>1</sup> H NMR. <i>Journal of Molecular Biology</i> , 1996, 264, 757-769.	2.0	35
117	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
118	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
119	Binding of fibronectin to phospholipid vesicles. <i>Journal of Biological Chemistry</i> , 1983, 258, 3327-31.	1.6	35
120	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
121	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
122	The planar distributions of surface proteins and intramembrane particles in <i>Acholeplasma laidlawii</i> are differentially affected by the physical state of membrane lipids. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1978, 508, 431-449.	1.4	33
123	A comparison of X-ray and NMR structures for human endothelin. <i>Protein Science</i> , 1995, 4, 75-83.	3.1	33
124	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
125	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
126	Antiamoebin can function as a carrier or as a pore-forming peptaibol. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1998, 1415, 255-260.	1.4	32



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127	Effects of Local Environment on the Circular Dichroism Spectra of Polypeptides. <i>Analytical Biochemistry</i> , 1995, 227, 90-100.	1.1	31
128	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
129	Co-crystals of gramicidin A and phospholipid. <i>Journal of Molecular Biology</i> , 1991, 217, 625-627.	2.0	30
130	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
131	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
132	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
133	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
134	Crystallographic studies of a transmembrane ion channel, gramicidin A. <i>Progress in Biophysics and Molecular Biology</i> , 1992, 57, 59-69.	1.4	26
135	Novel methods for secondary structure determination using low wavelength (VUV) circular dichroism spectroscopic data. <i>BMC Bioinformatics</i> , 2006, 7, 507.	1.2	26
136	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
137	Conductance Studies on Trichotoxin_A50E and Implications for Channel Structure. <i>Biophysical Journal</i> , 2004, 87, 1705-1710.	0.2	25
138	Conformation of an oligopeptide in phospholipid vesicles.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1979, 76, 1775-1779.	3.3	24
139	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
140	Synchrotron radiation circular dichroism and conventional circular dichroism spectroscopy: A comparison. <i>Spectroscopy</i> , 2002, 16, 121-125.	0.8	24
141	Solution NMR Studies of Antiamoebin, a Membrane Channel-Forming Polypeptide. <i>Biophysical Journal</i> , 2003, 84, 185-194.	0.2	24
142	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
143	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
144	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

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145	Cystine nooses and protein specificity. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 266-268.	3.6	22
146	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
147	Tetrameric Bacterial Sodium Channels: Characterization of Structure, Stability, and Drug Binding. <i>Biochemistry</i> , 2008, 47, 8114-8121.	1.2	22
148	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
149	Comparison of lipid/gramicidin dispersions and cocrystals by Raman scattering. <i>Biochemistry</i> , 1987, 26, 557-562.	1.2	21
150	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
151	Circular dichroism and synchrotron radiation circular dichroism spectroscopy: tools for drug discovery. <i>Biochemical Society Transactions</i> , 2003, 31, 631-633.	1.6	21
152	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
153	Deconstructing the DGAT1 enzyme: Binding sites and substrate interactions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 3145-3152.	1.4	21
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