

# Bonnie Ann Wallace

## List of Publications by Year in descending order

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267  
papers

19,653  
citations

17440

63  
h-index

12597

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. Protein Science, 2022, 31, 37-46.	7.6	208
2	The PCDDDB (Protein Circular Dichroism Data Bank): A Bioinformatics Resource for Protein Characterisations and Methods Development. Journal of Molecular Biology, 2022, 434, 167441.	4.2	14
3	The T1â€tetramerization Domain of Kv1.2 Rescues Expression and Preserves Function of a Truncated NaChBac Sodium Channel. FEBS Letters, 2022, , .	2.8	0
4	Tools and methods for circular dichroism spectroscopy of proteins: a tutorial review. Chemical Society Reviews, 2021, 50, 8400-8413.	38.1	107
5	A tamoxifen receptor within a voltage-gated sodium channel. Molecular Cell, 2021, 81, 1160-1169.e5.	9.7	19
6	Reference Protocol to Assess Analytical Performance of Higher Order Structural Analysis Measurements: Results from an Interlaboratory Comparison. Analytical Chemistry, 2021, 93, 9041-9048.	6.5	4
7	Interactions of amphipathic Î±-helical MEG proteins from Schistosoma mansoni with membranes. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183173.	2.6	8
8	Biopharmaceutical applications of protein characterisation by circular dichroism spectroscopy. , 2020, , 123-152.		3
9	Cannabidiol interactions with voltage-gated sodium channels. ELife, 2020, 9, .	6.0	40
10	Unveiling the binding and orientation of the antimicrobial peptide Plantaricin 149 in zwitterionic and negatively charged membranes. European Biophysics Journal, 2019, 48, 621-633.	2.2	9
11	The role of circular dichroism spectroscopy in the era of integrative structural biology. Current Opinion in Structural Biology, 2019, 58, 191-196.	5.7	33
12	Valproic acid interactions with the NavMs voltage-gated sodium channel. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26549-26554.	7.1	20
13	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
14	The intrinsically disordered Tarp protein from chlamydia binds actin with a partially preformed helix. Scientific Reports, 2018, 8, 1960.	3.3	18
15	Thermal Melt Circular Dichroism Spectroscopy of Membrane Proteins as a Tool for Cryo-EM Preparations. Biophysical Journal, 2018, 114, 634a.	0.5	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. Protein Science, 2018, 27, 10-13.	7.6	10
17	Thermal melt circular dichroism spectroscopic studies for identifying stabilising amphipathic molecules for the voltageâ€gated sodium channel NavMs. Biopolymers, 2018, 109, e23067.	2.4	12
18	Comparisons of voltage-gated sodium channel structures with open and closed gates and implications for state-dependent drug design. Biochemical Society Transactions, 2018, 46, 1567-1575.	3.4	9

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19	Role of the Interaction Motif in Maintaining the Open Gate of an Open Sodium Channel. Biophysical Journal, 2018, 115, 1920-1930.	0.5	13
20	Fenestration Mutants of a Voltage-Gated Sodium Channel that Modify Channel Blocker Ingress. Biophysical Journal, 2018, 114, 38a.	0.5	0
21	CDtoolX, a downloadable software package for processing and analyses of circular dichroism spectroscopic data. Protein Science, 2018, 27, 1717-1722.	7.6	89
22	Characterization of esterase activity from an Acetomicrobium hydrogeniformans enzyme with high structural stability in extreme conditions. Extremophiles, 2018, 22, 781-793.	2.3	10
23	Lipid binding attenuates channel closure of the outer membrane protein OmpF. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6691-6696.	7.1	39
24	Differential dehydration effects on globular proteins and intrinsically disordered proteins during film formation. Protein Science, 2017, 26, 718-726.	7.6	21
25	Structure and function of PspA and Vipp1 N-terminal peptides: Insights into the membrane stress sensing and mitigation. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 28-39.	2.6	35
26	Voltage-gated sodium channels as targets for pyrethroid insecticides. European Biophysics Journal, 2017, 46, 675-679.	2.2	116
27	The complete structure of an activated open sodium channel. Nature Communications, 2017, 8, 14205.	12.8	118
28	The Complete Crystal Structure of an Open Activated Sodium Channel. Biophysical Journal, 2017, 112, 18a-19a.	0.5	0
29	Interpreting the functional role of a novel interaction motif in prokaryotic sodium channels. Journal of General Physiology, 2017, 149, 613-622.	1.9	17
30	Oriented Circular Dichroism Spectroscopy as a Tool for Studying the Gating of Sodium Channels. Biophysical Journal, 2017, 112, 241a.	0.5	0
31	How C-Terminal Domain Stabilize the Gate of Voltage-Gated Sodium Channels. Biophysical Journal, 2017, 112, 106a.	0.5	0
32	Attenuation of Phosphorylation-dependent Activation of Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) by Disease-causing Mutations at the Transmission Interface. Journal of Biological Chemistry, 2017, 292, 1988-1999.	3.4	7
33	PCDDb: new developments at the Protein Circular Dichroism Data Bank. Nucleic Acids Research, 2017, 45, D303-D307.	14.5	52
34	Mutagenesis of the NaChBac sodium channel discloses a functional role for a conserved S6 asparagine. European Biophysics Journal, 2017, 46, 665-674.	2.2	12
35	Interaction of an esophageal MEG protein from schistosomes with a human S100 protein involved in inflammatory response. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 3490-3497.	2.4	13
36	Environmental Factors Modulating the Stability and Enzymatic Activity of the Petrotoga mobilis Esterase (PmEst). PLoS ONE, 2016, 11, e0158146.	2.5	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.	4.1	1
38	Molecular basis of ion permeability in a voltage-gated sodium channel. <i>EMBO Journal</i> , 2016, 35, 820-830.	7.8	95
39	Isolated pores dissected from human two-pore channel 2 are functional. <i>Scientific Reports</i> , 2016, 6, 38426.	3.3	9
40	Sodium Channel/Ligand Complex Structures as a Guide for Rational Drug Design. <i>Biophysical Journal</i> , 2016, 110, 33a.	0.5	0
41	Protein Design for Decreased Disorder: SHERP as an Exemplar Protein. <i>Biophysical Journal</i> , 2016, 110, 555a.	0.5	0
42	Structure of the C-terminal domain of the prokaryotic sodium channel orthologue NsvBa. <i>European Biophysics Journal</i> , 2016, 45, 807-814.	2.2	2
43	Circular dichroism spectroscopy of membrane proteins. <i>Chemical Society Reviews</i> , 2016, 45, 4859-4872.	38.1	234
44	Spectral Properties of $\alpha$ -Disordered and Polyproline II Structures Defined by Circular Dichroism Spectroscopy. <i>Biophysical Journal</i> , 2016, 110, 559a-560a.	0.5	0
45	Sodium Ion Coordination in the Selectivity Filter of a Voltage-Gated Sodium Channel. <i>Biophysical Journal</i> , 2015, 108, 490a.	0.5	0
46	Deconstructing the DGAT1 Enzyme: Membrane Interactions at Substrate Binding Sites. <i>PLoS ONE</i> , 2015, 10, e0118407.	2.5	8
47	Screening ion-channel ligand interactions with passive pumping in a microfluidic bilayer lipid membrane chip. <i>Biomicrofluidics</i> , 2015, 9, 014103.	2.4	4
48	Voltage-Gated Sodium Channels: Structure and Function of Complexes with Sodium Channel Blockers. <i>Biophysical Journal</i> , 2015, 108, 10a.	0.5	0
49	An evolutionarily unique heterodimeric voltage-gated cation channel found in aphids. <i>FEBS Letters</i> , 2015, 589, 598-607.	2.8	21
50	X-ray, spectroscopic and normal-mode dynamics of calexitin: 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.	0.8	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.	1.9	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.	2.5	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.	0.5	34
56	Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. <i>Nature Communications</i> , 2014, 5, 4863.	12.8	91
57	Deconstructing the DGAT1 enzyme: Binding sites and substrate interactions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 3145-3152.	2.6	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.	7.1	120
59	Lipid interactions of LAH4, a peptide with antimicrobial and nucleic acid transfection activities. <i>European Biophysics Journal</i> , 2014, 43, 499-507.	2.2	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.	7.6	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.	2.4	10
62	Predictive <scp>3D</scp> 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.	3.4	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.	0.5	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.	7.1	149
65	Stabilisation of Na,K-ATPase structure by the cardiotonic steroid ouabain. <i>Biochemical and Biophysical Research Communications</i> , 2013, 435, 300-305.	2.1	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.	2.6	37
67	Peptaibols. , 2013, , 150-156.		6
68	ValidDichro: a website for validating and quality control of protein circular dichroism spectra. <i>Nucleic Acids Research</i> , 2013, 41, W417-W421.	14.5	13
69	Role of the C-terminal domain in the structure and function of tetrameric sodium channels. <i>Nature Communications</i> , 2013, 4, 2465.	12.8	71
70	Differential Lipid Dependence of the Function of Bacterial Sodium Channels. <i>PLoS ONE</i> , 2013, 8, e61216.	2.5	18
71	Membrane Interactions of S100A12 (Calgranulin C). <i>PLoS ONE</i> , 2013, 8, e82555.	2.5	10
72	DichroMatch: a website for similarity searching of circular dichroism spectra. <i>Nucleic Acids Research</i> , 2012, 40, W547-W552.	14.5	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.	12.8	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.	2.5	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.	2.6	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.	2.5	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.	2.6	3
78	JCAMP-DX for circular dichroism spectra and metadata (IUPAC Recommendations 2012). <i>Pure and Applied Chemistry</i> , 2012, 84, 2171-2182.	1.9	4
79	The Metastasis-Associated Extracellular Matrix Protein Osteopontin Forms Transient Structure in Ligand Interaction Sites. <i>Biochemistry</i> , 2011, 50, 6113-6124.	2.5	64
80	NaChBac: The Long Lost Sodium Channel Ancestor. <i>Biochemistry</i> , 2011, 50, 6742-6752.	2.5	60
81	Molecular Dynamics Simulation of the Antiamoebin Ion Channel: Linking Structure and Conductance. <i>Biophysical Journal</i> , 2011, 100, 2394-2402.	0.5	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.	4.1	135
84	Validichro, a Software Tool for Validation of Circular Dichroism (CD) Spectroscopic Data. <i>Biophysical Journal</i> , 2011, 100, 320a.	0.5	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.	2.6	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.	2.8	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.	1.6	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.	7.1	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.	14.5	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.	14.5	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.	3.4	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.	3.4	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.	3.4	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.	3.3	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.	7.1	41
96	2Struc: the secondary structure server. <i>Bioinformatics</i> , 2010, 26, 2624-2625.	4.1	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.	0.5	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.	4.2	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.	5.4	66
100	SRCD2009. <i>Synchrotron Radiation News</i> , 2009, 22, 2-4.	0.8	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.	2.2	12
102	Thermal and chemical unfolding and refolding of a eukaryotic sodium channel. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009, 1788, 1279-1286.	2.6	24
103	Protein characterisation by synchrotron radiation circular dichroism spectroscopy. <i>Quarterly Reviews of Biophysics</i> , 2009, 42, 317-370.	5.7	99
104	Oriented Synchrotron Radiation Circular Dichroism and Linear Dichroism Spectroscopy of Peptides in Model Membranes. <i>Biophysical Journal</i> , 2009, 96, 337a.	0.5	1
105	Evaluating protein:protein complex formation using synchrotron radiation circular dichroism spectroscopy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1142-1146.	2.6	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.	2.4	91
107	Knockdown resistance to DDT and pyrethroids: from target site mutations to molecular modelling. <i>Pest Management Science</i> , 2008, 64, 1126-1130.	3.4	65
108	Protein secondary structure analyses from circular dichroism spectroscopy: Methods and reference databases. <i>Biopolymers</i> , 2008, 89, 392-400.	2.4	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.	9.7	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.	2.6	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.	2.5	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.	2.6	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.	3.4	40
115	Association of partially folded lens $\beta$ 2B2-crystallins with the $\beta$ 1-crystallin molecular chaperone. <i>Biochemical Journal</i> , 2008, 409, 691-699.	3.7	22
116	A reference dataset for circular dichroism spectroscopy tailored for the $\beta$ 2B3-crystallin lens proteins. <i>Experimental Eye Research</i> , 2007, 84, 1001-1008.	2.6	16
117	Opsin Stability and Folding: Modulation by Phospholipid Bicelles. <i>Journal of Molecular Biology</i> , 2007, 374, 1319-1332.	4.2	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.	4.1	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.	38.1	218
122	Novel methods for secondary structure determination using low wavelength (VUV) circular dichroism spectroscopic data. <i>BMC Bioinformatics</i> , 2006, 7, 507.	2.6	26
123	Protein circular dichroism data bank (PCDDb): Data bank and website design. <i>Chirality</i> , 2006, 18, 426-429.	2.6	10
124	Modelling insecticide-binding sites in the voltage-gated sodium channel. <i>Biochemical Journal</i> , 2006, 396, 255-263.	3.7	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.	2.4	41
126	The Protein Circular Dichroism Data Bank (PCDDb): A bioinformatics and spectroscopic resource. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 1-3.	2.6	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.	0.8	1
129	Effects of Deglycosylation of Sodium Channels on Their Structure and Function. <i>Biochemistry</i> , 2005, 44, 441-449.	2.5	44
130	Calcium Fluoride Micro Cells for Synchrotron Radiation Circular Dichroism Spectroscopy. <i>Applied Spectroscopy</i> , 2005, 59, 1109-1113.	2.2	65
131	Spectral magnitude effects on the analyses of secondary structure from circular dichroism spectroscopic data. <i>Protein Science</i> , 2005, 14, 368-374.	7.6	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.	2.4	43
133	Analysis of peptaibol sequence composition: implications for in vivo synthesis and channel formation. <i>European Biophysics Journal</i> , 2004, 33, 233-7.	2.2	39
134	CDtool—an integrated software package for circular dichroism spectroscopic data processing, analysis, and archiving. <i>Analytical Biochemistry</i> , 2004, 332, 285-289.	2.4	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.	3.2	33
136	The Peptaibol Database: a database for sequences and structures of naturally occurring peptaibols. <i>Nucleic Acids Research</i> , 2004, 32, 593D-594.	14.5	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.	14.5	2,106
138	Conductance Studies on Trichotoxin_A50E and Implications for Channel Structure. <i>Biophysical Journal</i> , 2004, 87, 1705-1710.	0.5	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.	4.2	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.	1.4	17
141	The peptaibol database: a sequence and structure resource. <i>Journal of Peptide Science</i> , 2003, 9, 663-665.	1.4	45
142	Analyses of circular dichroism spectra of membrane proteins. <i>Protein Science</i> , 2003, 12, 875-884.	7.6	149
143	Solution NMR Studies of Antiamoebin, a Membrane Channel-Forming Polypeptide. <i>Biophysical Journal</i> , 2003, 84, 185-194.	0.5	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.	3.4	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.	3.4	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.	0.9	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.	3.4	44
149	DICHROWEB: an interactive website for the analysis of protein secondary structure from circular dichroism spectra. <i>Bioinformatics</i> , 2002, 18, 211-212.	4.1	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.	2.5	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.	2.5	108
152	Structure and Function of Voltage-Dependent Ion Channel Regulatory $\hat{I}^2$ Subunits. <i>Biochemistry</i> , 2002, 41, 2886-2894.	2.5	95
153	Synchrotron radiation circular dichroism and conventional circular dichroism spectroscopy: A comparison. <i>Spectroscopy</i> , 2002, 16, 121-125.	0.8	24
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