Charles M Deber

List of Publications by Year
in descending order

160 papers	7,994 citations	47 h-index 47006	82 g-index 58581
165 all docs	165 docs citations	165 times ranked	7974 citing authors

#	Article	IF	Citations
1	Enhanced proteolytic resistance of cationic antimicrobial peptides through lysine side chain analogs and cyclization. Biochemical and Biophysical Research Communications, 2022, 612, 105-109.	2.1	3
2	Mechanistic Insight into Peptide-Based Efflux Pump Inhibitors Against Pathogenic Bacteria. Biophysical Journal, 2021, 120, 74a.	0.5	0
3	Peptide-Based Inhibition of AcrB Efflux Activity. Biophysical Journal, 2021, 120, 70a.	0.5	0
4	Heat treatment of thioredoxin fusions increases the purity of Î±â€helical transmembrane protein constructs. Protein Science, 2021, 30, 1974-1982.	7.6	4
5	Uncoupling Amphipathicity and Hydrophobicity: Role of Charge Clustering in Membrane Interactions of Cationic Antimicrobial Peptides. Biochemistry, 2021, 60, 2586-2592.	2.5	11
6	CFTR transmembrane segments are impaired in their conformational adaptability by a pathogenic loop mutation and dynamically stabilized by Lumacaftor. Journal of Biological Chemistry, 2020, 295, 1985-1991.	3.4	17
7	Peptide-Based Approach to Inhibition of the Multidrug Resistance Efflux Pump AcrB. Biochemistry, 2020, 59, 3973-3981.	2.5	9
8	Anti-Infectives Restore ORKAMBIÂ® Rescue of F508del-CFTR Function in Human Bronchial Epithelial Cells Infected with Clinical Strains of P. aeruginosa. Biomolecules, 2020, 10, 334.	4.0	32
9	Protection or Destruction: The LL-37/HNP1 Cooperativity Switch. Biophysical Journal, 2020, 119, 2370-2371.	0.5	1
10	Relative role(s) of leucine versus isoleucine in the folding of membrane proteins. Peptide Science, 2019, 111, e24075.	1.8	10
11	Peptide-Based Efflux Pump Inhibitors of the Small Multidrug Resistance Protein from Pseudomonas aeruginosa. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	19
12	Positive Charge Patterning and Hydrophobicity of Membrane-Active Antimicrobial Peptides as Determinants of Activity, Toxicity, and Pharmacokinetic Stability. Journal of Medicinal Chemistry, 2019, 62, 6276-6286.	6.4	43
13	Method to generate highly stable D-amino acid analogs of bioactive helical peptides using a mirror image of the entire PDB. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1505-1510.	7.1	89
14	Structural effects of extracellular loop mutations in CFTR helical hairpins. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 1092-1098.	2.6	5
15	Influence of hydrocarbon-stapling on membrane interactions of synthetic antimicrobial peptides. Bioorganic and Medicinal Chemistry, 2018, 26, 1189-1196.	3.0	32
16	A minimal helical-hairpin motif provides molecular-level insights into misfolding and pharmacological rescue of CFTR. Communications Biology, 2018, 1, 154.	4.4	25
17	Activity of a novel antimicrobial peptide against Pseudomonas aeruginosa biofilms. Scientific Reports, 2018, 8, 14728.	3.3	42
18	Structure of theEmrEmultidrug transporter and its use for inhibitor peptide design. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7932-E7941.	7.1	34

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19	Therapeutic design of peptide modulators of protein-protein interactions in membranes. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 577-585.	2.6	57
20	Structural impact of proline mutations in the loop region of an ancestral membrane protein. Biopolymers, 2016, 106, 37-42.	2.4	4
21	Hydrophobic Clusters Raise the Threshold Hydrophilicity for Insertion of Transmembrane Sequences in Vivo. Biochemistry, 2016, 55, 5772-5779.	2.5	4
22	Modulating Transmembrane Î±-Helix Interactions through pH-Sensitive Boundary Residues. Biochemistry, 2016, 55, 4306-4315.	2.5	4
23	Design and Characterization of a Membrane Protein Unfolding Platform in Lipid Bilayers. PLoS ONE, 2015, 10, e0120253.	2.5	3
24	Efflux by Small Multidrug Resistance Proteins Is Inhibited by Membrane-interactive Helix-stapled Peptides. Journal of Biological Chemistry, 2015, 290, 1752-1759.	3.4	26
25	Hydrophobic Blocks Facilitate Lipid Compatibility and Translocon Recognition of Transmembrane Protein Sequences. Biochemistry, 2015, 54, 1465-1473.	2.5	5
26	Helix-Helix Interactions: Is the Medium the Message?. Structure, 2015, 23, 437-438.	3.3	7
27	Functional response of the small multidrug resistance protein EmrE to mutations in transmembrane helix 2. FEBS Letters, 2014, 588, 3720-3725.	2.8	7
28	Terminal Residue Hydrophobicity Modulates Transmembrane Helixâ€“Helix Interactions. Biochemistry, 2014, 53, 3747-3757.	2.5	4
29	Design of Transmembrane Peptides: Coping with Sticky Situations. Methods in Molecular Biology, 2013, 1063, 197-210.	0.9	3
30	Correction factors for membrane protein molecular weight readouts on sodium dodecyl sulfateâ€“polyacrylamide gel electrophoresis. Analytical Biochemistry, 2013, 434, 67-72.	2.4	34
31	Loop Sequence Dictates the Secondary Structure of a Human Membrane Protein Hairpin. Biochemistry, 2013, 52, 2419-2426.	2.5	13
32	Effects of a polar amino acid substitution on helix formation and aggregate size along the detergent-induced peptide folding pathway. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 373-381.	2.6	9
33	Inside-out Signaling Promotes Dynamic Changes in the Carcinoembryonic Antigen-related Cellular Adhesion Molecule 1 (CEACAM1) Oligomeric State to Control Its Cell Adhesion Properties. Journal of Biological Chemistry, 2013, 288, 29654-29669.	3.4	29
34	Acrylamide concentration determines the direction and magnitude of helical membrane protein gel shifts. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15668-15673.	7.1	50
35	Congenital Heart Block Maternal Sera Autoantibodies Target an Extracellular Epitope on the Î±1G T-Type Calcium Channel in Human Fetal Hearts. PLoS ONE, 2013, 8, e72668.	2.5	28
36	Differential Binding of L- vs. D-isomers of Cationic Antimicrobial Peptides to the Biofilm Exopolysaccharide Alginate. Protein and Peptide Letters, 2013, 20, 843-847.	0.9	10

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37	Drug Efflux by a Small Multidrug Resistance Protein Is Inhibited by a Transmembrane Peptide. Antimicrobial Agents and Chemotherapy, 2012, 56, 3911-3916.	3.2	19
38	Design, expression, and purification of de novo transmembrane â€œhairpinâ€•peptides. Biopolymers, 2012, 98, 546-556.	2.4	2
39	Sequence Hydropathy Dominates Membrane Protein Response to Detergent Solubilization. Biochemistry, 2012, 51, 6228-6237.	2.5	9
40	Protein Structure in Membrane Domains. Annual Review of Biophysics, 2012, 41, 135-155.	10.0	26
41	Membrane protein misassembly in disease. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1115-1122.	2.6	75
42	Structural basis for misfolding at a disease phenotypic position in CFTR: Comparison of TM3/4 helix-loop-helix constructs with TM4 peptides. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 49-54.	2.6	5
43	Efficiency of detergents at maintaining membrane protein structures in their biologically relevant forms. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1351-1358.	2.6	51
44	Roles of Hydrophobicity and Charge Distribution of Cationic Antimicrobial Peptides in Peptide-Membrane Interactions. Journal of Biological Chemistry, 2012, 287, 7738-7745.	3.4	317
45	Positions of Polar Amino Acids Alter Interactions between Transmembrane Segments and Detergents. Biochemistry, 2011, 50, 3928-3935.	2.5	19
46	Converting a Marginally Hydrophobic Soluble Protein into a Membrane Protein. Journal of Molecular Biology, 2011, 407, 171-179.	4.2	5
47	3 Membrane protein folding in detergents. , 2011, , 23-46.		1
48	Beta-branched residues adjacent to GG4 motifs promote the efficient association of glycophorin a transmembrane helices. Biopolymers, 2011, 96, 340-347.	2.4	10
49	Modulation of Substrate Efflux in Bacterial Small Multidrug Resistance Proteins by Mutations at the Dimer Interface. Journal of Bacteriology, 2011, 193, 5929-5935.	2.2	10
50	Novel Hydrophobic Standards for Membrane Protein Molecular Weight Determinations via Sodium Dodecyl Sulfateâ^'Polyacrylamide Gel Electrophoresis. Biochemistry, 2010, 49, 10589-10591.	2.5	11
51	Modulation of the Oligomerization of Myelin Proteolipid Protein by Transmembrane Helix Interaction Motifs. Biochemistry, 2010, 49, 6896-6902.	2.5	18
52	Evidence that the translocon may function as a hydropathy partitioning filter. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 1995-1998.	2.6	5
53	Deletion of a terminal residue disrupts oligomerization of a transmembrane l±-helixThis paper is one of a selection of papers published in this special issue entitled â€œCanadian Society of Biochemistry, Molecular & Cellular Biology 52nd Annual Meeting â€" Protein Folding: Principles and Diseasesâ€• and has undergone the Journal's usual peer review process.. Biochemistry and Cell Biology, 2010, 88, 339-345.	2.0	11
54	Distinctions between Hydrophobic Helices in Globular Proteins and Transmembrane Segments as Factors in Protein Sorting. Journal of Biological Chemistry, 2009, 284, 5395-5402.	3.4	13

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55	The Assembly Motif of a Bacterial Small Multidrug Resistance Protein. Journal of Biological Chemistry, 2009, 284, 9870-9875.	3.4	26
56	A novel method for monitoring the cytosolic delivery of peptide cargo. Journal of Controlled Release, 2009, 137, 2-7.	9.9	30
57	Functional Rescue of DeltaF508-CFTR by Peptides Designed to Mimic Sorting Motifs. Chemistry and Biology, 2009, 16, 520-530.	6.0	19
58	Peptide Models of Membrane Protein Folding. Biochemistry, 2009, 48, 3036-3045.	2.5	42
59	Detergent binding explains anomalous SDS-PAGE migration of membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1760-1765.	7.1	659
60	SDS Micelles as a Membrane-Mimetic Environment for Transmembrane Segments. Biochemistry, 2009, 48, 12096-12103.	2.5	101
61	Surface recognition elements of membrane protein oligomerization. Proteins: Structure, Function and Bioinformatics, 2008, 70, 786-793.	2.6	15
62	Membrane interactions of designed cationic antimicrobial peptides: The two thresholds. Biopolymers, 2008, 89, 360-371.	2.4	78
63	Defining the Defect in F508 del CFTR: A Soluble Problem?. Chemistry and Biology, 2008, 15, 3-4.	6.0	0
64	Misfolding of the Cystic Fibrosis Transmembrane Conductance Regulator and Disease. Biochemistry, 2008, 47, 1465-1473.	2.5	62
65	Positional dependence of non-native polar mutations on folding of CFTR helical hairpins. Biochimica Et Biophysica Acta - Biomembranes, 2008, 1778, 79-87.	2.6	9
66	Optimizing synthesis and expression of transmembrane peptides and proteins. Methods, 2007, 41, 370-380.	3.8	46
67	Membrane interactions of the hydrophobic segment of diacylglycerol kinase epsilon. Biochimica Et Biophysica Acta - Biomembranes, 2007, 1768, 2549-2558.	2.6	14
68	Membrane protein assembly patterns reflect selection for non-proliferative structures. FEBS Letters, 2007, 581, 1335-1341.	2.8	13
69	Transmembrane Domain of Myelin Protein Zero Can Form Dimers:â€‰ Possible Implications for Myelin Construction. Biochemistry, 2007, 46, 12164-12173.	2.5	36
70	Role of the Extracellular Loop in the Folding of a CFTR Transmembrane Helical Hairpin. Biochemistry, 2007, 46, 7099-7106.	2.5	20
71	Aromatic and Cationâ^Ï€ Interactions Enhance Helixâ^'Helix Association in a Membrane Environment. Biochemistry, 2007, 46, 9208-9214.	2.5	92
72	Peptides as transmembrane segments: Decrypting the determinants for helixâ€“helix interactions in membrane proteins. Biopolymers, 2007, 88, 217-232.	2.4	28

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73	Hydrophobic Interactions in Complexes of Antimicrobial Peptides with Bacterial Polysaccharides. Chemical Biology and Drug Design, 2007, 69, 405-412.	3.2	32
74	The position of the Gly-xxx-Gly motif in transmembrane segments modulates dimer affinityThis paper is one of a selection of papers published in this Special Issue, entitled CSBMCB â€" Membrane Proteins in Health and Disease.. Biochemistry and Cell Biology, 2006, 84, 1006-1012.	2.0	23
75	Activity of novel non-amphipathic cationic antimicrobial peptides against Candida species. Journal of Antimicrobial Chemotherapy, 2006, 57, 899-907.	3.0	43
76	Lipid Solvation Effects Contribute to the Affinity of Gly-xxx-Gly Motif-Mediated Helixâ^'Helix Interactionsâ€. Biochemistry, 2006, 45, 8507-8515.	2.5	28
77	Self-association of the Transmembrane Domain of an Anthrax Toxin Receptor. Journal of Molecular Biology, 2006, 360, 145-156.	4.2	23
78	Evidence for Assembly of Small Multidrug Resistance Proteins by a â€œTwo-facedâ€•Transmembrane Helix. Journal of Biological Chemistry, 2006, 281, 15546-15553.	3.4	31
79	The structure of â€œunstructuredâ€•regions in peptides and proteins: Role of the polyproline II helix in protein folding and recognition*. Biopolymers, 2005, 80, 179-185.	2.4	181
80	Basis for Selectivity of Cationic Antimicrobial Peptides for Bacterial Versus Mammalian Membranes. Journal of Biological Chemistry, 2005, 280, 33960-33967.	3.4	244
81	Destabilization of the Transmembrane Domain Induces Misfolding in a Phenotypic Mutant of Cystic Fibrosis Transmembrane Conductance Regulator. Journal of Biological Chemistry, 2005, 280, 4968-4974.	3.4	22
82	Helix Induction in Antimicrobial Peptides by Alginate in Biofilms. Journal of Biological Chemistry, 2004, 279, 38749-38754.	3.4	88
83	The Affinity of GXXXG Motifs in Transmembrane Helix-Helix Interactions Is Modulated by Long-range Communication. Journal of Biological Chemistry, 2004, 279, 16591-16597.	3.4	103
84	Missense mutations in transmembrane domains of proteins: Phenotypic propensity of polar residues for human disease. Proteins: Structure, Function and Bioinformatics, 2004, 54, 648-656.	2.6	94
85	Aqueous solubility and membrane interactions of hydrophobic peptides with peptoid tags. Biopolymers, 2004, 76, 110-118.	2.4	17
86	Hydrophobic Helical Hairpins:â€‰ Design and Packing Interactions in Membrane Environments. Biochemistry, 2004, 43, 14361-14369.	2.5	36
87	Non-Native Interhelical Hydrogen Bonds in the Cystic Fibrosis Transmembrane Conductance Regulator Domain Modulated by Polar Mutations. Biochemistry, 2004, 43, 8077-8083.	2.5	30
88	Transmembrane segment peptides with double D-amino acid replacements: Helicity, hydrophobicity, and antimicrobial activity. Biopolymers, 2003, 71, 77-84.	2.4	8
89	Polar residue tagging of transmembrane peptides. Biopolymers, 2003, 71, 675-685.	2.4	86
90	Disease-associated mutations in conserved residues of ALK-1 kinase domain. European Journal of Human Genetics, 2003, 11, 279-287.	2.8	73

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91	Sequence Context Strongly Modulates Association of Polar Residues in Transmembrane Helices. Journal of Molecular Biology, 2003, 331, 255-262.	4.2	72
92	A Transmembrane Segment Mimic Derived from Escherichia coli Diacylglycerol Kinase Inhibits Protein Activity. Journal of Biological Chemistry, 2003, 278, 22056-22060.	3.4	38
93	Modulation of Na,K-ATPase by the Î³ Subunit. Journal of Biological Chemistry, 2003, 278, 40437-40441.	3.4	38
94	Blockade of G Protein-Coupled Receptors and the Dopamine Transporter by a Transmembrane Domain Peptide: Novel Strategy for Functional Inhibition of Membrane Proteins in Vivo. Journal of Pharmacology and Experimental Therapeutics, 2003, 307, 481-489.	2.5	29
95	Interhelical Packing in Detergent Micelles. Journal of Biological Chemistry, 2002, 277, 6067-6072.	3.4	29
96	The hydrophobicity threshold for peptide insertion into membranes. Current Topics in Membranes, 2002, 52, 465-479.	0.9	9
97	Cationic Hydrophobic Peptides with Antimicrobial Activity. Antimicrobial Agents and Chemotherapy, 2002, 46, 3585-3590.	3.2	194
98	Polar Residues in Membrane Domains of Proteins:Â Molecular Basis for Helixâ^'Helix Association in a Mutant CFTR Transmembrane Segmentâ€. Biochemistry, 2002, 41, 3647-3653.	2.5	53
99	Transmembrane domain mediated self-assembly of major coat protein subunits from Ff bacteriophage11Edited by G. von Heijne. Journal of Molecular Biology, 2002, 315, 63-72.	4.2	64
100	Expression and Purification of Two Hydrophobic Double-Spanning Membrane Proteins Derived from the Cystic Fibrosis Transmembrane Conductance Regulator. Protein Expression and Purification, 2002, 25, 81-86.	1.3	30
101	Oligomerization of a Peptide Derived from the Transmembrane Region of the Sodium Pump Î³ Subunit: Effect of the Pathological Mutation G41R. Journal of Molecular Biology, 2002, 322, 583-590.	4.2	48
102	Hydrophobicity and helicity of membrane-interactive peptides containing peptoid residues. Biopolymers, 2002, 65, 254-262.	2.4	31
103	Polar mutations in membrane proteins as a biophysical basis for disease. Biopolymers, 2002, 66, 350-358.	2.4	49
104	Putting the Î²-breaks on membrane protein misfolding. Nature Structural Biology, 2002, 9, 318-319.	9.7	39
105	Retention of Native-like Oligomerization States in Transmembrane Segment Peptides:â€‰ Application to the Escherichia coli Aspartate Receptor. Biochemistry, 2001, 40, 11106-11113.	2.5	88
106	TM Finder: A prediction program for transmembrane protein segments using a combination of hydrophobicity and nonpolar phase helicity scales. Protein Science, 2001, 10, 212-219.	7.6	128
107	Interhelical hydrogen bonds in the CFTR membrane domain. Nature Structural Biology, 2001, 8, 597-601.	9.7	90
108	Peptide Mimics of the M13 Coat Protein Transmembrane Segment. Journal of Biological Chemistry, 2000, 275, 16155-16159.	3.4	32

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109	Combining hydrophobicity and helicity: a novel approach to membrane protein structure prediction. Bioorganic and Medicinal Chemistry, 1999, 7, 1-7.	3.0	31
110	Conjugation of Polyethylene Glycol via a Disulfide Bond Confers Water Solubility upon a Peptide Model of a Protein Transmembrane Segment. Analytical Biochemistry, 1999, 275, 224-230.	2.4	8
111	Helicity of hydrophobic peptides in polar vs. non-polar environments. Physical Chemistry Chemical Physics, 1999, 1, 1539.	2.8	8
112	Threshold hydrophobicity dictates helical conformations of peptides in membrane environments. , 1998, 39, 465-470.		68
113	Guidelines for membrane protein engineering derived from de novo designed model peptides. , 1998, 47, 41-62.		105
114	Cystic fibrosis transmembrane conductance regulator: expression and helicity of a double membrane-spanning segment. FEBS Letters, 1998, 431, 29-33.	2.8	21
115	Solubilization of Hydrophobic Peptides by Reversible Cysteine PEGylation. Biochemical and Biophysical Research Communications, 1998, 245, 618-621.	2.1	16
116	Uncoupling Hydrophobicity and Helicity in Transmembrane Segments. Journal of Biological Chemistry, 1998, 273, 23645-23648.	3.4	85
117	The N Terminus of the Qcr7 Protein of the Cytochromebc 1 Complex Is Not Essential for Import into Mitochondria in Saccharomyces cerevisiae but Is Essential for Assembly of the Complex. Journal of Biological Chemistry, 1997, 272, 17495-17501.	3.4	14
118	Anionic Phospholipids Modulate Peptide Insertion into Membranes. Biochemistry, 1997, 36, 5476-5482.	2.5	115
119	Folding proteins into membranes. Nature Structural and Molecular Biology, 1996, 3, 815-818.	8.2	56
120	[4] Use of ionophores for manipulating intracellular ion concentrations. Methods in Neurosciences, 1995, 27, 52-68.	0.5	4
121	Manipulation of peptide conformations by fine-tuning of the environment and/or the primary sequence. Biopolymers, 1995, 35, 667-675.	2.4	16
122	Peptides in membranes: Helicity and hydrophobicity. Biopolymers, 1995, 37, 295-318.	2.4	108
123	Packing of Coat Protein Amphipathic and Transmembrane Helices in Filamentous Bacteriophage M13: Role of Small Residues in Protein Oligomeriza tion. Journal of Molecular Biology, 1995, 252, 6-14.	4.2	81
124	A measure of helical propensity for amino acids in membrane environments. Nature Structural and Molecular Biology, 1994, 1, 368-373.	8.2	171
125	Transmembrane Aromatic Amino Acid Distribution in P-glycoprotein. Journal of Molecular Biology, 1994, 235, 554-564.	4.2	114
126	Non-random Distribution of Amino Acids in the Transmembrane Segments of Human Type I Single Span Membrane Proteins. Journal of Molecular Biology, 1993, 229, 602-608.	4.2	361

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127	The Structure and Function of Central Nervous System Myelin. Critical Reviews in Clinical Laboratory Sciences, 1993, 30, 29-64.	6.1	44
128	Glycine and Î²-branched residues support and modulate peptide helicity in membrane environments. FEBS Letters, 1992, 311, 217-220.	2.8	92
129	Minimum energy conformations of proline-containing helices. Biopolymers, 1992, 32, 399-406.	2.4	36
130	Influence of glycine residues on peptide conformation in membran environments. International Journal of Peptide and Protein Research, 1992, 40, 243-248.	0.1	40
131	Proline residues in transmembrane helixes: structural or dynamic role?. Biochemistry, 1991, 30, 8919-8923.	2.5	263
132	Central nervous system myelin: structure, function, and pathology. Clinical Biochemistry, 1991, 24, 113-134.	1.9	101
133	Conformations of neurotensin in solution and in membrane environments studied by 2â€Ð NMR spectroscopy. International Journal of Peptide and Protein Research, 1991, 37, 528-535.	0.1	27
134	Conformations of proline residues in membrane environments. Biopolymers, 1990, 29, 149-157.	2.4	68
135	Conformation of proline residues in bacteriorhodopsin. Biochemical and Biophysical Research Communications, 1990, 172, 862-869.	2.1	19
136	A lipid vesicle system for probing voltage-dependent peptide-lipid interactions: Application to alamethicin channel formation. Biopolymers, 1989, 28, 267-272.	2.4	36
137	Deuterated Digoxin. Analytical Letters, 1989, 22, 2783-2790.	1.8	1
138	Evidence for similar function of transmembrane segments in receptor and membrane-anchored proteins. Biopolymers, 1988, 27, 1171-1182.	2.4	15
139	Potential-sensitive membrane association of a fluorescent dye. FEBS Letters, 1987, 224, 337-342.	2.8	37
140	D-glucose binding increases secondary structure of human erythrocyte monosaccharide transport protein. Biochemical and Biophysical Research Communications, 1987, 145, 1087-1091.	2.1	12
141	Peptides in membranes: Lipid-induced secondary structure of substance P. Biopolymers, 1987, 26, S109-S121.	2.4	70
142	Amino acid composition of the membrane and aqueous domains of integral membrane proteins. Archives of Biochemistry and Biophysics, 1986, 251, 68-76.	3.0	60
143	Binding of human normal and multiple sclerosis-derived myelin basic protein to phospholipid vesicles: Effects on membrane head group and bilayer regions. Archives of Biochemistry and Biophysics, 1986, 245, 455-463.	3.0	19
144	Calcium transport by ionophorous peptides in dog and human lymphocytes detected by quin-2 fluorescence. Biochemical and Biophysical Research Communications, 1986, 134, 731-735.	2.1	15

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145	The modulation of bovine milk d-galactosyltransferase by various phosphatidylethanolamines. Carbohydrate Research, 1986, 149, 47-58.	2.3	3
146	Transfer of peptide hormones from aqueous to membrane phases. Biopolymers, 1985, 24, 105-116.	2.4	48
147	Bromo-A23187: A nonfluorescent calcium ionophore for use with fluorescent probes. Analytical Biochemistry, 1985, 146, 349-352.	2.4	77
148	NMR investigation of the charge isomers of bovine myelin basic protein. Archives of Biochemistry and Biophysics, 1984, 233, 151-160.	3.0	42
149	Microheterogeneity of bovine myelin basic protein studied by nuclear magnetic resonance spectroscopy. Biopolymers, 1983, 22, 377-380.	2.4	10
150	Conformations of cyclic peptide/calcium complexes in solution. Biopolymers, 1982, 21, 169-179.	2.4	11
151	Complexation of Zn(II) to a native sequence tripeptide of human serum albumin studied by 13C nuclear magnetic resonance. Canadian Journal of Chemistry, 1980, 58, 757-766.	1.1	17
152	Peptide models for protein-mediated cation transport. Canadian Journal of Biochemistry, 1980, 58, 865-870.	1.4	15
153	Isosteric metal complexes of ionophore A23187. FEBS Letters, 1979, 105, 360-364.	2.8	16
154	Cyclic peptides. 17. Metal and amino acid complexes of cyclo(Pro-Gly)4 and analogs studied by nuclear magnetic resonance and circular dichroism. Journal of the American Chemical Society, 1977, 99, 4788-4798.	13.7	91
155	Why cyclic peptides? Complementary approaches to conformations. Accounts of Chemical Research, 1976, 9, 106-113.	15.6	205
156	Cyclic peptides. VIII. Carbon-13 and proton nuclear magnetic resonance evidence for slow cis'-trans' rotation in a cyclic tetrapeptide. Journal of the American Chemical Society, 1974, 96, 4015-4017.	13.7	54
157	Cyclic peptides. Amino acid-cyclic peptides complexes. Journal of the American Chemical Society, 1974, 96, 7566-7568.	13.7	47
158	Cyclic peptides. V. Proton and carbon-13 nuclear magnetic resonance determination of the preferred .beta. conformation for proline-containing cyclic hexapeptides. Journal of the American Chemical Society, 1973, 95, 258-260.	13.7	65
159	Cyclic peptides. I. Cyclo(tri-L-prolyl) and derivatives. Synthesis and molecular conformation from nuclear magnetic resonance. Journal of the American Chemical Society, 1971, 93, 4893-4897.	13.7	95
160	Conformational Aspects of Polypeptides. VII. Reversal of The Helical Sense of Poly-L-Aspartate Esters. Journal of the American Chemical Society, 1962, 84, 3773-3774.	13.7	55