

Charles M Deber

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

158 papers	6,922 citations	46 h-index	77 g-index
165 ext. papers	7,474 ext. citations	4.8 avg, IF	5.84 L-index

#	Paper	IF	Citations
158	Enhanced proteolytic resistance of cationic antimicrobial peptides through lysine side chain analogs and cyclization.. <i>Biochemical and Biophysical Research Communications</i> , 2022 , 612, 105-109	3.4	1
157	Heat treatment of thioredoxin fusions increases the purity of helical transmembrane protein constructs. <i>Protein Science</i> , 2021 , 30, 1974-1982	6.3	1
156	Uncoupling Amphipathicity and Hydrophobicity: Role of Charge Clustering in Membrane Interactions of Cationic Antimicrobial Peptides. <i>Biochemistry</i> , 2021 , 60, 2586-2592	3.2	3
155	Anti-Infectives Restore ORKAMBI Rescue of F508del-CFTR Function in Human Bronchial Epithelial Cells Infected with Clinical Strains of. <i>Biomolecules</i> , 2020 , 10,	5.9	21
154	Protection or Destruction: The LL-37/HNP1 Cooperativity Switch. <i>Biophysical Journal</i> , 2020 , 119, 2370-2374	3.7	1
153	CFTR transmembrane segments are impaired in their conformational adaptability by a pathogenic loop mutation and dynamically stabilized by Lumacaftor. <i>Journal of Biological Chemistry</i> , 2020 , 295, 19851-19914	5.4	4
152	Peptide-Based Approach to Inhibition of the Multidrug Resistance Efflux Pump AcrB. <i>Biochemistry</i> , 2020 , 59, 3973-3981	3.2	3
151	Peptide-Based Efflux Pump Inhibitors of the Small Multidrug Resistance Protein from <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	8
150	Positive Charge Patterning and Hydrophobicity of Membrane-Active Antimicrobial Peptides as Determinants of Activity, Toxicity, and Pharmacokinetic Stability. <i>Journal of Medicinal Chemistry</i> , 2019 , 62, 6276-6286	8.3	20
149	Relative role(s) of leucine versus isoleucine in the folding of membrane proteins. <i>Peptide Science</i> , 2019 , 111, e24075	3	5
148	Method to generate highly stable D-amino acid analogs of bioactive helical peptides using a mirror image of the entire PDB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 1505-1510	11.5	54
147	Structural effects of extracellular loop mutations in CFTR helical hairpins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018 , 1860, 1092-1098	3.8	3
146	Structure of the multidrug transporter and its use for inhibitor peptide design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E7932-E7941	11.5	22
145	Influence of hydrocarbon-stapling on membrane interactions of synthetic antimicrobial peptides. <i>Bioorganic and Medicinal Chemistry</i> , 2018 , 26, 1189-1196	3.4	24
144	A minimal helical-hairpin motif provides molecular-level insights into misfolding and pharmacological rescue of CFTR. <i>Communications Biology</i> , 2018 , 1, 154	6.7	13
143	Activity of a novel antimicrobial peptide against <i>Pseudomonas aeruginosa</i> biofilms. <i>Scientific Reports</i> , 2018 , 8, 14728	4.9	29
142	Therapeutic design of peptide modulators of protein-protein interactions in membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017 , 1859, 577-585	3.8	34

141	Hydrophobic Clusters Raise the Threshold Hydrophilicity for Insertion of Transmembrane Sequences in Vivo. <i>Biochemistry</i> , 2016 , 55, 5772-5779	3.2	2
140	Modulating Transmembrane α -Helix Interactions through pH-Sensitive Boundary Residues. <i>Biochemistry</i> , 2016 , 55, 4306-15	3.2	3
139	Structural impact of proline mutations in the loop region of an ancestral membrane protein. <i>Biopolymers</i> , 2016 , 106, 37-42	2.2	4
138	Helix-helix interactions: is the medium the message?. <i>Structure</i> , 2015 , 23, 437-438	5.2	5
137	Design and characterization of a membrane protein unfolding platform in lipid bilayers. <i>PLoS ONE</i> , 2015 , 10, e0120253	3.7	1
136	Efflux by small multidrug resistance proteins is inhibited by membrane-interactive helix-stapled peptides. <i>Journal of Biological Chemistry</i> , 2015 , 290, 1752-9	5.4	19
135	Hydrophobic blocks facilitate lipid compatibility and translocon recognition of transmembrane protein sequences. <i>Biochemistry</i> , 2015 , 54, 1465-73	3.2	4
134	Functional response of the small multidrug resistance protein EmrE to mutations in transmembrane helix 2. <i>FEBS Letters</i> , 2014 , 588, 3720-5	3.8	7
133	Terminal residue hydrophobicity modulates transmembrane helix-helix interactions. <i>Biochemistry</i> , 2014 , 53, 3747-57	3.2	3
132	Design of transmembrane peptides: coping with sticky situations. <i>Methods in Molecular Biology</i> , 2013 , 1063, 197-210	1.4	3
131	Correction factors for membrane protein molecular weight readouts on sodium dodecyl sulfate-polyacrylamide gel electrophoresis. <i>Analytical Biochemistry</i> , 2013 , 434, 67-72	3.1	23
130	Loop sequence dictates the secondary structure of a human membrane protein hairpin. <i>Biochemistry</i> , 2013 , 52, 2419-26	3.2	12
129	Effects of a polar amino acid substitution on helix formation and aggregate size along the detergent-induced peptide folding pathway. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013 , 1828, 373-81	3.8	8
128	Inside-out signaling promotes dynamic changes in the carcinoembryonic antigen-related cellular adhesion molecule 1 (CEACAM1) oligomeric state to control its cell adhesion properties. <i>Journal of Biological Chemistry</i> , 2013 , 288, 29654-69	5.4	20
127	Acrylamide concentration determines the direction and magnitude of helical membrane protein gel shifts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 15668-73	11.5	38
126	Congenital heart block maternal sera autoantibodies target an extracellular epitope on the α_1 G T-type calcium channel in human fetal hearts. <i>PLoS ONE</i> , 2013 , 8, e72668	3.7	23
125	Differential binding of L- vs. D-isomers of cationic antimicrobial peptides to the biofilm exopolysaccharide alginate. <i>Protein and Peptide Letters</i> , 2013 , 20, 843-7	1.9	8
124	Design, expression, and purification of de novo transmembrane "hairpin" peptides. <i>Biopolymers</i> , 2012 , 98, 546-56	2.2	2

123	Sequence hydropathy dominates membrane protein response to detergent solubilization. <i>Biochemistry</i> , 2012 , 51, 6228-37	3.2	8
122	Protein structure in membrane domains. <i>Annual Review of Biophysics</i> , 2012 , 41, 135-55	21.1	24
121	Membrane protein misassembly in disease. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1115-22	3.8	66
120	Structural basis for misfolding at a disease phenotypic position in CFTR: comparison of TM3/4 helix-loop-helix constructs with TM4 peptides. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 49-54	3.8	5
119	Efficiency of detergents at maintaining membrane protein structures in their biologically relevant forms. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1351-8	3.8	46
118	Roles of hydrophobicity and charge distribution of cationic antimicrobial peptides in peptide-membrane interactions. <i>Journal of Biological Chemistry</i> , 2012 , 287, 7738-45	5.4	238
117	Drug efflux by a small multidrug resistance protein is inhibited by a transmembrane peptide. <i>Antimicrobial Agents and Chemotherapy</i> , 2012 , 56, 3911-6	5.9	15
116	Converting a marginally hydrophobic soluble protein into a membrane protein. <i>Journal of Molecular Biology</i> , 2011 , 407, 171-9	6.5	5
115	3 Membrane protein folding in detergents 2011 ,		1
114	Beta-branched residues adjacent to GG4 motifs promote the efficient association of glycophorin A transmembrane helices. <i>Biopolymers</i> , 2011 , 96, 340-7	2.2	9
113	Positions of polar amino acids alter interactions between transmembrane segments and detergents. <i>Biochemistry</i> , 2011 , 50, 3928-35	3.2	16
112	Modulation of substrate efflux in bacterial small multidrug resistance proteins by mutations at the dimer interface. <i>Journal of Bacteriology</i> , 2011 , 193, 5929-35	3.5	10
111	Novel hydrophobic standards for membrane protein molecular weight determinations via sodium dodecyl sulfate-polyacrylamide gel electrophoresis. <i>Biochemistry</i> , 2010 , 49, 10589-91	3.2	10
110	Modulation of the oligomerization of myelin proteolipid protein by transmembrane helix interaction motifs. <i>Biochemistry</i> , 2010 , 49, 6896-902	3.2	17
109	Evidence that the translocon may function as a hydropathy partitioning filter. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010 , 1798, 1995-8	3.8	5
108	Proline Residues in Proteins 2010 ,		5
107	Deletion of a terminal residue disrupts oligomerization of a transmembrane alpha-helix. <i>Biochemistry and Cell Biology</i> , 2010 , 88, 339-45	3.6	11
106	Distinctions between hydrophobic helices in globular proteins and transmembrane segments as factors in protein sorting. <i>Journal of Biological Chemistry</i> , 2009 , 284, 5395-402	5.4	12

105	The assembly motif of a bacterial small multidrug resistance protein. <i>Journal of Biological Chemistry</i> , 2009 , 284, 9870-5	5.4	23
104	A novel method for monitoring the cytosolic delivery of peptide cargo. <i>Journal of Controlled Release</i> , 2009 , 137, 2-7	11.7	27
103	Functional rescue of DeltaF508-CFTR by peptides designed to mimic sorting motifs. <i>Chemistry and Biology</i> , 2009 , 16, 520-30		18
102	Peptide models of membrane protein folding. <i>Biochemistry</i> , 2009 , 48, 3036-45	3.2	42
101	Detergent binding explains anomalous SDS-PAGE migration of membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 1760-5	11.5	547
100	SDS micelles as a membrane-mimetic environment for transmembrane segments. <i>Biochemistry</i> , 2009 , 48, 12096-103	3.2	82
99	Misfolding of the cystic fibrosis transmembrane conductance regulator and disease. <i>Biochemistry</i> , 2008 , 47, 1465-73	3.2	56
98	Positional dependence of non-native polar mutations on folding of CFTR helical hairpins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2008 , 1778, 79-87	3.8	9
97	Surface recognition elements of membrane protein oligomerization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 786-93	4.2	15
96	Membrane interactions of designed cationic antimicrobial peptides: the two thresholds. <i>Biopolymers</i> , 2008 , 89, 360-71	2.2	64
95	Defining the defect in F508 del CFTR: a soluble problem?. <i>Chemistry and Biology</i> , 2008 , 15, 3-4		
94	Transmembrane domain of myelin protein zero can form dimers: possible implications for myelin construction. <i>Biochemistry</i> , 2007 , 46, 12164-73	3.2	29
93	Role of the extracellular loop in the folding of a CFTR transmembrane helical hairpin. <i>Biochemistry</i> , 2007 , 46, 7099-106	3.2	19
92	Aromatic and cation-pi interactions enhance helix-helix association in a membrane environment. <i>Biochemistry</i> , 2007 , 46, 9208-14	3.2	83
91	Peptides as transmembrane segments: decrypting the determinants for helix-helix interactions in membrane proteins. <i>Biopolymers</i> , 2007 , 88, 217-32	2.2	26
90	Hydrophobic interactions in complexes of antimicrobial peptides with bacterial polysaccharides. <i>Chemical Biology and Drug Design</i> , 2007 , 69, 405-12	2.9	28
89	Optimizing synthesis and expression of transmembrane peptides and proteins. <i>Methods</i> , 2007 , 41, 370-80	4.6	43
88	Membrane interactions of the hydrophobic segment of diacylglycerol kinase epsilon. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 2549-58	3.8	13

87	Membrane protein assembly patterns reflect selection for non-proliferative structures. <i>FEBS Letters</i> , 2007 , 581, 1335-41	3.8	12
86	Evidence for assembly of small multidrug resistance proteins by a "two-faced" transmembrane helix. <i>Journal of Biological Chemistry</i> , 2006 , 281, 15546-53	5.4	30
85	The position of the Gly-xxx-Gly motif in transmembrane segments modulates dimer affinity. <i>Biochemistry and Cell Biology</i> , 2006 , 84, 1006-12	3.6	20
84	Activity of novel non-amphipathic cationic antimicrobial peptides against <i>Candida</i> species. <i>Journal of Antimicrobial Chemotherapy</i> , 2006 , 57, 899-907	5.1	41
83	Lipid solvation effects contribute to the affinity of Gly-xxx-Gly motif-mediated helix-helix interactions. <i>Biochemistry</i> , 2006 , 45, 8507-15	3.2	25
82	Self-association of the transmembrane domain of an anthrax toxin receptor. <i>Journal of Molecular Biology</i> , 2006 , 360, 145-56	6.5	23
81	The structure of "unstructured" regions in peptides and proteins: role of the polyproline II helix in protein folding and recognition. <i>Biopolymers</i> , 2005 , 80, 179-85	2.2	170
80	Basis for selectivity of cationic antimicrobial peptides for bacterial versus mammalian membranes. <i>Journal of Biological Chemistry</i> , 2005 , 280, 33960-7	5.4	198
79	Destabilization of the transmembrane domain induces misfolding in a phenotypic mutant of cystic fibrosis transmembrane conductance regulator. <i>Journal of Biological Chemistry</i> , 2005 , 280, 4968-74	5.4	21
78	Helix induction in antimicrobial peptides by alginate in biofilms. <i>Journal of Biological Chemistry</i> , 2004 , 279, 38749-54	5.4	74
77	The affinity of GXXXG motifs in transmembrane helix-helix interactions is modulated by long-range communication. <i>Journal of Biological Chemistry</i> , 2004 , 279, 16591-7	5.4	97
76	Missense mutations in transmembrane domains of proteins: phenotypic propensity of polar residues for human disease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 648-56	4.2	80
75	Aqueous solubility and membrane interactions of hydrophobic peptides with peptoid tags. <i>Biopolymers</i> , 2004 , 76, 110-8	2.2	17
74	Hydrophobic helical hairpins: design and packing interactions in membrane environments. <i>Biochemistry</i> , 2004 , 43, 14361-9	3.2	36
73	Non-native interhelical hydrogen bonds in the cystic fibrosis transmembrane conductance regulator domain modulated by polar mutations. <i>Biochemistry</i> , 2004 , 43, 8077-83	3.2	29
72	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. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2003 , 307, 481-9	4.7	26
71	Transmembrane segment peptides with double D-amino acid replacements: helicity, hydrophobicity, and antimicrobial activity. <i>Biopolymers</i> , 2003 , 71, 77-84	2.2	7
70	Polar residue tagging of transmembrane peptides. <i>Biopolymers</i> , 2003 , 71, 675-85	2.2	80

69	Disease-associated mutations in conserved residues of ALK-1 kinase domain. <i>European Journal of Human Genetics</i> , 2003 , 11, 279-87	5.3	61
68	Sequence context strongly modulates association of polar residues in transmembrane helices. <i>Journal of Molecular Biology</i> , 2003 , 331, 255-62	6.5	71
67	A transmembrane segment mimic derived from Escherichia coli diacylglycerol kinase inhibits protein activity. <i>Journal of Biological Chemistry</i> , 2003 , 278, 22056-60	5.4	36
66	Modulation of Na,K-ATPase by the gamma subunit: studies with transfected cells and transmembrane mimetic peptides. <i>Journal of Biological Chemistry</i> , 2003 , 278, 40437-41	5.4	34
65	Hydrophobicity and helicity of membrane-interactive peptides containing peptoid residues. <i>Biopolymers</i> , 2002 , 65, 254-62	2.2	28
64	Polar mutations in membrane proteins as a biophysical basis for disease. <i>Biopolymers</i> , 2002 , 66, 350-8	2.2	46
63	Interhelical packing in detergent micelles. Folding of a cystic fibrosis transmembrane conductance regulator construct. <i>Journal of Biological Chemistry</i> , 2002 , 277, 6067-72	5.4	28
62	The hydrophobicity threshold for peptide insertion into membranes. <i>Current Topics in Membranes</i> , 2002 , 52, 465-479	2.2	7
61	Cationic hydrophobic peptides with antimicrobial activity. <i>Antimicrobial Agents and Chemotherapy</i> , 2002 , 46, 3585-90	5.9	167
60	Polar residues in membrane domains of proteins: molecular basis for helix-helix association in a mutant CFTR transmembrane segment. <i>Biochemistry</i> , 2002 , 41, 3647-53	3.2	53
59	Transmembrane domain mediated self-assembly of major coat protein subunits from Ff bacteriophage. <i>Journal of Molecular Biology</i> , 2002 , 315, 63-72	6.5	62
58	Expression and purification of two hydrophobic double-spanning membrane proteins derived from the cystic fibrosis transmembrane conductance regulator. <i>Protein Expression and Purification</i> , 2002 , 25, 81-6	2	30
57	Oligomerization of a peptide derived from the transmembrane region of the sodium pump gamma subunit: effect of the pathological mutation G41R. <i>Journal of Molecular Biology</i> , 2002 , 322, 583-50	6.5	46
56	Proline Residues in Proteins 2001 ,		2
55	TM Finder: a prediction program for transmembrane protein segments using a combination of hydrophobicity and nonpolar phase helicity scales. <i>Protein Science</i> , 2001 , 10, 212-9	6.3	117
54	Interhelical hydrogen bonds in the CFTR membrane domain. <i>Nature Structural Biology</i> , 2001 , 8, 597-601		87
53	Retention of native-like oligomerization states in transmembrane segment peptides: application to the Escherichia coli aspartate receptor. <i>Biochemistry</i> , 2001 , 40, 11106-13	3.2	87
52	Peptide mimics of the M13 coat protein transmembrane segment. Retention of helix-helix interaction motifs. <i>Journal of Biological Chemistry</i> , 2000 , 275, 16155-9	5.4	31

51	Combining hydrophobicity and helicity: a novel approach to membrane protein structure prediction. <i>Bioorganic and Medicinal Chemistry</i> , 1999 , 7, 1-7	3.4	27
50	Conjugation of polyethylene glycol via a disulfide bond confers water solubility upon a peptide model of a protein transmembrane segment. <i>Analytical Biochemistry</i> , 1999 , 275, 224-30	3.1	8
49	Helicity of hydrophobic peptides in polar vs. non-polar environments. <i>Physical Chemistry Chemical Physics</i> , 1999 , 1, 1539	3.6	8
48	Guidelines for membrane protein engineering derived from de novo designed model peptides. <i>Biopolymers</i> , 1998 , 47, 41-62	2.2	94
47	Cystic fibrosis transmembrane conductance regulator: expression and helicity of a double membrane-spanning segment. <i>FEBS Letters</i> , 1998 , 431, 29-33	3.8	21
46	Solubilization of hydrophobic peptides by reversible cysteine PEGylation. <i>Biochemical and Biophysical Research Communications</i> , 1998 , 245, 618-21	3.4	15
45	Uncoupling hydrophobicity and helicity in transmembrane segments. Alpha-helical propensities of the amino acids in non-polar environments. <i>Journal of Biological Chemistry</i> , 1998 , 273, 23645-8	5.4	72
44	The N terminus of the Qcr7 protein of the cytochrome bc1 complex is not essential for import into mitochondria in <i>Saccharomyces cerevisiae</i> but is essential for assembly of the complex. <i>Journal of Biological Chemistry</i> , 1997 , 272, 17495-501	5.4	11
43	Anionic phospholipids modulate peptide insertion into membranes. <i>Biochemistry</i> , 1997 , 36, 5476-82	3.2	110
42	Threshold hydrophobicity dictates helical conformations of peptides in membrane environments. <i>Biopolymers</i> , 1996 , 39, 465-70	2.2	64
41	Packing of coat protein amphipathic and transmembrane helices in filamentous bacteriophage M13: role of small residues in protein oligomerization. <i>Journal of Molecular Biology</i> , 1995 , 252, 6-14	6.5	74
40	[4] Use of ionophores for manipulating intracellular ion concentrations. <i>Methods in Neurosciences</i> , 1995 , 27, 52-68		3
39	Manipulation of peptide conformations by fine-tuning of the environment and/or the primary sequence. <i>Biopolymers</i> , 1995 , 35, 667-75	2.2	16
38	Peptides in membranes: helicity and hydrophobicity. <i>Biopolymers</i> , 1995 , 37, 295-318	2.2	95
37	A measure of helical propensity for amino acids in membrane environments. <i>Nature Structural and Molecular Biology</i> , 1994 , 1, 368-73	17.6	158
36	Transmembrane aromatic amino acid distribution in P-glycoprotein. A functional role in broad substrate specificity. <i>Journal of Molecular Biology</i> , 1994 , 235, 554-64	6.5	107
35	Non-random distribution of amino acids in the transmembrane segments of human type I single span membrane proteins. <i>Journal of Molecular Biology</i> , 1993 , 229, 602-8	6.5	337
34	The structure and function of central nervous system myelin. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 1993 , 30, 29-64	9.4	29

33	Influence of glycine residues on peptide conformation in membrane environments. <i>International Journal of Peptide and Protein Research</i> , 1992 , 40, 243-8		33
32	Glycine and beta-branched residues support and modulate peptide helicity in membrane environments. <i>FEBS Letters</i> , 1992 , 311, 217-20	3.8	69
31	Minimum energy conformations of proline-containing helices. <i>Biopolymers</i> , 1992 , 32, 399-406	2.2	35
30	Conformations of neurotensin in solution and in membrane environments studied by 2-D NMR spectroscopy. <i>International Journal of Peptide and Protein Research</i> , 1991 , 37, 528-35		26
29	Central nervous system myelin: structure, function, and pathology. <i>Clinical Biochemistry</i> , 1991 , 24, 113-34.5		86
28	Proline residues in transmembrane helices: structural or dynamic role?. <i>Biochemistry</i> , 1991 , 30, 8919-23	3.2	239
27	Conformations of proline residues in membrane environments. <i>Biopolymers</i> , 1990 , 29, 149-57	2.2	61
26	Conformation of proline residues in bacteriorhodopsin. <i>Biochemical and Biophysical Research Communications</i> , 1990 , 172, 862-9	3.4	18
25	A lipid vesicle system for probing voltage-dependent peptide-lipid interactions: application to alamethicin channel formation. <i>Biopolymers</i> , 1989 , 28, 267-72	2.2	28
24	Deuterated Digoxin. <i>Analytical Letters</i> , 1989 , 22, 2783-2790	2.2	1
23	Evidence for similar function of transmembrane segments in receptor and membrane-anchored proteins. <i>Biopolymers</i> , 1988 , 27, 1171-82	2.2	14
22	Potential-sensitive membrane association of a fluorescent dye. <i>FEBS Letters</i> , 1987 , 224, 337-342	3.8	34
21	D-glucose binding increases secondary structure of human erythrocyte monosaccharide transport protein. <i>Biochemical and Biophysical Research Communications</i> , 1987 , 145, 1087-91	3.4	11
20	Peptides in membranes: lipid-induced secondary structure of substance P. <i>Biopolymers</i> , 1987 , 26 Suppl, S109-21	2.2	65
19	The modulation of bovine milk D-galactosyltransferase by various phosphatidylethanolamines. <i>Carbohydrate Research</i> , 1986 , 149, 47-58	2.9	3
18	Amino acid composition of the membrane and aqueous domains of integral membrane proteins. <i>Archives of Biochemistry and Biophysics</i> , 1986 , 251, 68-76	4.1	54
17	Binding of human normal and multiple sclerosis-derived myelin basic protein to phospholipid vesicles: effects on membrane head group and bilayer regions. <i>Archives of Biochemistry and Biophysics</i> , 1986 , 245, 455-63	4.1	18
16	Calcium transport by ionophorous peptides in dog and human lymphocytes detected by quin-2 fluorescence. <i>Biochemical and Biophysical Research Communications</i> , 1986 , 134, 731-5	3.4	14

15	Transfer of peptide hormones from aqueous to membrane phases. <i>Biopolymers</i> , 1985 , 24, 105-116	2.2	46
14	Bromo-A23187: a nonfluorescent calcium ionophore for use with fluorescent probes. <i>Analytical Biochemistry</i> , 1985 , 146, 349-52	3.1	69
13	NMR investigation of the charge isomers of bovine myelin basic protein. <i>Archives of Biochemistry and Biophysics</i> , 1984 , 233, 151-60	4.1	40
12	Microheterogeneity of bovine myelin basic protein studied by nuclear magnetic resonance spectroscopy. <i>Biopolymers</i> , 1983 , 22, 377-80	2.2	9
11	Conformations of cyclic peptide/calcium complexes in solution. <i>Biopolymers</i> , 1982 , 21, 169-79	2.2	10
10	Complexation of Zn(II) to a native sequence tripeptide of human serum albumin studied by ¹³ C nuclear magnetic resonance. <i>Canadian Journal of Chemistry</i> , 1980 , 58, 757-766	0.9	11
9	Peptide models for protein-mediated cation transport. <i>Canadian Journal of Biochemistry</i> , 1980 , 58, 865-70		14
8	Isosteric metal complexes of ionophore A23187: a basis for cation selectivity. <i>FEBS Letters</i> , 1979 , 105, 360-4	3.8	15
7	Cyclic peptides. 17. Metal and amino acid complexes of cyclo(pro-gly) ₄ and analogues studied by nuclear magnetic resonance and circular dichroism. <i>Journal of the American Chemical Society</i> , 1977 , 99, 4788-98	16.4	75
6	Why cyclic peptides? Complementary approaches to conformations. <i>Accounts of Chemical Research</i> , 1976 , 9, 106-113	24.3	188
5	Cyclic peptides. 8. ¹³ C and ¹ H nuclear magnetic resonance evidence for slow cis-trans rotation in a cyclic tetrapeptide. <i>Journal of the American Chemical Society</i> , 1974 , 96, 4015-7	16.4	48
4	Letter: Amino acid-cyclic peptide complexes. <i>Journal of the American Chemical Society</i> , 1974 , 96, 7566-8	16.4	32
3	Cyclic peptides. V. ¹ H and ¹³ C nuclear magnetic resonance determination of the preferred beta conformation for proline-containing cyclic hexapeptides. <i>Journal of the American Chemical Society</i> , 1973 , 95, 258-60	16.4	59
2	Cyclic peptides. I. Cyclo(tri-L-prolyl) and derivatives. Synthesis and molecular conformation from nuclear magnetic resonance. <i>Journal of the American Chemical Society</i> , 1971 , 93, 4893-7	16.4	79
1	Conformational Aspects of Polypeptides. VII. Reversal of The Helical Sense of Poly-L-Aspartate Esters. <i>Journal of the American Chemical Society</i> , 1962 , 84, 3773-3774	16.4	43