# Charles M Deber

## List of Publications by Year
## in descending order

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160

papers

7,994

citations

47006

47

h-index

58581

82

g-index

165

all docs

165

docs citations

165

times ranked

7974

citing authors

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | Proline residues in transmembrane helixes: structural or dynamic role?. Biochemistry, 1991, 30, 8919-8923. | 2.5 | 263 |
| 5 | Basis for Selectivity of Cationic Antimicrobial Peptides for Bacterial Versus Mammalian Membranes. Journal of Biological Chemistry, 2005, 280, 33960-33967. | 3.4 | 244 |
| 6 | Why cyclic peptides? Complementary approaches to conformations. Accounts of Chemical Research, 1976, 9, 106-113. | 15.6 | 205 |
| 7 | Cationic Hydrophobic Peptides with Antimicrobial Activity. Antimicrobial Agents and Chemotherapy, 2002, 46, 3585-3590. | 3.2 | 194 |
| 8 | 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 |
| 9 | A measure of helical propensity for amino acids in membrane environments. Nature Structural and Molecular Biology, 1994, 1, 368-373. | 8.2 | 171 |
| 10 | 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 |
| 11 | Anionic Phospholipids Modulate Peptide Insertion into Membranes. Biochemistry, 1997, 36, 5476-5482. | 2.5 | 115 |
| 12 | Transmembrane Aromatic Amino Acid Distribution in P-glycoprotein. Journal of Molecular Biology, 1994, 235, 554-564. | 4.2 | 114 |
| 13 | Peptides in membranes: Helicity and hydrophobicity. Biopolymers, 1995, 37, 295-318. | 2.4 | 108 |
| 14 | Guidelines for membrane protein engineering derived from de novo designed model peptides. , 1998, 47, 41-62. | | 105 |
| 15 | 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 |
| 16 | Central nervous system myelin: structure, function, and pathology. Clinical Biochemistry, 1991, 24, 113-134. | 1.9 | 101 |
| 17 | SDS Micelles as a Membrane-Mimetic Environment for Transmembrane Segments. Biochemistry, 2009, 48, 12096-12103. | 2.5 | 101 |
| 18 | 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 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 19 | 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 |
| 20 | Glycine and Î²-branched residues support and modulate peptide helicity in membrane environments. FEBS Letters, 1992, 311, 217-220. | 2.8 | 92 |
| 21 | Aromatic and Cationâˆ'Ï€ Interactions Enhance Helixâˆ'Helix Association in a Membrane Environment. Biochemistry, 2007, 46, 9208-9214. | 2.5 | 92 |
| 22 | 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 |
| 23 | Interhelical hydrogen bonds in the CFTR membrane domain. Nature Structural Biology, 2001, 8, 597-601. | 9.7 | 90 |
| 24 | 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 |
| 25 | 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 |
| 26 | Helix Induction in Antimicrobial Peptides by Alginate in Biofilms. Journal of Biological Chemistry, 2004, 279, 38749-38754. | 3.4 | 88 |
| 27 | Polar residue tagging of transmembrane peptides. Biopolymers, 2003, 71, 675-685. | 2.4 | 86 |
| 28 | Uncoupling Hydrophobicity and Helicity in Transmembrane Segments. Journal of Biological Chemistry, 1998, 273, 23645-23648. | 3.4 | 85 |
| 29 | 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 |
| 30 | Membrane interactions of designed cationic antimicrobial peptides: The two thresholds. Biopolymers, 2008, 89, 360-371. | 2.4 | 78 |
| 31 | Bromo-A23187: A nonfluorescent calcium ionophore for use with fluorescent probes. Analytical Biochemistry, 1985, 146, 349-352. | 2.4 | 77 |
| 32 | Membrane protein misassembly in disease. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1115-1122. | 2.6 | 75 |
| 33 | Disease-associated mutations in conserved residues of ALK-1 kinase domain. European Journal of Human Genetics, 2003, 11, 279-287. | 2.8 | 73 |
| 34 | Sequence Context Strongly Modulates Association of Polar Residues in Transmembrane Helices. Journal of Molecular Biology, 2003, 331, 255-262. | 4.2 | 72 |
| 35 | Peptides in membranes: Lipid-induced secondary structure of substance P. Biopolymers, 1987, 26, S109-S121. | 2.4 | 70 |
| 36 | Conformations of proline residues in membrane environments. Biopolymers, 1990, 29, 149-157. | 2.4 | 68 |

| # | ARTICLE | IF | CITATIONS |
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| 37 | Threshold hydrophobicity dictates helical conformations of peptides in membrane environments. , 1998, 39, 465-470. | | 68 |
| 38 | 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 |
| 39 | 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 |
| 40 | Misfolding of the Cystic Fibrosis Transmembrane Conductance Regulator and Disease. Biochemistry, 2008, 47, 1465-1473. | 2.5 | 62 |
| 41 | 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 |
| 42 | Therapeutic design of peptide modulators of protein-protein interactions in membranes. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 577-585. | 2.6 | 57 |
| 43 | Folding proteins into membranes. Nature Structural and Molecular Biology, 1996, 3, 815-818. | 8.2 | 56 |
| 44 | 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 |
| 45 | 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 |
| 46 | Polar Residues in Membrane Domains of Proteins:Â Molecular Basis for Helixâˆ'Helix Association in a Mutant CFTR Transmembrane Segmentâ€. Biochemistry, 2002, 41, 3647-3653. | 2.5 | 53 |
| 47 | 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 |
| 48 | 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 |
| 49 | Polar mutations in membrane proteins as a biophysical basis for disease. Biopolymers, 2002, 66, 350-358. | 2.4 | 49 |
| 50 | Transfer of peptide hormones from aqueous to membrane phases. Biopolymers, 1985, 24, 105-116. | 2.4 | 48 |
| 51 | 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 |
| 52 | Cyclic peptides. Amino acid-cyclic peptides complexes. Journal of the American Chemical Society, 1974, 96, 7566-7568. | 13.7 | 47 |
| 53 | Optimizing synthesis and expression of transmembrane peptides and proteins. Methods, 2007, 41, 370-380. | 3.8 | 46 |
| 54 | The Structure and Function of Central Nervous System Myelin. Critical Reviews in Clinical Laboratory Sciences, 1993, 30, 29-64. | 6.1 | 44 |

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|---|---|---|---|
| 55 | Activity of novel non-amphipathic cationic antimicrobial peptides against Candida species. Journal of Antimicrobial Chemotherapy, 2006, 57, 899-907. | 3.0 | 43 |
| 56 | 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 |
| 57 | NMR investigation of the charge isomers of bovine myelin basic protein. Archives of Biochemistry and Biophysics, 1984, 233, 151-160. | 3.0 | 42 |
| 58 | Peptide Models of Membrane Protein Folding. Biochemistry, 2009, 48, 3036-3045. | 2.5 | 42 |
| 59 | Activity of a novel antimicrobial peptide against Pseudomonas aeruginosa biofilms. Scientific Reports, 2018, 8, 14728. | 3.3 | 42 |
| 60 | Influence of glycine residues on peptide conformation in membran environments. International Journal of Peptide and Protein Research, 1992, 40, 243-248. | 0.1 | 40 |
| 61 | Putting the Î²-breaks on membrane protein misfolding. Nature Structural Biology, 2002, 9, 318-319. | 9.7 | 39 |
| 62 | A Transmembrane Segment Mimic Derived from Escherichia coli Diacylglycerol Kinase Inhibits Protein Activity. Journal of Biological Chemistry, 2003, 278, 22056-22060. | 3.4 | 38 |
| 63 | Modulation of Na,K-ATPase by the Î³ Subunit. Journal of Biological Chemistry, 2003, 278, 40437-40441. | 3.4 | 38 |
| 64 | Potential-sensitive membrane association of a fluorescent dye. FEBS Letters, 1987, 224, 337-342. | 2.8 | 37 |
| 65 | A lipid vesicle system for probing voltage-dependent peptide-lipid interactions: Application to alamethicin channel formation. Biopolymers, 1989, 28, 267-272. | 2.4 | 36 |
| 66 | Minimum energy conformations of proline-containing helices. Biopolymers, 1992, 32, 399-406. | 2.4 | 36 |
| 67 | Hydrophobic Helical Hairpins:â€‰ Design and Packing Interactions in Membrane Environments. Biochemistry, 2004, 43, 14361-14369. | 2.5 | 36 |
| 68 | Transmembrane Domain of Myelin Protein Zero Can Form Dimers:â€‰ Possible Implications for Myelin Construction. Biochemistry, 2007, 46, 12164-12173. | 2.5 | 36 |
| 69 | Correction factors for membrane protein molecular weight readouts on sodium dodecyl sulfateâ€“polyacrylamide gel electrophoresis. Analytical Biochemistry, 2013, 434, 67-72. | 2.4 | 34 |
| 70 | 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 |
| 71 | Peptide Mimics of the M13 Coat Protein Transmembrane Segment. Journal of Biological Chemistry, 2000, 275, 16155-16159. | 3.4 | 32 |
| 72 | Hydrophobic Interactions in Complexes of Antimicrobial Peptides with Bacterial Polysaccharides. Chemical Biology and Drug Design, 2007, 69, 405-412. | 3.2 | 32 |

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| 73 | Influence of hydrocarbon-stapling on membrane interactions of synthetic antimicrobial peptides. Bioorganic and Medicinal Chemistry, 2018, 26, 1189-1196. | 3.0 | 32 |
| 74 | 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 |
| 75 | Combining hydrophobicity and helicity: a novel approach to membrane protein structure prediction. Bioorganic and Medicinal Chemistry, 1999, 7, 1-7. | 3.0 | 31 |
| 76 | Hydrophobicity and helicity of membrane-interactive peptides containing peptoid residues. Biopolymers, 2002, 65, 254-262. | 2.4 | 31 |
| 77 | 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 |
| 78 | 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 |
| 79 | 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 |
| 80 | A novel method for monitoring the cytosolic delivery of peptide cargo. Journal of Controlled Release, 2009, 137, 2-7. | 9.9 | 30 |
| 81 | Interhelical Packing in Detergent Micelles. Journal of Biological Chemistry, 2002, 277, 6067-6072. | 3.4 | 29 |
| 82 | 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 |
| 83 | 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 |
| 84 | Lipid Solvation Effects Contribute to the Affinity of Gly-xxx-Gly Motif-Mediated Helixâˆ’Helix Interactionsâ€. Biochemistry, 2006, 45, 8507-8515. | 2.5 | 28 |
| 85 | Peptides as transmembrane segments: Decrypting the determinants for helixâ€“helix interactions in membrane proteins. Biopolymers, 2007, 88, 217-232. | 2.4 | 28 |
| 86 | 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 |
| 87 | Conformations of neurotensin in solution and in membrane environments studied by 2â€D NMR spectroscopy. International Journal of Peptide and Protein Research, 1991, 37, 528-535. | 0.1 | 27 |
| 88 | The Assembly Motif of a Bacterial Small Multidrug Resistance Protein. Journal of Biological Chemistry, 2009, 284, 9870-9875. | 3.4 | 26 |
| 89 | Protein Structure in Membrane Domains. Annual Review of Biophysics, 2012, 41, 135-155. | 10.0 | 26 |
| 90 | 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 |

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| 91 | A minimal helical-hairpin motif provides molecular-level insights into misfolding and pharmacological rescue of CFTR. Communications Biology, 2018, 1, 154. | 4.4 | 25 |
| 92 | 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 |
| 93 | Self-association of the Transmembrane Domain of an Anthrax Toxin Receptor. Journal of Molecular Biology, 2006, 360, 145-156. | 4.2 | 23 |
| 94 | 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 |
| 95 | Cystic fibrosis transmembrane conductance regulator: expression and helicity of a double membrane-spanning segment. FEBS Letters, 1998, 431, 29-33. | 2.8 | 21 |
| 96 | Role of the Extracellular Loop in the Folding of a CFTR Transmembrane Helical Hairpin. Biochemistry, 2007, 46, 7099-7106. | 2.5 | 20 |
| 97 | 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 |
| 98 | Conformation of proline residues in bacteriorhodopsin. Biochemical and Biophysical Research Communications, 1990, 172, 862-869. | 2.1 | 19 |
| 99 | Functional Rescue of DeltaF508-CFTR by Peptides Designed to Mimic Sorting Motifs. Chemistry and Biology, 2009, 16, 520-530. | 6.0 | 19 |
| 100 | Positions of Polar Amino Acids Alter Interactions between Transmembrane Segments and Detergents. Biochemistry, 2011, 50, 3928-3935. | 2.5 | 19 |
| 101 | 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 |
| 102 | Peptide-Based Efflux Pump Inhibitors of the Small Multidrug Resistance Protein from Pseudomonas aeruginosa. Antimicrobial Agents and Chemotherapy, 2019, 63, . | 3.2 | 19 |
| 103 | Modulation of the Oligomerization of Myelin Proteolipid Protein by Transmembrane Helix Interaction Motifs. Biochemistry, 2010, 49, 6896-6902. | 2.5 | 18 |
| 104 | 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 |
| 105 | Aqueous solubility and membrane interactions of hydrophobic peptides with peptoid tags. Biopolymers, 2004, 76, 110-118. | 2.4 | 17 |
| 106 | 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 |
| 107 | Isosteric metal complexes of ionophore A23187. FEBS Letters, 1979, 105, 360-364. | 2.8 | 16 |
| 108 | Manipulation of peptide conformations by fine-tuning of the environment and/or the primary sequence. Biopolymers, 1995, 35, 667-675. | 2.4 | 16 |

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|---|---|---|---|
| 109 | Solubilization of Hydrophobic Peptides by Reversible Cysteine PEGylation. Biochemical and Biophysical Research Communications, 1998, 245, 618-621. | 2.1 | 16 |
| 110 | Peptide models for protein-mediated cation transport. Canadian Journal of Biochemistry, 1980, 58, 865-870. | 1.4 | 15 |
| 111 | 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 |
| 112 | Evidence for similar function of transmembrane segments in receptor and membrane-anchored proteins. Biopolymers, 1988, 27, 1171-1182. | 2.4 | 15 |
| 113 | Surface recognition elements of membrane protein oligomerization. Proteins: Structure, Function and Bioinformatics, 2008, 70, 786-793. | 2.6 | 15 |
| 114 | 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 |
| 115 | Membrane interactions of the hydrophobic segment of diacylglycerol kinase epsilon. Biochimica Et Biophysica Acta - Biomembranes, 2007, 1768, 2549-2558. | 2.6 | 14 |
| 116 | Membrane protein assembly patterns reflect selection for non-proliferative structures. FEBS Letters, 2007, 581, 1335-1341. | 2.8 | 13 |
| 117 | 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 |
| 118 | Loop Sequence Dictates the Secondary Structure of a Human Membrane Protein Hairpin. Biochemistry, 2013, 52, 2419-2426. | 2.5 | 13 |
| 119 | D-glucose binding increases secondary structure of human erythrocyte monosaccharide transport protein. Biochemical and Biophysical Research Communications, 1987, 145, 1087-1091. | 2.1 | 12 |
| 120 | Conformations of cyclic peptide/calcium complexes in solution. Biopolymers, 1982, 21, 169-179. | 2.4 | 11 |
| 121 | Novel Hydrophobic Standards for Membrane Protein Molecular Weight Determinations via Sodium Dodecyl Sulfateâˆ'Polyacrylamide Gel Electrophoresis. Biochemistry, 2010, 49, 10589-10591. | 2.5 | 11 |
| 122 | Deletion of a terminal residue disrupts oligomerization of a transmembrane Î±-helixThis paper is one of a selection of papers published in this special issue entitled â€œCanadian Society of Biochemistry, Molecular &amp; 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 |
| 123 | Uncoupling Amphipathicity and Hydrophobicity: Role of Charge Clustering in Membrane Interactions of Cationic Antimicrobial Peptides. Biochemistry, 2021, 60, 2586-2592. | 2.5 | 11 |
| 124 | Microheterogeneity of bovine myelin basic protein studied by nuclear magnetic resonance spectroscopy. Biopolymers, 1983, 22, 377-380. | 2.4 | 10 |
| 125 | Beta-branched residues adjacent to GG4 motifs promote the efficient association of glycophorin a transmembrane helices. Biopolymers, 2011, 96, 340-347. | 2.4 | 10 |
| 126 | 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 |

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| 127 | Relative role(s) of leucine versus isoleucine in the folding of membrane proteins. Peptide Science, 2019, 111, e24075. | 1.8 | 10 |
| 128 | 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 |
| 129 | The hydrophobicity threshold for peptide insertion into membranes. Current Topics in Membranes, 2002, 52, 465-479. | 0.9 | 9 |
| 130 | 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 |
| 131 | Sequence Hydropathy Dominates Membrane Protein Response to Detergent Solubilization. Biochemistry, 2012, 51, 6228-6237. | 2.5 | 9 |
| 132 | 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 |
| 133 | Peptide-Based Approach to Inhibition of the Multidrug Resistance Efflux Pump AcrB. Biochemistry, 2020, 59, 3973-3981. | 2.5 | 9 |
| 134 | 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 |
| 135 | Helicity of hydrophobic peptides in polar vs. non-polar environments. Physical Chemistry Chemical Physics, 1999, 1, 1539. | 2.8 | 8 |
| 136 | Transmembrane segment peptides with double D-amino acid replacements: Helicity, hydrophobicity, and antimicrobial activity. Biopolymers, 2003, 71, 77-84. | 2.4 | 8 |
| 137 | Functional response of the small multidrug resistance protein EmrE to mutations in transmembrane helix 2. FEBS Letters, 2014, 588, 3720-3725. | 2.8 | 7 |
| 138 | Helix-Helix Interactions: Is the Medium the Message?. Structure, 2015, 23, 437-438. | 3.3 | 7 |
| 139 | Evidence that the translocon may function as a hydropathy partitioning filter. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 1995-1998. | 2.6 | 5 |
| 140 | Converting a Marginally Hydrophobic Soluble Protein into a Membrane Protein. Journal of Molecular Biology, 2011, 407, 171-179. | 4.2 | 5 |
| 141 | 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 |
| 142 | Hydrophobic Blocks Facilitate Lipid Compatibility and Translocon Recognition of Transmembrane Protein Sequences. Biochemistry, 2015, 54, 1465-1473. | 2.5 | 5 |
| 143 | Structural effects of extracellular loop mutations in CFTR helical hairpins. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 1092-1098. | 2.6 | 5 |
| 144 | [4] Use of ionophores for manipulating intracellular ion concentrations. Methods in Neurosciences, 1995, 27, 52-68. | 0.5 | 4 |

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| 145 | Terminal Residue Hydrophobicity Modulates Transmembrane Helixâ€“Helix Interactions. Biochemistry, 2014, 53, 3747-3757. | 2.5 | 4 |
| 146 | Structural impact of proline mutations in the loop region of an ancestral membrane protein. Biopolymers, 2016, 106, 37-42. | 2.4 | 4 |
| 147 | Hydrophobic Clusters Raise the Threshold Hydrophilicity for Insertion of Transmembrane Sequences in Vivo. Biochemistry, 2016, 55, 5772-5779. | 2.5 | 4 |
| 148 | Modulating Transmembrane Î±-Helix Interactions through pH-Sensitive Boundary Residues. Biochemistry, 2016, 55, 4306-4315. | 2.5 | 4 |
| 149 | Heat treatment of thioredoxin fusions increases the purity of Î±â€helical transmembrane protein constructs. Protein Science, 2021, 30, 1974-1982. | 7.6 | 4 |
| 150 | The modulation of bovine milk d-galactosyltransferase by various phosphatidylethanolamines. Carbohydrate Research, 1986, 149, 47-58. | 2.3 | 3 |
| 151 | Design of Transmembrane Peptides: Coping with Sticky Situations. Methods in Molecular Biology, 2013, 1063, 197-210. | 0.9 | 3 |
| 152 | Design and Characterization of a Membrane Protein Unfolding Platform in Lipid Bilayers. PLoS ONE, 2015, 10, e0120253. | 2.5 | 3 |
| 153 | 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 |
| 154 | Design, expression, and purification of de novo transmembrane â€œhairpinâ€peptides. Biopolymers, 2012, 98, 546-556. | 2.4 | 2 |
| 155 | Deuterated Digoxin. Analytical Letters, 1989, 22, 2783-2790. | 1.8 | 1 |
| 156 | 3 Membrane protein folding in detergents. , 2011, , 23-46. |  | 1 |
| 157 | Protection or Destruction: The LL-37/HNP1 Cooperativity Switch. Biophysical Journal, 2020, 119, 2370-2371. | 0.5 | 1 |
| 158 | Defining the Defect in F508 del CFTR: A Soluble Problem?. Chemistry and Biology, 2008, 15, 3-4. | 6.0 | 0 |
| 159 | Mechanistic Insight into Peptide-Based Efflux Pump Inhibitors Against Pathogenic Bacteria. Biophysical Journal, 2021, 120, 74a. | 0.5 | 0 |
| 160 | Peptide-Based Inhibition of AcrB Efflux Activity. Biophysical Journal, 2021, 120, 70a. | 0.5 | 0 |