William F Degrado

List of Publications by Citations

268 papers	21,349 citations	80 h-index	140 g-index
285 ext. papers	23,418 ext. citations	10.8 avg, IF	6.84 L-index

#	Paper	IF	Citations
268	beta-Peptides: from structure to function. *Chemical Reviews*, **2001**, 101, 3219-32	68.1	1633
267	Design and synthesis of multi-haem proteins. *Nature*, **1994**, 368, 425-32	50.4	535
266	De novo design and structural characterization of proteins and metalloproteins. *Annual Review of Biochemistry*, **1999**, 68, 779-819	29.1	529
265	Structure of the amantadine binding site of influenza M2 proton channels in lipid bilayers. *Nature*, **2010**, 463, 689-92	50.4	519
264	Structural basis for the function and inhibition of an influenza virus proton channel. *Nature*, **2008**, 451, 596-9	50.4	501
263	De novo design of antimicrobial polymers, foldamers, and small molecules: from discovery to practical applications. *Accounts of Chemical Research*, **2010**, 43, 30-9	24.3	447
262	De novo design of biomimetic antimicrobial polymers. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 5110-4	11.5	387
261	Folding of helical membrane proteins: the role of polar, GxxxG-like and proline motifs. *Current Opinion in Structural Biology*, **2004**, 14, 465-79	8.1	368
260	Short peptides self-assemble to produce catalytic amyloids. *Nature Chemistry*, **2014**, 6, 303-9	17.6	364
259	De Novo Design of Antibacterial β-Peptides. *Journal of the American Chemical Society*, **1999**, 121, 12200-12201	16.4	325
258	Asparagine-mediated self-association of a model transmembrane helix. *Nature Structural Biology*, **2000**, 7, 161-6		311
257	De novo design, synthesis, and characterization of antimicrobial beta-peptides. *Journal of the American Chemical Society*, **2001**, 123, 7553-9	16.4	303
256	Using nitrile-derivatized amino acids as infrared probes of local environment. *Journal of the American Chemical Society*, **2003**, 125, 405-11	16.4	278
255	De novo design of helical bundles as models for understanding protein folding and function. *Accounts of Chemical Research*, **2000**, 33, 745-54	24.3	274
254	Activation of integrin alphaIIbbeta3 by modulation of transmembrane helix associations. *Science*, **2003**, 300, 795-8	33.3	270
253	Design of a 4-helix bundle protein: synthesis of peptides which self-associate into a helical protein. *Journal of the American Chemical Society*, **1987**, 109, 6751-6758	16.4	265
252	De novo design and in vivo activity of conformationally restrained antimicrobial arylamide foldamers. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 6968-73	11.5	253

251	Computational design of peptides that target transmembrane helices. *Science*, **2007**, 315, 1817-22	33.3	240
250	Design of peptides and proteins. *Advances in Protein Chemistry*, **1988**, 39, 51-124		240
249	The role of hydrophobicity in the antimicrobial and hemolytic activities of polymethacrylate derivatives. *Chemistry - A European Journal*, **2009**, 15, 1123-33	4.8	236
248	Design of a heme-binding four-helix bundle. *Journal of the American Chemical Society*, **1994**, 116, 856-865	16.4	236
247	De novo design of a transmembrane Zn□+-transporting four-helix bundle. *Science*, **2014**, 346, 1520-4	33.3	220
246	Salt bridges: geometrically specific, designable interactions. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 898-915	4.2	212
245	Structure and mechanism of proton transport through the transmembrane tetrameric M2 protein bundle of the influenza A virus. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 15075-80	11.5	208
244	Development of □helical calpain probes by mimicking a natural protein-protein interaction. *Journal of the American Chemical Society*, **2012**, 134, 17704-13	16.4	205
243	Helix formation via conformation diffusion search. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 2788-93	11.5	204
242	Self-assembling dipeptide antibacterial nanostructures with membrane disrupting activity. *Nature Communications*, **2017**, 8, 1365	17.4	200
241	Synthetic peptides as models for ion channel proteins. *Accounts of Chemical Research*, **1993**, 26, 191-197	24.3	191
240	Nontoxic membrane-active antimicrobial arylamide oligomers. *Angewandte Chemie - International Edition*, **2004**, 43, 1158-62	16.4	189
239	Computational design of virus-like protein assemblies on carbon nanotube surfaces. *Science*, **2011**, 332, 1071-6	33.3	178
238	The □□1 integrin plays a critical in vivo role in tissue fibrosis. *Science Translational Medicine*, **2015**, 7, 288ra79	17.5	174
237	Structure and inhibition of the drug-resistant S31N mutant of the M2 ion channel of influenza A virus. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 1315-20	11.5	167
236	Design, synthesis, and characterization of a cytotoxic peptide with melittin-like activity. *Journal of the American Chemical Society*, **1981**, 103, 679-681	16.4	159
235	Signal transduction in histidine kinases: insights from new structures. *Structure*, **2015**, 23, 981-94	5.2	154
234	De novo designed synthetic mimics of antimicrobial peptides. *Current Opinion in Biotechnology*, **2008**, 19, 620-7	11.4	154

233	Probing designability via a generalized model of helical bundle geometry. *Journal of Molecular Biology*, **2011**, 405, 1079-100	6.5	152
232	An artificial di-iron oxo-protein with phenol oxidase activity. *Nature Chemical Biology*, **2009**, 5, 882-4	11.7	152
231	Computational de novo design and characterization of a four-helix bundle protein that selectively binds a nonbiological cofactor. *Journal of the American Chemical Society*, **2005**, 127, 1346-7	16.4	152
230	De Novo Design of Mercury-Binding Two- and Three-Helical Bundles. *Journal of the American Chemical Society*, **1997**, 119, 6195-6196	16.4	146
229	How do helix-helix interactions help determine the folds of membrane proteins? Perspectives from the study of homo-oligomeric helical bundles. *Protein Science*, **2003**, 12, 647-65	6.3	145
228	pH-dependent tetramerization and amantadine binding of the transmembrane helix of M2 from the influenza A virus. *Biochemistry*, **2000**, 39, 14160-70	3.2	145
227	Protein-protein interactions in the membrane: sequence, structural, and biological motifs. *Structure* , **2008**, 16, 991-1001	5.2	140
226	Computational design of a protein crystal. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 7304-9	11.5	138
225	Tetraphilin: a four-helix proton channel built on a tetraphenylporphyrin framework. *Journal of the American Chemical Society*, **1992**, 114, 9656-9657	16.4	138
224	The hydration of amides in helices; a comprehensive picture from molecular dynamics, IR, and NMR. *Protein Science*, **2003**, 12, 520-31	6.3	136
223	Identification of the functional core of the influenza A virus A/M2 proton-selective ion channel. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 12283-8	11.5	135
222	Pump/probe self heterodyned 2D spectroscopy of vibrational transitions of a small globular peptide. *Journal of Chemical Physics*, **2000**, 112, 1907-1916	3.9	135
221	Solution Structure of 2D, a Nativelike de Novo Designed Protein. *Journal of the American Chemical Society*, **1998**, 120, 1138-1145	16.4	132
220	Temperature-dependent helix-coil transition of an alanine based peptide. *Journal of the American Chemical Society*, **2001**, 123, 9235-8	16.4	131
219	E(z), a depth-dependent potential for assessing the energies of insertion of amino acid side-chains into membranes: derivation and applications to determining the orientation of transmembrane and interfacial helices. *Journal of Molecular Biology*, **2007**, 366, 436-48	6.5	130
218	The crystal structure of the designed trimeric coiled coil coil-VaLd: implications for engineering crystals and supramolecular assemblies. *Protein Science*, **1997**, 6, 80-8	6.3	128
217	Use of thiol-disulfide equilibria to measure the energetics of assembly of transmembrane helices in phospholipid bilayers. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 14772-7	11.5	126
216	From coiled coils to small globular proteins: design of a native-like three-helix bundle. *Protein Science*, **1998**, 7, 1404-14	6.3	125

215	Distinct synthetic A□prion strains producing different amyloid deposits in bigenic mice. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 10329-34	11.5	124
214	Computational design and characterization of a monomeric helical dinuclear metalloprotein. *Journal of Molecular Biology*, **2003**, 334, 1101-15	6.5	119
213	Computational de novo design, and characterization of an A(2)B(2) diiron protein. *Journal of Molecular Biology*, **2002**, 321, 923-38	6.5	119
212	The role of protonation and metal chelation preferences in defining the properties of mercury-binding coiled coils. *Journal of Molecular Biology*, **1998**, 280, 897-912	6.5	115
211	De novo design of a redox-active minimal rubredoxin mimic. *Journal of the American Chemical Society*, **2005**, 127, 5804-5	16.4	114
210	Comparative mechanistic studies of brilacidin, daptomycin, and the antimicrobial peptide LL16. *Antimicrobial Agents and Chemotherapy*, **2014**, 58, 5136-45	5.9	113
209	A push-pull mechanism for regulating integrin function. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 1424-9	11.5	112
208	Controlling topology and native-like behavior of de novo-designed peptides: design and characterization of antiparallel four-stranded coiled coils. *Biochemistry*, **1996**, 35, 6955-62	3.2	110
207	Molecular dynamics simulation directed rational design of inhibitors targeting drug-resistant mutants of influenza A virus M2. *Journal of the American Chemical Society*, **2011**, 133, 12834-41	16.4	109
206	Toward the Synthesis of a Photosynthetic Reaction Center Maquette: A Cofacial Porphyrin Pair Assembled between Two Subunits of a Synthetic Four-Helix Bundle Multiheme Protein. *Journal of the American Chemical Society*, **1996**, 118, 473-474	16.4	106
205	Molecular dynamics calculations suggest a conduction mechanism for the M2 proton channel from influenza A virus. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 1069-74	11.5	103
204	Structural basis for proton conduction and inhibition by the influenza M2 protein. *Protein Science*, **2012**, 21, 1620-33	6.3	101
203	Alteration of the oxygen-dependent reactivity of de novo Due Ferri proteins. *Nature Chemistry*, **2012**, 4, 900-6	17.6	100
202	De novo design and molecular assembly of a transmembrane diporphyrin-binding protein complex. *Journal of the American Chemical Society*, **2010**, 132, 15516-8	16.4	99
201	Functional studies and modeling of pore-lining residue mutants of the influenza a virus M2 ion channel. *Biochemistry*, **2010**, 49, 696-708	3.2	99
200	A de Novo Designed Protein Mimics the Native State of Natural Proteins. *Journal of the American Chemical Society*, **1995**, 117, 7558-7559	16.4	95
199	Toward the de novo design of a catalytically active helix bundle: a substrate-accessible carboxylate-bridged dinuclear metal center. *Journal of the American Chemical Society*, **2001**, 123, 12749-57	16.4	92
198	Specific binding of adamantane drugs and direction of their polar amines in the pore of the influenza M2 transmembrane domain in lipid bilayers and dodecylphosphocholine micelles determined by NMR spectroscopy. *Journal of the American Chemical Society*, **2011**, 133, 4274-84	16.4	88

197	The role of helix formation in the folding of a fully alpha-helical coiled coil. *Proteins: Structure, Function and Bioinformatics*, **1996**, 24, 427-32	4.2	88
196	Tidal surge in the M2 proton channel, sensed by 2D IR spectroscopy. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 6115-20	11.5	85
195	Catalytic efficiency of designed catalytic proteins. *Current Opinion in Structural Biology*, **2014**, 27, 113-21	8.1	84
194	The conformation of the pore region of the M2 proton channel depends on lipid bilayer environment. *Protein Science*, **2005**, 14, 856-61	6.3	84
193	Cys-scanning disulfide crosslinking and bayesian modeling probe the transmembrane signaling mechanism of the histidine kinase, PhoQ. *Structure*, **2014**, 22, 1239-1251	5.2	83
192	De novo design of native proteins: characterization of proteins intended to fold into antiparallel, rop-like, four-helix bundles. *Biochemistry*, **1997**, 36, 2450-8	3.2	83
191	Thermodynamic analysis of a designed three-stranded coiled coil. *Biochemistry*, **1996**, 35, 14480-5	3.2	81
190	Influenza virus A M2 protein generates negative Gaussian membrane curvature necessary for budding and scission. *Journal of the American Chemical Society*, **2013**, 135, 13710-9	16.4	80
189	De novo design of a single-chain diphenylporphyrin metalloprotein. *Journal of the American Chemical Society*, **2007**, 129, 10732-40	16.4	80
188	Characterization of nonbiological antimicrobial polymers in aqueous solution and at water-lipid interfaces from all-atom molecular dynamics. *Journal of the American Chemical Society*, **2006**, 128, 1778-9	16.4	77
187	Zinc-binding structure of a catalytic amyloid from solid-state NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 6191-6196	11.5	71
186	Small-molecule inhibitors of integrin alpha2beta1 that prevent pathological thrombus formation via an allosteric mechanism. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 719-24	11.5	70
185	Molecular Motions and Protein Folding: Characterization of the Backbone Dynamics and Folding Equilibrium of 2D Using 13C NMR Spin Relaxation. *Journal of the American Chemical Society*, **2000**, 122, 11610-11619	16.4	70
184	Stimulated Photon Echoes from Amide I Vibrations. *Journal of Physical Chemistry A*, **1999**, 103, 10049-10053	2.8	70
183	Structural heterogeneity and intersubject variability of A in familial and sporadic Alzheimer disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E782-E791	11.5	69
182	Design of a three-helix bundle capable of binding heavy metals in a triscysteine environment. *Angewandte Chemie - International Edition*, **2011**, 50, 2049-53	16.4	69
181	De novo design of a D2-symmetrical protein that reproduces the diheme four-helix bundle in cytochrome bc1. *Journal of the American Chemical Society*, **2004**, 126, 8141-7	16.4	69
180	Proton and cation transport activity of the M2 proton channel from influenza A virus. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 15409-14	11.5	67

179	A Designed Buried Salt Bridge in a Heterodimeric Coiled Coil. *Journal of the American Chemical Society*, **1997**, 119, 5742-5743	16.4	67
178	Preorganization of molecular binding sites in designed diiron proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 3772-7	11.5	67
177	Exploration of the structural features defining the conduction properties of a synthetic ion channel. *Biophysical Journal*, **1999**, 76, 618-30	2.9	67
176	De Novo Design of Four-Helix Bundle Metalloproteins: One Scaffold, Diverse Reactivities. *Accounts of Chemical Research*, **2019**, 52, 1148-1159	24.3	66
175	protein design, a retrospective. *Quarterly Reviews of Biophysics*, **2020**, 53, e3	7	66
174	High-resolution structures of the M2 channel from influenza A virus reveal dynamic pathways for proton stabilization and transduction. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 14260-5	11.5	65
173	Consensus motif for integrin transmembrane helix association. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 703-8	11.5	65
172	Position-dependence of stabilizing polar interactions of asparagine in transmembrane helical bundles. *Biochemistry*, **2003**, 42, 6400-7	3.2	65
171	Antibacterial mechanism of action of arylamide foldamers. *Antimicrobial Agents and Chemotherapy*, **2011**, 55, 5043-53	5.9	64
170	Exploring the size limit of templates for inhibitors of the M2 ion channel of influenza A virus. *Journal of Medicinal Chemistry*, **2011**, 54, 2646-57	8.3	64
169	Flipping in the pore: discovery of dual inhibitors that bind in different orientations to the wild-type versus the amantadine-resistant S31N mutant of the influenza A virus M2 proton channel. *Journal of the American Chemical Society*, **2014**, 136, 17987-95	16.4	63
168	Sequence determinants of the energetics of folding of a transmembrane four-helix-bundle protein. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 8568-72	11.5	63
167	Water Distribution, Dynamics, and Interactions with Alzheimer□Amyloid Fibrils Investigated by Solid-State NMR. *Journal of the American Chemical Society*, **2017**, 139, 6242-6252	16.4	61
166	Blue fluorescent amino acid for biological spectroscopy and microscopy. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 6005-6009	11.5	61
165	Structural Polymorphism of Alzheimer□Amyloid Fibrils as Controlled by an E22 Switch: A Solid-State NMR Study. *Journal of the American Chemical Society*, **2016**, 138, 9840-52	16.4	61
164	De novo design of a hyperstable non-natural protein-ligand complex with sub-□accuracy. *Nature Chemistry*, **2017**, 9, 1157-1164	17.6	60
163	Transmembrane orientation and possible role of the fusogenic peptide from parainfluenza virus 5 (PIV5) in promoting fusion. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 3958-63	11.5	60
162	Length Dependent Helix-Coil Transition Kinetics of Nine Alanine-Based Peptides. *Journal of Physical Chemistry B*, **2004**, 108,	3.4	60

161	Knowledge-based potential for positioning membrane-associated structures and assessing residue-specific energetic contributions. *Structure*, **2012**, 20, 924-35	5.2	58
160	Noncovalent self-assembly of a heterotetrameric diiron protein. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 5150-4	11.5	58
159	Sequence determinants of a transmembrane proton channel: an inverse relationship between stability and function. *Journal of Molecular Biology*, **2005**, 347, 169-79	6.5	57
158	Tertiary templates for the design of diiron proteins. *Current Opinion in Structural Biology*, **1999**, 9, 500-8	8.1	57
157	Computationally designed peptide inhibitors of protein-protein interactions in membranes. *Biochemistry*, **2008**, 47, 8600-6	3.2	56
156	A and tau prion-like activities decline with longevity in the Alzheimer disease human brain. *Science Translational Medicine*, **2019**, 11,	17.5	55
155	Actionable Activating Oncogenic ERBB2/HER2 Transmembrane and Juxtamembrane Domain Mutations. *Cancer Cell*, **2018**, 34, 792-806.e5	24.3	55
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152	Analysis and design of turns in alpha-helical hairpins. *Journal of Molecular Biology*, **2005**, 346, 1441-54	6.5	53
151	High-density grids for efficient data collection from multiple crystals. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 2-11	5.5	52
150	Analysis and design of three-stranded coiled coils and three-helix bundles. *Folding & Design*, **1998**, 3, R29-40		52
149	Acid activation mechanism of the influenza A M2 proton channel. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E6955-E6964	11.5	51
148	Inhibitors of the M2 Proton Channel Engage and Disrupt Transmembrane Networks of Hydrogen-Bonded Waters. *Journal of the American Chemical Society*, **2018**, 140, 15219-15226	16.4	51
147	Artificial Diiron Enzymes with a De Novo Designed Four-Helix Bundle Structure. *European Journal of Inorganic Chemistry*, **2015**, 2015, 3371-3390	2.3	50
146	Computational design and elaboration of a de novo heterotetrameric alpha-helical protein that selectively binds an emissive abiological (porphinato)zinc chromophore. *Journal of the American Chemical Society*, **2010**, 132, 3997-4005	16.4	50
145	Proton and metal ion-dependent assembly of a model diiron protein. *Protein Science*, **2001**, 10, 958-69	6.3	50
144	Computational design of a -peptide that targets transmembrane helices. *Journal of the American Chemical Society*, **2011**, 133, 12378-81	16.4	49

143	The interplay of functional tuning, drug resistance, and thermodynamic stability in the evolution of the M2 proton channel from the influenza A virus. *Structure*, **2008**, 16, 1067-76	5.2	48
142	Probing Membrane Insertion Activity of Antimicrobial Polymers via Coarse-grain Molecular Dynamics. *Journal of Chemical Theory and Computation*, **2006**, 2, 649-655	6.4	48
141	Characterization of a membrane protein folding motif, the Ser zipper, using designed peptides. *Journal of Molecular Biology*, **2006**, 359, 930-9	6.5	48
140	Sliding helix and change of coordination geometry in a model di-MnII protein. *Angewandte Chemie - International Edition*, **2003**, 42, 417-20	16.4	48
139	Protein-directed self-assembly of a fullerene crystal. *Nature Communications*, **2016**, 7, 11429	17.4	47
138	A 31-residue peptide induces aggregation of tau's microtubule-binding region in cells. *Nature Chemistry*, **2017**, 9, 874-881	17.6	46
137	The membrane- and soluble-protein helix-helix interactome: similar geometry via different interactions. *Structure*, **2015**, 23, 527-541	5.2	46
136	Computational de novo design and characterization of a protein that selectively binds a highly hyperpolarizable abiological chromophore. *Journal of the American Chemical Society*, **2013**, 135, 13914-26	16.4	46
135	XFEL structures of the influenza M2 proton channel: Room temperature water networks and insights into proton conduction. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 13357-13362	11.5	45
134	Spontaneous and specific chemical cross-linking in live cells to capture and identify protein interactions. *Nature Communications*, **2017**, 8, 2240	17.4	45
133	De novo design of covalently constrained mesosize protein scaffolds with unique tertiary structures. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 10852-10857	11.5	44
132	In vitro 0N4R tau fibrils contain a monomorphic β-sheet core enclosed by dynamically heterogeneous fuzzy coat segments. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 16357-16366	11.5	44
131	Exploring the Requirements for the Hydrophobic Scaffold and Polar Amine in inhibitors of M2 from Influenza A Virus. *ACS Medicinal Chemistry Letters*, **2011**, 2, 307-312	4.3	44
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127	Discovery of Highly Potent Inhibitors Targeting the Predominant Drug-Resistant S31N Mutant of the Influenza A Virus M2 Proton Channel. *Journal of Medicinal Chemistry*, **2016**, 59, 1207-16	8.3	40
126	Inhibitors of the influenza A virus M2 proton channel discovered using a high-throughput yeast growth restoration assay. *PLoS ONE*, **2013**, 8, e55271	3.7	40

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121	De novo design of heterotrimeric coiled coils **1996**, 40, 495-504		38
120	Proximity-enhanced SuFEx chemical cross-linker for specific and multitargeting cross-linking mass spectrometry. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 11162-11167	11.5	38
119	Designed peptides that assemble into cross-β amyloid-like structures. *Nature Chemical Biology*, **2018**, 14, 870-875	11.7	37
118	From synthetic coiled coils to functional proteins: automated design of a receptor for the calmodulin-binding domain of calcineurin. *Journal of Molecular Biology*, **1998**, 281, 379-91	6.5	37
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115	The structure of a designed diiron(III) protein: implications for cofactor stabilization and catalysis. *Angewandte Chemie - International Edition*, **2006**, 45, 4951-4	16.4	33
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112	The Design of Efficient α-Helical C-Capping Auxiliaries. *Journal of the American Chemical Society*, **1998**, 120, 2764-2767	16.4	30
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110	Experimental and computational evaluation of forces directing the association of transmembrane helices. *Journal of the American Chemical Society*, **2009**, 131, 11341-3	16.4	29
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106	Artificial di-iron proteins: solution characterization of four helix bundles containing two distinct types of inter-helical loops. *Journal of Biological Inorganic Chemistry*, **2005**, 10, 539-49	3.7	28
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104	Asp44 stabilizes the Trp41 gate of the M2 proton channel of influenza A virus. *Structure*, **2013**, 21, 2033-41	5.2	27
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