

William F Degrado

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/9453040/william-f-degrado-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

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	Soluble TREM2 inhibits secondary nucleation of A β fibrillization and enhances cellular uptake of fibrillar A β . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	2
267	Brilacidin, a COVID-19 Drug Candidate, demonstrates broad-spectrum antiviral activity against human coronaviruses OC43, 229E and NL63 through targeting both the virus and the host cell.. <i>Journal of Medical Virology</i> , 2022 ,	19.7	4
266	De novo metalloprotein design. <i>Nature Reviews Chemistry</i> , 2022 , 6, 31-50	34.6	2
265	Spiers Memorial Lecture: Analysis and design of membrane-interactive peptides. <i>Faraday Discussions</i> , 2021 ,	3.6	1
264	Design, Solution Characterization, and Crystallographic Structure of an Abiological Mn-Porphyrin-Binding Protein Capable of Stabilizing a Mn(V) Species. <i>Journal of the American Chemical Society</i> , 2021 , 143, 252-259	16.4	2
263	Protein design-scapes generated by microfluidic DNA assembly elucidate domain coupling in the bacterial histidine kinase CpxA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
262	Visualization of Platelet Integrins via Two-Photon Microscopy Using Anti-transmembrane Domain Peptides Containing a Blue Fluorescent Amino Acid. <i>Biochemistry</i> , 2021 , 60, 1722-1730	3.2	0
261	Constructing ion channels from water-soluble β helical barrels. <i>Nature Chemistry</i> , 2021 , 13, 643-650	17.6	14
260	Inclusion of the C-Terminal Domain in the β -Sheet Core of Heparin-Fibrillized Three-Repeat Tau Protein Revealed by Solid-State Nuclear Magnetic Resonance Spectroscopy. <i>Journal of the American Chemical Society</i> , 2021 , 143, 7839-7851	16.4	4
259	Elucidation of the molecular interactions that enable stable assembly and structural diversity in multicomponent immune receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
258	Acyl Transfer Catalytic Activity in De Novo Designed Protein with N-Terminus of β -Helix As Oxyanion-Binding Site. <i>Journal of the American Chemical Society</i> , 2021 , 143, 3330-3339	16.4	4
257	Rimantadine Binds to and Inhibits the Influenza A M2 Proton Channel without Enantiomeric Specificity. <i>Biochemistry</i> , 2021 ,	3.2	3
256	Cleavage of talin by calpain promotes platelet-mediated fibrin clot contraction. <i>Blood Advances</i> , 2021 , 5, 4901-4909	7.8	0
255	Emergence of distinct and heterogeneous strains of amyloid beta with advanced Alzheimer's disease pathology in Down syndrome.. <i>Acta Neuropathologica Communications</i> , 2021 , 9, 201	7.3	0
254	Platform to Discover Protease-Activated Antibiotics and Application to Siderophore-Antibiotic Conjugates. <i>Journal of the American Chemical Society</i> , 2020 , 142, 21310-21321	16.4	8
253	Deep mutational scanning reveals the structural basis for β synuclein activity. <i>Nature Chemical Biology</i> , 2020 , 16, 653-659	11.7	27
252	protein design, a retrospective. <i>Quarterly Reviews of Biophysics</i> , 2020 , 53, e3	7	66

251	X-ray Crystal Structures of the Influenza M2 Proton Channel Drug-Resistant V27A Mutant Bound to a Spiro-Adamantyl Amine Inhibitor Reveal the Mechanism of Adamantane Resistance. <i>Biochemistry</i> , 2020 , 59, 627-634	3.2	12
250	Dual antagonists of β_1/α_1 integrin for airway hyperresponsiveness. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2020 , 30, 127578	2.9	1
249	Robust Sequence Determinants of β Synuclein Toxicity in Yeast Implicate Membrane Binding. <i>ACS Chemical Biology</i> , 2020 , 15, 2137-2153	4.9	3
248	A defined structural unit enables de novo design of small-molecule-binding proteins. <i>Science</i> , 2020 , 369, 1227-1233	33.3	24
247	Prion biology: implications for Alzheimer's disease therapeutics. <i>Lancet Neurology</i> , 2020 , 19, 802-803	4.1	4
246	Influenza A M2 Inhibitor Binding Understood through Mechanisms of Excess Proton Stabilization and Channel Dynamics. <i>Journal of the American Chemical Society</i> , 2020 , 142, 17425-17433	16.4	9
245	Allosteric cooperation in a de novo-designed two-domain protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 33246-33253	11.5	15
244	Exposing the Nucleation Site in β -Helix Folding: A Joint Experimental and Simulation Study. <i>Journal of Physical Chemistry B</i> , 2019 , 123, 1797-1807	3.4	8
243	Unique transmembrane domain interactions differentially modulate integrin $\alpha_3\beta_1$ and $\alpha_5\beta_1$ function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 12295-12300	11.5	10
242	X-ray Crystal Structure of the Influenza A M2 Proton Channel S31N Mutant in Two Conformational States: An Open and Shut Case. <i>Journal of the American Chemical Society</i> , 2019 , 141, 11481-11488	16.4	11
241	α and tau prion-like activities decline with longevity in the Alzheimer's disease human brain. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	55
240	Glutamine Side Chain C=O as a Nonperturbative IR Probe of Amyloid Fibril Hydration and Assembly. <i>Journal of the American Chemical Society</i> , 2019 , 141, 7320-7326	16.4	10
239	4-Cyanoindole-2'-deoxyribonucleoside as a Dual Fluorescence and Infrared Probe of DNA Structure and Dynamics. <i>Molecules</i> , 2019 , 24,	4.8	4
238	SNAC-tag for sequence-specific chemical protein cleavage. <i>Nature Methods</i> , 2019 , 16, 319-322	21.6	13
237	Packing of apolar side chains enables accurate design of highly stable membrane proteins. <i>Science</i> , 2019 , 363, 1418-1423	33.3	53
236	De Novo Design of Four-Helix Bundle Metalloproteins: One Scaffold, Diverse Reactivities. <i>Accounts of Chemical Research</i> , 2019 , 52, 1148-1159	24.3	66
235	In vitro 0N4R tau fibrils contain a monomorphic β -sheet core enclosed by dynamically heterogeneous fuzzy coat segments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16357-16366	11.5	44
234	Proton-Induced Conformational and Hydration Dynamics in the Influenza A M2 Channel. <i>Journal of the American Chemical Society</i> , 2019 , 141, 11667-11676	16.4	12

233	Modulating Integrin α β Activity through Mutagenesis of Allosterically Regulated Intersubunit Contacts. <i>Biochemistry</i> , 2019 , 58, 3251-3259	3.2	5
232	A disease-associated mutation in fibrillin-1 differentially regulates integrin-mediated cell adhesion. <i>Journal of Biological Chemistry</i> , 2019 , 294, 18232-18243	5.4	5
231	De novo design of a homo-trimeric amantadine-binding protein. <i>ELife</i> , 2019 , 8,	8.9	10
230	Direct Visualization of Platelet Integrins Using ANTI-Transmembrane Domain Peptides Containing a BLUE Fluorescent Amino Acid. <i>Blood</i> , 2019 , 134, 2344-2344	2.2	
229	Design of a Short Thermally Stable α Helix Embedded in a Macrocyclic. <i>ChemBioChem</i> , 2018 , 19, 902-906	3.8	8
228	De Novo Design of Tetranuclear Transition Metal Clusters Stabilized by Hydrogen-Bonded Networks in Helical Bundles. <i>Journal of the American Chemical Society</i> , 2018 , 140, 1294-1304	16.4	28
227	Structural heterogeneity and intersubject variability of A β in familial and sporadic Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E782-E791	11.5	69
226	A long-lived A β oligomer resistant to fibrillization. <i>Biopolymers</i> , 2018 , 109, e23096	2.2	17
225	Designed peptides that assemble into cross- β amyloid-like structures. <i>Nature Chemical Biology</i> , 2018 , 14, 870-875	11.7	37
224	De novo designed transmembrane peptides activating the β α integrin. <i>Protein Engineering, Design and Selection</i> , 2018 , 31, 181-190	1.9	8
223	Entry from the Lipid Bilayer: A Possible Pathway for Inhibition of a Peptide G Protein-Coupled Receptor by a Lipophilic Small Molecule. <i>Biochemistry</i> , 2018 , 57, 5748-5758	3.2	16
222	Building and Breaking Bonds via a Compact S-Propargyl-Cysteine to Chemically Control Enzymes and Modify Proteins. <i>Angewandte Chemie</i> , 2018 , 130, 12884-12888	3.6	1
221	Building and Breaking Bonds via a Compact S-Propargyl-Cysteine to Chemically Control Enzymes and Modify Proteins. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 12702-12706	16.4	9
220	Active Calpain Promotes Fibrin Clot Contraction By Strengthening the Coupling of Fibrin-Bound α β to the Platelet Cytoskeleton. <i>Blood</i> , 2018 , 132, 1128-1128	2.2	
219	Actionable Activating Oncogenic ERBB2/HER2 Transmembrane and Juxtamembrane Domain Mutations. <i>Cancer Cell</i> , 2018 , 34, 792-806.e5	24.3	55
218	Proximity-enhanced SuFEx chemical cross-linker for specific and multitargeting cross-linking mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 11162-11167	11.5	38
217	Spectroscopic and metal binding properties of a de novo metalloprotein binding a tetrazinc cluster. <i>Biopolymers</i> , 2018 , 109, e23339	2.2	11
216	Inhibitors of the M2 Proton Channel Engage and Disrupt Transmembrane Networks of Hydrogen-Bonded Waters. <i>Journal of the American Chemical Society</i> , 2018 , 140, 15219-15226	16.4	51

215	Peptide-Programmable Nanoparticle Superstructures with Tailored Electrocatalytic Activity. <i>ACS Nano</i> , 2018 , 12, 6554-6562	16.7	12
214	Structure and Function of the Transmembrane Domain of NsaS, an Antibiotic Sensing Histidine Kinase in <i>Staphylococcus aureus</i> . <i>Journal of the American Chemical Society</i> , 2018 , 140, 7471-7485	16.4	13
213	An M2-V27A channel blocker demonstrates potent <i>in vitro</i> and <i>in vivo</i> antiviral activities against amantadine-sensitive and -resistant influenza A viruses. <i>Antiviral Research</i> , 2017 , 140, 45-54	10.8	32
212	Pharmacologic Blockade of α_1 Integrin Ameliorates Renal Failure and Fibrosis. <i>Journal of the American Society of Nephrology: JASN</i> , 2017 , 28, 1998-2005	12.7	39
211	Water Distribution, Dynamics, and Interactions with Alzheimer β -Amyloid Fibrils Investigated by Solid-State NMR. <i>Journal of the American Chemical Society</i> , 2017 , 139, 6242-6252	16.4	61
210	Activation pH and Gating Dynamics of Influenza A M2 Proton Channel Revealed by Single-Molecule Spectroscopy. <i>Angewandte Chemie</i> , 2017 , 129, 5367-5371	3.6	
209	Stapled Voltage-Gated Calcium Channel (Ca β) Interaction Domain (AID) Peptides Act As Selective Protein-Protein Interaction Inhibitors of Ca β Function. <i>ACS Chemical Neuroscience</i> , 2017 , 8, 1313-1326	5.7	23
208	Design of self-assembling transmembrane helical bundles to elucidate principles required for membrane protein folding and ion transport. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	17
207	Blue fluorescent amino acid for biological spectroscopy and microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 6005-6009	11.5	61
206	Zinc-binding structure of a catalytic amyloid from solid-state NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 6191-6196	11.5	71
205	A 31-residue peptide induces aggregation of tau β microtubule-binding region in cells. <i>Nature Chemistry</i> , 2017 , 9, 874-881	17.6	46
204	Activation pH and Gating Dynamics of Influenza A M2 Proton Channel Revealed by Single-Molecule Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 5283-5287	16.4	6
203	The accommodation index measures the perturbation associated with insertions and deletions in coiled-coils: Application to understand signaling in histidine kinases. <i>Protein Science</i> , 2017 , 26, 414-435	6.3	20
202	De novo design of covalently constrained mesosize protein scaffolds with unique tertiary structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 10852-10857	11.5	44
201	XFEL structures of the influenza M2 proton channel: Room temperature water networks and insights into proton conduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 13357-13362	11.5	45
200	De novo design of a hyperstable non-natural protein-ligand complex with sub- \AA accuracy. <i>Nature Chemistry</i> , 2017 , 9, 1157-1164	17.6	60
199	Self-assembling dipeptide antibacterial nanostructures with membrane disrupting activity. <i>Nature Communications</i> , 2017 , 8, 1365	17.4	200
198	Spontaneous and specific chemical cross-linking in live cells to capture and identify protein interactions. <i>Nature Communications</i> , 2017 , 8, 2240	17.4	45

197	Exploring α -Arylsulfonyl-L-proline Scaffold as a Platform for Potent and Selective α 1 Integrin Inhibitors. <i>ACS Medicinal Chemistry Letters</i> , 2016 , 7, 902-907	4.3	17
196	Structural Polymorphism of Alzheimer's β -Amyloid Fibrils as Controlled by an E22 Switch: A Solid-State NMR Study. <i>Journal of the American Chemical Society</i> , 2016 , 138, 9840-52	16.4	61
195	Protein-directed self-assembly of a fullerene crystal. <i>Nature Communications</i> , 2016 , 7, 11429	17.4	47
194	Acid activation mechanism of the influenza A M2 proton channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E6955-E6964	11.5	51
193	High-density grids for efficient data collection from multiple crystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 2-11	5.5	52
192	Photoactivatable protein labeling by singlet oxygen mediated reactions. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2016 , 26, 3359-3363	2.9	20
191	Graphene Symmetry Amplified by Designed Peptide Self-Assembly. <i>Biophysical Journal</i> , 2016 , 110, 2507-2516	25.16	23
190	Discovery of Highly Potent Inhibitors Targeting the Predominant Drug-Resistant S31N Mutant of the Influenza A Virus M2 Proton Channel. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 1207-16	8.3	40
189	Designed metalloprotein stabilizes a semiquinone radical. <i>Nature Chemistry</i> , 2016 , 8, 354-9	17.6	53
188	Crystal structure of the drug-resistant S31N influenza M2 proton channel. <i>Protein Science</i> , 2016 , 25, 1551-4	15.4	30
187	Directly Activating the Integrin β 1 Initiates Outside-In Signaling by Causing β 1 Clustering. <i>Journal of Biological Chemistry</i> , 2016 , 291, 11706-16	5.4	23
186	Infrared and fluorescence assessment of the hydration status of the tryptophan gate in the influenza A M2 proton channel. <i>Physical Chemistry Chemical Physics</i> , 2016 , 18, 28939-28950	3.6	13
185	The membrane- and soluble-protein helix-helix interactome: similar geometry via different interactions. <i>Structure</i> , 2015 , 23, 527-541	5.2	46
184	Systematic Perturbations of Binuclear Non-heme Iron Sites: Structure and Dioxygen Reactivity of de Novo Due Ferri Proteins. <i>Biochemistry</i> , 2015 , 54, 4637-51	3.2	15
183	Molecular-Level Insight into the Differential Oxidase and Oxygenase Reactivities of de Novo Due Ferri Proteins. <i>Journal of the American Chemical Society</i> , 2015 , 137, 9302-14	16.4	21
182	The Tyrosine Kinase c-Src Specifically Binds to the Active Integrin β 1 to Initiate Outside-in Signaling in Platelets. <i>Journal of Biological Chemistry</i> , 2015 , 290, 15825-15834	5.4	18
181	Artificial Diiron Enzymes with a De Novo Designed Four-Helix Bundle Structure. <i>European Journal of Inorganic Chemistry</i> , 2015 , 2015, 3371-3390	2.3	50
180	The α 1 integrin plays a critical in vivo role in tissue fibrosis. <i>Science Translational Medicine</i> , 2015 , 7, 288ra79	17.5	174

179	Signal transduction in histidine kinases: insights from new structures. <i>Structure</i> , 2015 , 23, 981-94	5.2	154
178	High-resolution structures of the M2 channel from influenza A virus reveal dynamic pathways for proton stabilization and transduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 14260-5	11.5	65
177	Hydrogen-bonded water molecules in the M2 channel of the influenza A virus guide the binding preferences of ammonium-based inhibitors. <i>Journal of Physical Chemistry B</i> , 2015 , 119, 1173-83	3.4	25
176	Computational design and experimental characterization of peptides intended for pH-dependent membrane insertion and pore formation. <i>ACS Chemical Biology</i> , 2015 , 10, 1082-93	4.9	18
175	Specific aromatic foldamers potently inhibit spontaneous and seeded A β 42 and A β 43 fibril assembly. <i>Biochemical Journal</i> , 2014 , 464, 85-98	3.8	12
174	Distinct synthetic A β prion strains producing different amyloid deposits in bigenic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 10329-34	11.5	124
173	Cys-scanning disulfide crosslinking and bayesian modeling probe the transmembrane signaling mechanism of the histidine kinase, PhoQ. <i>Structure</i> , 2014 , 22, 1239-1251	5.2	83
172	Comparative mechanistic studies of brilacidin, daptomycin, and the antimicrobial peptide LL16. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 5136-45	5.9	113
171	Mechanistic insights from functional characterization of an unnatural His37 mutant of the influenza A/M2 protein. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 1082-7	3.8	4
170	Catalytic efficiency of designed catalytic proteins. <i>Current Opinion in Structural Biology</i> , 2014 , 27, 113-218.1		84
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. <i>Journal of the American Chemical Society</i> , 2014 , 136, 17987-95	16.4	63
168	De novo design of a transmembrane Zn $^{2+}$ -transporting four-helix bundle. <i>Science</i> , 2014 , 346, 1520-4	33.3	220
167	2D IR spectroscopy reveals the role of water in the binding of channel-blocking drugs to the influenza M2 channel. <i>Journal of Chemical Physics</i> , 2014 , 140, 235105	3.9	22
166	Short peptides self-assemble to produce catalytic amyloids. <i>Nature Chemistry</i> , 2014 , 6, 303-9	17.6	364
165	Crystal structure of an amphiphilic foldamer reveals a 48-mer assembly comprising a hollow truncated octahedron. <i>Nature Communications</i> , 2014 , 5, 3581	17.4	11
164	Influenza virus A M2 protein generates negative Gaussian membrane curvature necessary for budding and scission. <i>Journal of the American Chemical Society</i> , 2013 , 135, 13710-9	16.4	80
163	Computational de novo design and characterization of a protein that selectively binds a highly hyperpolarizable abiological chromophore. <i>Journal of the American Chemical Society</i> , 2013 , 135, 13914-26	16.4	46
162	3-Azatetracyclo[5.2.1.1(5,8).0(1,5)]undecane derivatives: From wild-type inhibitors of the M2 ion channel of influenza A virus to derivatives with potent activity against the V27A mutant. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 9265-74	8.3	39

161	Structural Stability and Binding Strength of a Designed Peptide-Carbon Nanotube Hybrid. <i>Journal of Physical Chemistry C</i> , 2013 , 117, 26255-26261	3.8	11
160	Asp44 stabilizes the Trp41 gate of the M2 proton channel of influenza A virus. <i>Structure</i> , 2013 , 21, 2033-41	4.1	27
159	Structure and inhibition of the drug-resistant S31N mutant of the M2 ion channel of influenza A virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 1315-20	11.5	167
158	Inhibitors of the influenza A virus M2 proton channel discovered using a high-throughput yeast growth restoration assay. <i>PLoS ONE</i> , 2013 , 8, e55271	3.7	40
157	Activating Individual $\beta\beta$ Molecules Using An Anti- β -Transmembrane Domain Peptide Causes $\beta\beta$ Oligomerization and $\beta\beta$ -Mediated Outside-In Signaling. <i>Blood</i> , 2013 , 122, 3506-3506	2.2	
156	Knowledge-based potential for positioning membrane-associated structures and assessing residue-specific energetic contributions. <i>Structure</i> , 2012 , 20, 924-35	5.2	58
155	Structural basis for proton conduction and inhibition by the influenza M2 protein. <i>Protein Science</i> , 2012 , 21, 1620-33	6.3	101
154	Alteration of the oxygen-dependent reactivity of de novo Dufrenoy proteins. <i>Nature Chemistry</i> , 2012 , 4, 900-6	17.6	100
153	Development of Helical calpain probes by mimicking a natural protein-protein interaction. <i>Journal of the American Chemical Society</i> , 2012 , 134, 17704-13	16.4	205
152	Cysteine-linked aromatic nitriles as UV resonance Raman probes of protein structure. <i>Journal of Raman Spectroscopy</i> , 2012 , 43, 1244-1249	2.3	11
151	Computational design of a protein crystal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 7304-9	11.5	138
150	Selection of improved peptide ligases by yeast surface display. <i>FASEB Journal</i> , 2012 , 26, 549.3	0.9	
149	Analysis of β Binding to the c-Src SH3 Domain. <i>Blood</i> , 2012 , 120, 383-383	2.2	
148	Molecular dynamics simulation directed rational design of inhibitors targeting drug-resistant mutants of influenza A virus M2. <i>Journal of the American Chemical Society</i> , 2011 , 133, 12834-41	16.4	109
147	Antibacterial mechanism of action of arylamide foldamers. <i>Antimicrobial Agents and Chemotherapy</i> , 2011 , 55, 5043-53	5.9	64
146	Computational design of a β -peptide that targets transmembrane helices. <i>Journal of the American Chemical Society</i> , 2011 , 133, 12378-81	16.4	49
145	Exploring the Requirements for the Hydrophobic Scaffold and Polar Amine in inhibitors of M2 from Influenza A Virus. <i>ACS Medicinal Chemistry Letters</i> , 2011 , 2, 307-312	4.3	44
144	Probing designability via a generalized model of helical bundle geometry. <i>Journal of Molecular Biology</i> , 2011 , 405, 1079-100	6.5	152

143	Exploring the size limit of templates for inhibitors of the M2 ion channel of influenza A virus. <i>Journal of Medicinal Chemistry</i> , 2011 , 54, 2646-57	8.3	64
142	Computational design of virus-like protein assemblies on carbon nanotube surfaces. <i>Science</i> , 2011 , 332, 1071-6	33.3	178
141	Salt bridges: geometrically specific, designable interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 898-915	4.2	212
140	Design of a Three-Helix Bundle Capable of Binding Heavy Metals in a Triscysteine Environment. <i>Angewandte Chemie</i> , 2011 , 123, 2097-2101	3.6	13
139	Innentitelbild: Design of a Three-Helix Bundle Capable of Binding Heavy Metals in a Triscysteine Environment (Angew. Chem. 9/2011). <i>Angewandte Chemie</i> , 2011 , 123, 1990-1990	3.6	
138	Design of a three-helix bundle capable of binding heavy metals in a triscysteine environment. <i>Angewandte Chemie - International Edition</i> , 2011 , 50, 2049-53	16.4	69
137	Inside Cover: Design of a Three-Helix Bundle Capable of Binding Heavy Metals in a Triscysteine Environment (Angew. Chem. Int. Ed. 9/2011). <i>Angewandte Chemie - International Edition</i> , 2011 , 50, 1948-1948	16.4	
136	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. <i>Journal of the American Chemical Society</i> , 2011 , 133, 4274-84	16.4	88
135	Tidal surge in the M2 proton channel, sensed by 2D IR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 6115-20	11.5	85
134	Transmembrane orientation and possible role of the fusogenic peptide from parainfluenza virus 5 (PIV5) in promoting fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 3958-63	11.5	60
133	Kindlin-3 Undergoes Endoproteolysis in Stored Platelets and After Platelet Stimulation. <i>Blood</i> , 2011 , 118, 1255-1255	2.2	1
132	Structure of the amantadine binding site of influenza M2 proton channels in lipid bilayers. <i>Nature</i> , 2010 , 463, 689-92	50.4	519
131	Consensus motif for integrin transmembrane helix association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 703-8	11.5	65
130	Structure and mechanism of proton transport through the transmembrane tetrameric M2 protein bundle of the influenza A virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 15075-80	11.5	208
129	Proton and cation transport activity of the M2 proton channel from influenza A virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 15409-14	11.5	67
128	Computational design and elaboration of a de novo heterotetrameric alpha-helical protein that selectively binds an emissive abiological (porphinato)zinc chromophore. <i>Journal of the American Chemical Society</i> , 2010 , 132, 3997-4005	16.4	50
127	De novo design and molecular assembly of a transmembrane diporphyrin-binding protein complex. <i>Journal of the American Chemical Society</i> , 2010 , 132, 15516-8	16.4	99
126	A pH-dependent conformational ensemble mediates proton transport through the influenza A/M2 protein. <i>Biochemistry</i> , 2010 , 49, 10061-71	3.2	20

125	Functional studies and modeling of pore-lining residue mutants of the influenza a virus M2 ion channel. <i>Biochemistry</i> , 2010 , 49, 696-708	3.2	99
124	De novo design of antimicrobial polymers, foldamers, and small molecules: from discovery to practical applications. <i>Accounts of Chemical Research</i> , 2010 , 43, 30-9	24.3	447
123	Role of the Conformational Rigidity in the Design of Biomimetic Antimicrobial Compounds. <i>Angewandte Chemie</i> , 2010 , 122, 8640-8643	3.6	3
122	Assessing the Biochemistry of Kindlin-3 In Human Platelets. <i>Blood</i> , 2010 , 116, 2011-2011	2.2	
121	Arylamides: Discovery of a Novel Class of Fully-Synthetic Small Molecule Heparin and LMWH Antagonists.. <i>Blood</i> , 2010 , 116, 1096-1096	2.2	
120	Optimized Fully-Synthetic Salicylamide Heparin Antagonists Have Greater Efficacy Versus LMWHs and Display Improved Hemodynamic Responses as Compared to Protamine. <i>Blood</i> , 2010 , 116, 191-191	2.2	
119	Small-molecule inhibitors of integrin alpha2beta1 that prevent pathological thrombus formation via an allosteric mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 719-24	11.5	70
118	De novo design and in vivo activity of conformationally restrained antimicrobial arylamide foldamers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 6968-73	11.5	253
117	Molecular dynamics calculations suggest a conduction mechanism for the M2 proton channel from influenza A virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 1069-74	11.5	103
116	The role of hydrophobicity in the antimicrobial and hemolytic activities of polymethacrylate derivatives. <i>Chemistry - A European Journal</i> , 2009 , 15, 1123-33	4.8	236
115	An artificial di-iron oxo-protein with phenol oxidase activity. <i>Nature Chemical Biology</i> , 2009 , 5, 882-4	11.7	152
114	Experimental and computational evaluation of forces directing the association of transmembrane helices. <i>Journal of the American Chemical Society</i> , 2009 , 131, 11341-3	16.4	29
113	Spectroscopic definition of the biferrous and biferric sites in de novo designed four-helix bundle DFsc peptides: implications for O2 reactivity of binuclear non-heme iron enzymes. <i>Biochemistry</i> , 2009 , 48, 59-73	3.2	22
112	Multiple approaches converge on the structure of the integrin alpha11b/beta3 transmembrane heterodimer. <i>Journal of Molecular Biology</i> , 2009 , 392, 1087-101	6.5	20
111	Identification of the functional core of the influenza A virus A/M2 proton-selective ion channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 12283-8	11.5	135
110	Identification of Stalk Mutations That Stabilize the High Affinity Conformation of $\beta\beta$ by Negative Design.. <i>Blood</i> , 2009 , 114, 4017-4017	2.2	
109	Protein-Protein and Protein-Lipid Interactions Modulate $\beta\beta$ Inside-out Signaling.. <i>Blood</i> , 2009 , 114, 152-152	2.2	
108	Structural basis for the function and inhibition of an influenza virus proton channel. <i>Nature</i> , 2008 , 451, 596-9	50.4	501

107	The interplay of functional tuning, drug resistance, and thermodynamic stability in the evolution of the M2 proton channel from the influenza A virus. <i>Structure</i> , 2008 , 16, 1067-76	5.2	48
106	Protein-protein interactions in the membrane: sequence, structural, and biological motifs. <i>Structure</i> , 2008 , 16, 991-1001	5.2	140
105	Computationally designed peptide inhibitors of protein-protein interactions in membranes. <i>Biochemistry</i> , 2008 , 47, 8600-6	3.2	56
104	De novo designed synthetic mimics of antimicrobial peptides. <i>Current Opinion in Biotechnology</i> , 2008 , 19, 620-7	11.4	154
103	A Conserved Transmembrane Domain Interface Regulates Integrin Function. <i>Blood</i> , 2008 , 112, 2858-2858.2		1
102	NMR Structure of a Disulfide-Crosslinked $\beta\beta$ Cytoplasmic Domain Heterodimer. <i>Blood</i> , 2008 , 112, 2866-2866	2.2	
101	Factors That Influence the Homo- and Hetero-Oligomerization of the Leukocyte Integrin Transmembrane Domains. <i>Blood</i> , 2008 , 112, 3556-3556	2.2	
100	Characterization of the Weak Interaction of C-Src with the β Cytoplasmic Tail. <i>Blood</i> , 2008 , 112, 2856-2856		
99	De novo design of a single-chain diphenylporphyrin metalloprotein. <i>Journal of the American Chemical Society</i> , 2007 , 129, 10732-40	16.4	80
98	Enthalpic and entropic stages in alpha-helical peptide unfolding, from laser T-jump/UV Raman spectroscopy. <i>Journal of the American Chemical Society</i> , 2007 , 129, 12801-8	16.4	29
97	Diiron-containing metalloproteins: Developing functional models. <i>Comptes Rendus Chimie</i> , 2007 , 10, 703-720		39
96	Computational design of peptides that target transmembrane helices. <i>Science</i> , 2007 , 315, 1817-22	33.3	240
95	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. <i>Journal of Molecular Biology</i> , 2007 , 366, 436-48	6.5	130
94	The Design and Synthesis of Small Molecule Inhibitors of Collagen Binding to Integrin $\alpha 1$ as Antithrombotic Agents.. <i>Blood</i> , 2007 , 110, 306-306	2.2	
93	Characterization of a Disulfide-Crosslinked $\beta\beta$ Cytoplasmic Domain Heterodimer by NMR.. <i>Blood</i> , 2007 , 110, 415-415	2.2	
92	Identification of Oligomerization Motifs in the β Transmembrane Domain.. <i>Blood</i> , 2007 , 110, 416-416	2.2	
91	The Structure of a Designed Diiron(III) Protein: Implications for Cofactor Stabilization and Catalysis. <i>Angewandte Chemie</i> , 2006 , 118, 5073-5076	3.6	4
90	Characterization of nonbiological antimicrobial polymers in aqueous solution and at water-lipid interfaces from all-atom molecular dynamics. <i>Journal of the American Chemical Society</i> , 2006 , 128, 1778-9	16.4	77

89	The structure of a designed diiron(III) protein: implications for cofactor stabilization and catalysis. <i>Angewandte Chemie - International Edition</i> , 2006 , 45, 4951-4	16.4	33
88	Probing Membrane Insertion Activity of Antimicrobial Polymers via Coarse-grain Molecular Dynamics. <i>Journal of Chemical Theory and Computation</i> , 2006 , 2, 649-655	6.4	48
87	Polar networks control oligomeric assembly in membranes. <i>Journal of the American Chemical Society</i> , 2006 , 128, 4170-1	16.4	29
86	Characterization of a membrane protein folding motif, the Ser zipper, using designed peptides. <i>Journal of Molecular Biology</i> , 2006 , 359, 930-9	6.5	48
85	Factors Influencing the Homomeric and Heteromeric Association of Platelet Integrin Transmembrane Domains.. <i>Blood</i> , 2006 , 108, 212-212	2.2	
84	Regulation of the Function of α IIb in Platelets by a Designed Peptide Targeting the α Transmembrane Domain.. <i>Blood</i> , 2006 , 108, 1504-1504	2.2	
83	Computational Design of a Model for the Platelet Integrin α IIb β 3.. <i>Blood</i> , 2006 , 108, 1528-1528	2.2	
82	The Leech Product Saratin Is a Potent Inhibitor of Both VWF and Integrin α 1 Binding to Collagen.. <i>Blood</i> , 2006 , 108, 3928-3928	2.2	1
81	Response of a designed metalloprotein to changes in metal ion coordination, exogenous ligands, and active site volume determined by X-ray crystallography. <i>Journal of the American Chemical Society</i> , 2005 , 127, 17266-76	16.4	41
80	Spectroscopic and computational studies of the de novo designed protein DF2t: correlation to the biferrrous active site of ribonucleotide reductase and factors that affect O2 reactivity. <i>Journal of the American Chemical Society</i> , 2005 , 127, 16098-106	16.4	40
79	De novo design of a redox-active minimal rubredoxin mimic. <i>Journal of the American Chemical Society</i> , 2005 , 127, 5804-5	16.4	114
78	Computational de novo design and characterization of a four-helix bundle protein that selectively binds a nonbiological cofactor. <i>Journal of the American Chemical Society</i> , 2005 , 127, 1346-7	16.4	152
77	Analysis and design of turns in alpha-helical hairpins. <i>Journal of Molecular Biology</i> , 2005 , 346, 1441-54	6.5	53
76	Sequence determinants of a transmembrane proton channel: an inverse relationship between stability and function. <i>Journal of Molecular Biology</i> , 2005 , 347, 169-79	6.5	57
75	The conformation of the pore region of the M2 proton channel depends on lipid bilayer environment. <i>Protein Science</i> , 2005 , 14, 856-61	6.3	84
74	Artificial di-iron proteins: solution characterization of four helix bundles containing two distinct types of inter-helical loops. <i>Journal of Biological Inorganic Chemistry</i> , 2005 , 10, 539-49	3.7	28
73	Alpha-alpha linking motifs and interhelical orientations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 325-37	4.2	23
72	A push-pull mechanism for regulating integrin function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 1424-9	11.5	112

71	Activation of Platelet α IIb β 3 by Exogenous Peptides Corresponding to the Transmembrane Domains of α Ib and α 3.. <i>Blood</i> , 2005 , 106, 384-384	2.2	
70	The Development of Small Molecule Inhibitors of Collagen Binding to the Integrin α 1 as Antithrombotic Drugs.. <i>Blood</i> , 2005 , 106, 3677-3677	2.2	1
69	Two Specific Domains on the Upper Surface of the α IIb β 3 Propeller Determine the Sensitivity of α IIb β 3 for RGD-Containing Peptides.. <i>Blood</i> , 2005 , 106, 2653-2653	2.2	
68	Folding of helical membrane proteins: the role of polar, GxxxG-like and proline motifs. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 465-79	8.1	368
67	Nontoxic membrane-active antimicrobial arylamide oligomers. <i>Angewandte Chemie - International Edition</i> , 2004 , 43, 1158-62	16.4	189
66	Length Dependent Helix-Coil Transition Kinetics of Nine Alanine-Based Peptides. <i>Journal of Physical Chemistry B</i> , 2004 , 108,	3.4	60
65	De novo design of a D2-symmetrical protein that reproduces the diheme four-helix bundle in cytochrome bc1. <i>Journal of the American Chemical Society</i> , 2004 , 126, 8141-7	16.4	69
64	Association of a model transmembrane peptide containing gly in a heptad sequence motif. <i>Biophysical Journal</i> , 2004 , 87, 3421-9	2.9	36
63	Heteromeric and Homomeric Transmembrane Domain Associations Regulate α IIb β 3 Function.. <i>Blood</i> , 2004 , 104, 329-329	2.2	
62	Preorganization of molecular binding sites in designed diiron proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 3772-7	11.5	67
61	Position-dependence of stabilizing polar interactions of asparagine in transmembrane helical bundles. <i>Biochemistry</i> , 2003 , 42, 6400-7	3.2	65
60	Sliding helix and change of coordination geometry in a model di-MnII protein. <i>Angewandte Chemie - International Edition</i> , 2003 , 42, 417-20	16.4	48
59	The hydration of amides in helices; a comprehensive picture from molecular dynamics, IR, and NMR. <i>Protein Science</i> , 2003 , 12, 520-31	6.3	136
58	How do helix-helix interactions help determine the folds of membrane proteins? Perspectives from the study of homo-oligomeric helical bundles. <i>Protein Science</i> , 2003 , 12, 647-65	6.3	145
57	Using nitrile-derivatized amino acids as infrared probes of local environment. <i>Journal of the American Chemical Society</i> , 2003 , 125, 405-11	16.4	278
56	Computational design and characterization of a monomeric helical dinuclear metalloprotein. <i>Journal of Molecular Biology</i> , 2003 , 334, 1101-15	6.5	119
55	Use of thiol-disulfide equilibria to measure the energetics of assembly of transmembrane helices in phospholipid bilayers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 14772-7	11.5	126
54	Activation of integrin α IIb β 3 by modulation of transmembrane helix associations. <i>Science</i> , 2003 , 300, 795-8	33.3	270

53	Sequence determinants of the energetics of folding of a transmembrane four-helix-bundle protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 8568-72	11.5	63
52	De novo design of biomimetic antimicrobial polymers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 5110-4	11.5	387
51	Helix formation via conformation diffusion search. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 2788-93	11.5	204
50	Noncovalent self-assembly of a heterotetrameric diiron protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 5150-4	11.5	58
49	Computational de novo design, and characterization of an A(2)B(2) diiron protein. <i>Journal of Molecular Biology</i> , 2002 , 321, 923-38	6.5	119
48	Proton and metal ion-dependent assembly of a model diiron protein. <i>Protein Science</i> , 2001 , 10, 958-69	6.3	50
47	beta-Peptides: from structure to function. <i>Chemical Reviews</i> , 2001 , 101, 3219-32	68.1	1633
46	De novo design, synthesis, and characterization of antimicrobial beta-peptides. <i>Journal of the American Chemical Society</i> , 2001 , 123, 7553-9	16.4	303
45	Toward the de novo design of a catalytically active helix bundle: a substrate-accessible carboxylate-bridged dinuclear metal center. <i>Journal of the American Chemical Society</i> , 2001 , 123, 12749-57	16.4	92
44	Temperature-dependent helix-coil transition of an alanine based peptide. <i>Journal of the American Chemical Society</i> , 2001 , 123, 9235-8	16.4	131
43	Dynamics of a de novo designed three-helix bundle protein studied by ¹⁵ N, ¹³ C, and ² H NMR relaxation methods. <i>Biochemistry</i> , 2001 , 40, 9560-9	3.2	42
42	Introduction: protein design. <i>Chemical Reviews</i> , 2001 , 101, 3025-6	68.1	25
41	Structural consequences of an amino acid deletion in the B1 domain of protein G. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 41, 323-33	4.2	7
40	Asparagine-mediated self-association of a model transmembrane helix. <i>Nature Structural Biology</i> , 2000 , 7, 161-6		311
39	Evolution of binding affinity in a WW domain probed by phage display. <i>Protein Science</i> , 2000 , 9, 2366-76	6.3	30
38	Pump/probe self heterodyned 2D spectroscopy of vibrational transitions of a small globular peptide. <i>Journal of Chemical Physics</i> , 2000 , 112, 1907-1916	3.9	135
37	pH-dependent tetramerization and amantadine binding of the transmembrane helix of M2 from the influenza A virus. <i>Biochemistry</i> , 2000 , 39, 14160-70	3.2	145
36	Molecular Motions and Protein Folding: Characterization of the Backbone Dynamics and Folding Equilibrium of β D Using ¹³ C NMR Spin Relaxation. <i>Journal of the American Chemical Society</i> , 2000 , 122, 11610-11619	16.4	70

35	De novo design of helical bundles as models for understanding protein folding and function. <i>Accounts of Chemical Research</i> , 2000 , 33, 745-54	24.3	274
34	Evolution of binding affinity in a WW domain probed by phage display 2000 , 9, 2366		5
33	Centrosymmetric bilayers in the 0.75 Å resolution structure of a designed alpha-helical peptide, D,L-Alpha-1. <i>Protein Science</i> , 1999 , 8, 1410-22	6.3	41
32	Tertiary templates for the design of diiron proteins. <i>Current Opinion in Structural Biology</i> , 1999 , 9, 500-8	8.1	57
31	De novo design and structural characterization of proteins and metalloproteins. <i>Annual Review of Biochemistry</i> , 1999 , 68, 779-819	29.1	529
30	Exploration of the structural features defining the conduction properties of a synthetic ion channel. <i>Biophysical Journal</i> , 1999 , 76, 618-30	2.9	67
29	De Novo Design of Antibacterial α -Peptides. <i>Journal of the American Chemical Society</i> , 1999 , 121, 12200-12201	16.4	325
28	Stimulated Photon Echoes from Amide I Vibrations. <i>Journal of Physical Chemistry A</i> , 1999 , 103, 10049-10053	5.3	70
27	Analysis and design of three-stranded coiled coils and three-helix bundles. <i>Folding & Design</i> , 1998 , 3, R29-40		52
26	From coiled coils to small globular proteins: design of a native-like three-helix bundle. <i>Protein Science</i> , 1998 , 7, 1404-14	6.3	125
25	The Design of Efficient β -Helical C-Capping Auxiliaries. <i>Journal of the American Chemical Society</i> , 1998 , 120, 2764-2767	16.4	30
24	Solution Structure of β D, a Nativelike de Novo Designed Protein. <i>Journal of the American Chemical Society</i> , 1998 , 120, 1138-1145	16.4	132
23	The role of protonation and metal chelation preferences in defining the properties of mercury-binding coiled coils. <i>Journal of Molecular Biology</i> , 1998 , 280, 897-912	6.5	115
22	From synthetic coiled coils to functional proteins: automated design of a receptor for the calmodulin-binding domain of calcineurin. <i>Journal of Molecular Biology</i> , 1998 , 281, 379-91	6.5	37
21	Design of a Synthetic Receptor for the Calmodulin-Binding Domain of Calcineurin. <i>Journal of the American Chemical Society</i> , 1997 , 119, 12378-12379	16.4	16
20	De Novo Design of Mercury-Binding Two- and Three-Helical Bundles. <i>Journal of the American Chemical Society</i> , 1997 , 119, 6195-6196	16.4	146
19	De novo design of native proteins: characterization of proteins intended to fold into antiparallel, rop-like, four-helix bundles. <i>Biochemistry</i> , 1997 , 36, 2450-8	3.2	83
18	A Designed Buried Salt Bridge in a Heterodimeric Coiled Coil. <i>Journal of the American Chemical Society</i> , 1997 , 119, 5742-5743	16.4	67

17	The crystal structure of the designed trimeric coiled coil coil-VaLd: implications for engineering crystals and supramolecular assemblies. <i>Protein Science</i> , 1997 , 6, 80-8	6.3	128
16	Controlling topology and native-like behavior of de novo-designed peptides: design and characterization of antiparallel four-stranded coiled coils. <i>Biochemistry</i> , 1996 , 35, 6955-62	3.2	110
15	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. <i>Journal of the American Chemical Society</i> , 1996 , 118, 473-474	16.4	106
14	Thermodynamic analysis of a designed three-stranded coiled coil. <i>Biochemistry</i> , 1996 , 35, 14480-5	3.2	81
13	The role of helix formation in the folding of a fully alpha-helical coiled coil. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 24, 427-32	4.2	88
12	De novo design of heterotrimeric coiled coils 1996 , 40, 495-504		38
11	The role of helix formation in the folding of a fully helical coiled coil 1996 , 24, 427		3
10	Thermodynamic genetics of the folding of the B1 immunoglobulin-binding domain from streptococcal protein G. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 21, 11-21	4.2	35
9	A de Novo Designed Protein Mimics the Native State of Natural Proteins. <i>Journal of the American Chemical Society</i> , 1995 , 117, 7558-7559	16.4	95
8	Design and synthesis of multi-haem proteins. <i>Nature</i> , 1994 , 368, 425-32	50.4	535
7	Design of a heme-binding four-helix bundle. <i>Journal of the American Chemical Society</i> , 1994 , 116, 856-865	16.4	236
6	Synthetic peptides as models for ion channel proteins. <i>Accounts of Chemical Research</i> , 1993 , 26, 191-197	24.3	191
5	Tetraphilin: a four-helix proton channel built on a tetraphenylporphyrin framework. <i>Journal of the American Chemical Society</i> , 1992 , 114, 9656-9657	16.4	138
4	Crystallization of proton channel peptides. <i>Protein Science</i> , 1992 , 1, 1073-7	6.3	8
3	Design of peptides and proteins. <i>Advances in Protein Chemistry</i> , 1988 , 39, 51-124		240
2	Design of a 4-helix bundle protein: synthesis of peptides which self-associate into a helical protein. <i>Journal of the American Chemical Society</i> , 1987 , 109, 6751-6758	16.4	265
1	Design, synthesis, and characterization of a cytotoxic peptide with melittin-like activity. <i>Journal of the American Chemical Society</i> , 1981 , 103, 679-681	16.4	159