William F Degrado

List of Publications by Year
in descending order

270 papers	25,228 citations	4942 84 h-index	7931 149 g-index
285 all docs	285 docs citations	285 times ranked	19576 citing authors

#	Article	IF	Citations
1	Î²-Peptides:â€‰ From Structure to Function. Chemical Reviews, 2001, 101, 3219-3232.	23.0	1,772
2	Design and synthesis of multi-haem proteins. Nature, 1994, 368, 425-432.	13.7	592
3	Structure of the amantadine binding site of influenza M2 proton channels in lipid bilayers. Nature, 2010, 463, 689-692.	13.7	590
4	De Novo Design and Structural Characterization of Proteins and Metalloproteins. Annual Review of Biochemistry, 1999, 68, 779-819.	5.0	576
5	Structural basis for the function and inhibition of an influenza virus proton channel. Nature, 2008, 451, 596-599.	13.7	549
6	Short peptides self-assemble to produce catalytic amyloids. Nature Chemistry, 2014, 6, 303-309.	6.6	510
7	De Novo Design of Antimicrobial Polymers, Foldamers, and Small Molecules: From Discovery to Practical Applications. Accounts of Chemical Research, 2010, 43, 30-39.	7.6	489
8	De novo design of biomimetic antimicrobial polymers. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5110-5114.	3.3	419
9	Folding of helical membrane proteins: the role of polar, GxxxG-like and proline motifs. Current Opinion in Structural Biology, 2004, 14, 465-479.	2.6	402
10	De Novo Design of Antibacterial Î²-Peptides. Journal of the American Chemical Society, 1999, 121, 12200-12201.	6.6	358
11	De Novo Design, Synthesis, and Characterization of Antimicrobial Î²-Peptides. Journal of the American Chemical Society, 2001, 123, 7553-7559.	6.6	338
12	Asparagine-mediated self-association of a model transmembrane helix. Nature Structural Biology, 2000, 7, 161-166.	9.7	334
13	Using Nitrile-Derivatized Amino Acids as Infrared Probes of Local Environment. Journal of the American Chemical Society, 2003, 125, 405-411.	6.6	318
14	De Novo Design of Helical Bundles as Models for Understanding Protein Folding and Function. Accounts of Chemical Research, 2000, 33, 745-754.	7.6	311
15	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.	6.6	300
16	Self-assembling dipeptide antibacterial nanostructures with membrane disrupting activity. Nature Communications, 2017, 8, 1365.	5.8	299
17	Salt bridges: Geometrically specific, designable interactions. Proteins: Structure, Function and Bioinformatics, 2011, 79, 898-915.	1.5	285
18	Activation of Integrin alphaIIbbeta3 by Modulation of Transmembrane Helix Associations. Science, 2003, 300, 795-798.	6.0	284

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19	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, 6968-6973.	3.3	280
20	The Role of Hydrophobicity in the Antimicrobial and Hemolytic Activities of Polymethacrylate Derivatives. Chemistry - A European Journal, 2009, 15, 1123-1133.	1.7	280
21	Design of Peptides and Proteins. Advances in Protein Chemistry, 1988, 39, 51-124.	4.4	275
22	De novo design of a transmembrane Zn ²⁺ -transporting four-helix bundle. Science, 2014, 346, 1520-1524.	6.0	275
23	Computational Design of Peptides That Target Transmembrane Helices. Science, 2007, 315, 1817-1822.	6.0	271
24	Design of a heme-binding four-helix bundle. Journal of the American Chemical Society, 1994, 116, 856-865.	6.6	261
25	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, 15075-15080.	3.3	243
26	The Î± _v Î² ₁ integrin plays a critical in vivo role in tissue fibrosis. Science Translational Medicine, 2015, 7, 288ra79.	5.8	227
27	Development of Î±-Helical Calpain Probes by Mimicking a Natural Proteinâ€“Protein Interaction. Journal of the American Chemical Society, 2012, 134, 17704-17713.	6.6	225
28	Synthetic peptides as models for ion channel proteins. Accounts of Chemical Research, 1993, 26, 191-197.	7.6	217
29	Signal Transduction in Histidine Kinases: Insights from New Structures. Structure, 2015, 23, 981-994.	1.6	213
30	Helix formation via conformation diffusion search. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 2788-2793.	3.3	212
31	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, 1315-1320.	3.3	204
32	Probing Designability via a Generalized Model of Helical Bundle Geometry. Journal of Molecular Biology, 2011, 405, 1079-1100.	2.0	203
33	Nontoxic Membrane-Active Antimicrobial Arylamide Oligomers. Angewandte Chemie - International Edition, 2004, 43, 1158-1162.	7.2	199
34	Computational Design of Virus-Like Protein Assemblies on Carbon Nanotube Surfaces. Science, 2011, 332, 1071-1076.	6.0	196
35	Design, synthesis, and characterization of a cytotoxic peptide with melittin-like activity. Journal of the American Chemical Society, 1981, 103, 679-681.	6.6	175
36	De novo designed synthetic mimics of antimicrobial peptides. Current Opinion in Biotechnology, 2008, 19, 620-627.	3.3	175

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37	An artificial di-iron oxo-protein with phenol oxidase activity. Nature Chemical Biology, 2009, 5, 882-884.	3.9	170
38	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, 1346-1347.	6.6	167
39	Protein-Protein Interactions in the Membrane: Sequence, Structural, and Biological Motifs. Structure, 2008, 16, 991-1001.	1.6	162
40	De NovoDesign of Mercury-Binding Two- and Three-Helical Bundles. Journal of the American Chemical Society, 1997, 119, 6195-6196.	6.6	157
41	Computational design of a protein crystal. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7304-7309.	3.3	157
42	pH-Dependent Tetramerization and Amantadine Binding of the Transmembrane Helix of M2 from the Influenza A Virusâ€. Biochemistry, 2000, 39, 14160-14170.	1.2	156
43	Tetraphilin: a four-helix proton channel built on a tetraphenylporphyrin framework. Journal of the American Chemical Society, 1992, 114, 9656-9657.	6.6	151
44	The hydration of amides in helices; a comprehensive picture from molecular dynamics, IR, and NMR. Protein Science, 2003, 12, 520-531.	3.1	150
45	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, 647-665.	3.1	150
46	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, 12283-12288.	3.3	150
47	Solution Structure of Î±2D, a Nativelike de Novo Designed Protein. Journal of the American Chemical Society, 1998, 120, 1138-1145.	6.6	146
48	Pump/probe self heterodyned 2D spectroscopy of vibrational transitions of a small globular peptide. Journal of Chemical Physics, 2000, 112, 1907-1916.	1.2	144
49	De novo protein design, a retrospective. Quarterly Reviews of Biophysics, 2020, 53, e3.	2.4	144
50	Ez, 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, 436-448.	2.0	143
51	Comparative Mechanistic Studies of Brilacidin, Daptomycin, and the Antimicrobial Peptide LL16. Antimicrobial Agents and Chemotherapy, 2014, 58, 5136-5145.	1.4	142
52	Distinct synthetic Aî² prion strains producing different amyloid deposits in bigenic mice. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10329-10334.	3.3	140
53	The crystal structure of the designed trimeric coiled coil coilâ€V_aL_d: Implications for engineering crystals and supramolecular assemblies. Protein Science, 1997, 6, 80-88.	3.1	138
54	Temperature-Dependent Helixâ^'Coil Transition of an Alanine Based Peptide. Journal of the American Chemical Society, 2001, 123, 9235-9238.	6.6	138

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55	Computational Design and Characterization of a Monomeric Helical Dinuclear Metalloprotein. Journal of Molecular Biology, 2003, 334, 1101-1115.	2.0	138
56	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, 14772-14777.	3.3	137
57	From coiled coils to small globular proteins: Design of a nativeâ€like threeâ€helix bundle. Protein Science, 1998, 7, 1404-1414.	3.1	132
58	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, 12834-12841.	6.6	127
59	De Novo Design of a Redox-Active Minimal Rubredoxin Mimic. Journal of the American Chemical Society, 2005, 127, 5804-5805.	6.6	126
60	Controlling Topology and Native-like Behavior ofdeNovo-Designed Peptides:Â Design and Characterization of Antiparallel Four-Stranded Coiled Coils. Biochemistry, 1996, 35, 6955-6962.	1.2	124
61	Computational de novo Design, and Characterization of an A2B2 Diiron Protein. Journal of Molecular Biology, 2002, 321, 923-938.	2.0	124
62	Structural basis for proton conduction and inhibition by the influenza M2 protein. Protein Science, 2012, 21, 1620-1633.	3.1	124
63	The role of protonation and metal chelation preferences in defining the properties of mercury-binding coiled coils 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 280, 897-912.	2.0	121
64	Toward the Synthesis of a Photosynthetic Reaction Center Maquette:â€‰ 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.	6.6	119
65	A push-pull mechanism for regulating integrin function. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1424-1429.	3.3	118
66	Alteration of the oxygen-dependent reactivity of de novo Due Ferri proteins. Nature Chemistry, 2012, 4, 900-906.	6.6	118
67	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, 1069-1074.	3.3	111
68	De Novo Design and Molecular Assembly of a Transmembrane Diporphyrin-Binding Protein Complex. Journal of the American Chemical Society, 2010, 132, 15516-15518.	6.6	110
69	Functional Studies and Modeling of Pore-Lining Residue Mutants of the Influenza A Virus M2 Ion Channel. Biochemistry, 2010, 49, 696-708.	1.2	107
70	Structural heterogeneity and intersubject variability of Aî² in familial and sporadic Alzheimerâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E782-E791.	3.3	105
71	Catalytic efficiency of designed catalytic proteins. Current Opinion in Structural Biology, 2014, 27, 113-121.	2.6	104
72	Cys-Scanning Disulfide Crosslinking and Bayesian Modeling Probe the Transmembrane Signaling Mechanism of the Histidine Kinase, PhoQ. Structure, 2014, 22, 1239-1251.	1.6	103

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73	A de Novo Designed Protein Mimics the Native State of Natural Proteins. Journal of the American Chemical Society, 1995, 117, 7558-7559.	6.6	102
74	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.	3.3	102
75	Actionable Activating Oncogenic ERBB2/HER2 Transmembrane and Juxtamembrane Domain Mutations. Cancer Cell, 2018, 34, 792-806.e5.	7.7	102
76	Influenza Virus A M2 Protein Generates Negative Gaussian Membrane Curvature Necessary for Budding and Scission. Journal of the American Chemical Society, 2013, 135, 13710-13719.	6.6	101
77	Toward the de Novo Design of a Catalytically Active Helix Bundle:Â A Substrate-Accessible Carboxylate-Bridged Dinuclear Metal Center. Journal of the American Chemical Society, 2001, 123, 12749-12757.	6.6	100
78	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, 4274-4284.	6.6	100
79	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.	3.3	100
80	De Novo Design of Four-Helix Bundle Metalloproteins: One Scaffold, Diverse Reactivities. Accounts of Chemical Research, 2019, 52, 1148-1159.	7.6	99
81	The role of helix formation in the folding of a fully Î±-helical coiled coil. , 1996, 24, 427-432.		98
82	AÎ² and tau prion-like activities decline with longevity in the Alzheimerâ€™s disease human brain. Science Translational Medicine, 2019, 11, .	5.8	96
83	Packing of apolar side chains enables accurate design of highly stable membrane proteins. Science, 2019, 363, 1418-1423.	6.0	94
84	De novo design of a hyperstable non-natural proteinâ€“ligand complex with sub-Ã... accuracy. Nature Chemistry, 2017, 9, 1157-1164.	6.6	93
85	Characterization of Nonbiological Antimicrobial Polymers in Aqueous Solution and at Waterâ^'Lipid Interfaces from All-Atom Molecular Dynamics. Journal of the American Chemical Society, 2006, 128, 1778-1779.	6.6	92
86	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, 14260-14265.	3.3	92
87	De NovoDesign of Native Proteins:Â Characterization of Proteins Intended To Fold into Antiparallel, Rop-like, Four-Helix Bundlesâ€. Biochemistry, 1997, 36, 2450-2458.	1.2	91
88	The conformation of the pore region of the M2 proton channel depends on lipid bilayer environment. Protein Science, 2005, 14, 856-861.	3.1	91
89	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, 6115-6120.	3.3	91
90	De Novo Design of a Single-Chain Diphenylporphyrin Metalloprotein. Journal of the American Chemical Society, 2007, 129, 10732-10740.	6.6	90

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91	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.	6.6	87
92	Small-molecule inhibitors of integrin Î± ₂ Î² ₁ that prevent pathological thrombus formation via an allosteric mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 719-724.	3.3	83
93	Thermodynamic Analysis of a Designed Three-Stranded Coiled Coil. Biochemistry, 1996, 35, 14480-14485.	1.2	82
94	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, 15409-15414.	3.3	81
95	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.	3.3	81
96	Structural Polymorphism of Alzheimerâ€™s Î²-Amyloid Fibrils as Controlled by an E22 Switch: A Solid-State NMR Study. Journal of the American Chemical Society, 2016, 138, 9840-9852.	6.6	79
97	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, 8141-8147.	6.6	78
98	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, 17987-17995.	6.6	78
99	Water Distribution, Dynamics, and Interactions with Alzheimerâ€™s Î²-Amyloid Fibrils Investigated by Solid-State NMR. Journal of the American Chemical Society, 2017, 139, 6242-6252.	6.6	77
100	Stimulated Photon Echoes from Amide I Vibrations. Journal of Physical Chemistry A, 1999, 103, 10049-10053.	1.1	76
101	Design of a Threeâ€Helix Bundle Capable of Binding Heavy Metals in a Triscysteine Environment. Angewandte Chemie - International Edition, 2011, 50, 2049-2053.	7.2	76
102	In vitro 0N4R tau fibrils contain a monomorphic Î²-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.	3.3	76
103	Antibacterial Mechanism of Action of Arylamide Foldamers. Antimicrobial Agents and Chemotherapy, 2011, 55, 5043-5053.	1.4	75
104	Designed metalloprotein stabilizes a semiquinone radical. Nature Chemistry, 2016, 8, 354-359.	6.6	74
105	Spontaneous and specific chemical cross-linking in live cells to capture and identify protein interactions. Nature Communications, 2017, 8, 2240.	5.8	74
106	Molecular Motions and Protein Folding:â€‰ Characterization of the Backbone Dynamics and Folding Equilibrium of Î±2D Using 13C NMR Spin Relaxation. Journal of the American Chemical Society, 2000, 122, 11610-11619.	6.6	73
107	Preorganization of molecular binding sites in designed diiron proteins. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3772-3777.	3.3	73
108	A Designed Buried Salt Bridge in a Heterodimeric Coiled Coil. Journal of the American Chemical Society, 1997, 119, 5742-5743.	6.6	72

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109	Exploration of the Structural Features Defining the Conduction Properties of a Synthetic Ion Channel. Biophysical Journal, 1999, 76, 618-630.	0.2	72
110	Position-Dependence of Stabilizing Polar Interactions of Asparagine in Transmembrane Helical Bundlesâ€. Biochemistry, 2003, 42, 6400-6407.	1.2	70
111	Exploring the Size Limit of Templates for Inhibitors of the M2 Ion Channel of Influenza A Virus. Journal of Medicinal Chemistry, 2011, 54, 2646-2657.	2.9	69
112	Consensus motif for integrin transmembrane helix association. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 703-708.	3.3	68
113	A 31-residue peptide induces aggregation of tau's microtubule-binding region in cells. Nature Chemistry, 2017, 9, 874-881.	6.6	67
114	Deep mutational scanning reveals the structural basis for Î±-synuclein activity. Nature Chemical Biology, 2020, 16, 653-659.	3.9	67
115	Length Dependent Helixâ"Coil Transition Kinetics of Nine Alanine-Based Peptides. Journal of Physical Chemistry B, 2004, 108, 15301-15310.	1.2	66
116	Knowledge-Based Potential for Positioning Membrane-Associated Structures and Assessing Residue-Specific Energetic Contributions. Structure, 2012, 20, 924-935.	1.6	66
117	Noncovalent self-assembly of a heterotetrameric diiron protein. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5150-5154.	3.3	65
118	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, 3958-3963.	3.3	65
119	Artificial Diiron Enzymes with a De Novo Designed Fourâ€Helix Bundle Structure. European Journal of Inorganic Chemistry, 2015, 2015, 3371-3390.	1.0	65
120	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, 8568-8572.	3.3	64
121	The Membrane- and Soluble-Protein Helix-Helix Interactome: Similar Geometry via Different Interactions. Structure, 2015, 23, 527-541.	1.6	64
122	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.	3.3	64
123	A defined structural unit enables de novo design of small-moleculeâ€"binding proteins. Science, 2020, 369, 1227-1233.	6.0	64
124	Tertiary templates for the design of diiron proteins. Current Opinion in Structural Biology, 1999, 9, 500-508.	2.6	63
125	High-density grids for efficient data collection from multiple crystals. Acta Crystallographica Section D: Structural Biology, 2016, 72, 2-11.	1.1	62
126	Designed peptides that assemble into cross-Î± amyloid-like structures. Nature Chemical Biology, 2018, 14, 870-875.	3.9	62

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127	Computationally Designed Peptide Inhibitors of Proteinâ"Protein Interactions in Membranes. Biochemistry, 2008, 47, 8600-8606.	1.2	61
128	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.	3.3	61
129	Analysis and Design of Turns in Î±-Helical Hairpins. Journal of Molecular Biology, 2005, 346, 1441-1454.	2.0	59
130	Sequence Determinants of a Transmembrane Proton Channel: An Inverse Relationship between Stability and Function. Journal of Molecular Biology, 2005, 347, 169-179.	2.0	59
131	Characterization of a Membrane Protein Folding Motif, the Ser Zipper, Using Designed Peptides. Journal of Molecular Biology, 2006, 359, 930-939.	2.0	59
132	Constructing ion channels from water-soluble Î±-helical barrels. Nature Chemistry, 2021, 13, 643-650.	6.6	59
133	Analysis and design of three-stranded coiled coils and three-helix bundles. Folding & Design, 1998, 3, R29-R40.	4.5	57
134	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, 13914-13926.	6.6	55
135	Protein-directed self-assembly of a fullerene crystal. Nature Communications, 2016, 7, 11429.	5.8	55
136	Proton and metal ion-dependent assembly of a model diiron protein. Protein Science, 2001, 10, 958-969.	3.1	54
137	Computational Design and Elaboration of a de Novo Heterotetrameric Î±-Helical Protein That Selectively Binds an Emissive Abiological (Porphinato)zinc Chromophore. Journal of the American Chemical Society, 2010, 132, 3997-4005.	6.6	54
138	Computational Design of a Î²-Peptide That Targets Transmembrane Helices. Journal of the American Chemical Society, 2011, 133, 12378-12381.	6.6	54
139	Sliding Helix and Change of Coordination Geometry in a Model Di-MnII Protein. Angewandte Chemie - International Edition, 2003, 42, 417-420.	7.2	52
140	Probing Membrane Insertion Activity of Antimicrobial Polymers via Coarse-Grain Molecular Dynamics. Journal of Chemical Theory and Computation, 2006, 2, 649-655.	2.3	52
141	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, 1067-1076.	1.6	52
142	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.	3.3	52
143	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.	1.3	51
144	Pharmacologic Blockade of Î±vÎ²1 Integrin Ameliorates Renal Failure and Fibrosis In Vivo. Journal of the American Society of Nephrology: JASN, 2017, 28, 1998-2005.	3.0	51

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145	Response of a Designed Metalloprotein to Changes in Metal Ion Coordination, Exogenous Ligands, and Active Site Volume Determined by X-ray Crystallography. Journal of the American Chemical Society, 2005, 127, 17266-17276.	6.6	49
146	Inhibitors of the Influenza A Virus M2 Proton Channel Discovered Using a High-Throughput Yeast Growth Restoration Assay. PLoS ONE, 2013, 8, e55271.	1.1	48
147	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. Journal of Medicinal Chemistry, 2013, 56, 9265-9274.	2.9	46
148	De novo design of heterotrimeric coiled coils. , 1996, 40, 495-504.		45
149	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, 1207-1216.	2.9	45
150	Dynamics of a De Novo Designed Three-Helix Bundle Protein Studied by15N,13C, and2H NMR Relaxation Methodsâ€. Biochemistry, 2001, 40, 9560-9569.	1.2	44
151	An M2-V27A channel blocker demonstrates potent inÂvitro and inÂvivo antiviral activities against amantadine-sensitive and -resistant influenza A viruses. Antiviral Research, 2017, 140, 45-54.	1.9	44
152	De novo metalloprotein design. Nature Reviews Chemistry, 2022, 6, 31-50.	13.8	44
153	Centrosymmetric bilayers in the 0.75 Ã¥ resolution structure of a designed alphaâ€helical peptide, D, Lâ€Alphaâ€1. Protein Science, 1999, 8, 1410-1422.	3.1	43
154	Diiron-containing metalloproteins: Developing functional models. Comptes Rendus Chimie, 2007, 10, 703-720.	0.2	42
155	Spectroscopic and Computational Studies of the de Novo Designed Protein DF2t:Â Correlation to the Biferrous Active Site of Ribonucleotide Reductase and Factors That Affect O2Reactivity. Journal of the American Chemical Society, 2005, 127, 16098-16106.	6.6	41
156	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, 379-391.	2.0	40
157	Association of a Model Transmembrane Peptide Containing Gly in a Heptad Sequence Motif. Biophysical Journal, 2004, 87, 3421-3429.	0.2	39
158	Crystal structure of the drugâ€resistant S31N influenza M2 proton channel. Protein Science, 2016, 25, 1551-1554.	3.1	38
159	Kindlin-3 Undergoes Endoproteolysis in Stored Platelets and After Platelet Stimulation. Blood, 2011, 118, 1255-1255.	0.6	38
160	Thermodynamic genetics of the folding of the B1 immunoglobulin-binding domain from streptococcal protein G. Proteins: Structure, Function and Bioinformatics, 1995, 21, 11-21.	1.5	37
161	SNAC-tag for sequence-specific chemical protein cleavage. Nature Methods, 2019, 16, 319-322.	9.0	36
162	The Structure of a Designed Diiron(III) Protein: Implications for Cofactor Stabilization and Catalysis. Angewandte Chemie - International Edition, 2006, 45, 4951-4954.	7.2	35

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163	Allosteric cooperation in a de novo-designed two-domain protein. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 33246-33253.	3.3	35
164	The Design of Efficient Î±-Helical C-Capping Auxiliaries. Journal of the American Chemical Society, 1998, 120, 2764-2767.	6.6	34
165	Evolution of binding affinity in a WW domain probed by phage display. Protein Science, 2000, 9, 2366-2376.	3.1	34
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