

Lila M Gierasch

List of Publications by Year in Descending Order

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

160
papers

10,783
citations

58
h-index

101
g-index

203
ext. papers

11,614
ext. citations

9.5
avg, IF

6.49
L-index

#	Paper	IF	Citations
160	There are more Hsp90 chaperone mechanisms in heaven and earth, dear reader, than are dreamt of in your philosophy.. <i>Molecular Cell</i> , 2022 , 82, 1403-1404	17.6	2
159	Physics-based modeling provides predictive understanding of selectively promiscuous substrate binding by Hsp70 chaperones. <i>PLoS Computational Biology</i> , 2021 , 17, e1009567	5	1
158	Selective promiscuity in the binding of Hsp70 to an unfolded protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
157	The Proteome Folding Problem and Cellular Proteostasis. <i>Journal of Molecular Biology</i> , 2021 , 433, 16719-1675	7.5	4
156	How the Protein Data Bank changed biology: An introduction to the JBC Reviews thematic series, part 1. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100608	5.4	5
155	How the Protein Data Bank changed biology: An introduction to the JBC Reviews thematic series, part 2. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100748	5.4	
154	Opening ASBMB publications freely to all. <i>Journal of Biological Chemistry</i> , 2020 , 295, 7814-7815	5.4	0
153	2021 JBC Herbert Tabor Early Career Investigator Awards: Call for nominations. <i>Journal of Biological Chemistry</i> , 2020 , 295, 13697	5.4	
152	Hsp70 molecular chaperones: multifunctional allosteric holding and unfolding machines. <i>Biochemical Journal</i> , 2019 , 476, 1653-1677	3.8	36
151	Kinetic versus thermodynamic control of mutational effects on protein homeostasis: A perspective from computational modeling and experiment. <i>Protein Science</i> , 2019 , 28, 1324-1339	6.3	4
150	Celebrating the scientific legacy of Herbert Tabor. <i>Journal of Biological Chemistry</i> , 2019 , 294, 1635-1637	5.4	1
149	Proper secretion of the serpin antithrombin relies strictly on thiol-dependent quality control. <i>Journal of Biological Chemistry</i> , 2019 , 294, 18992-19011	5.4	3
148	Recent advances in the structural and mechanistic aspects of Hsp70 molecular chaperones. <i>Journal of Biological Chemistry</i> , 2019 , 294, 2085-2097	5.4	130
147	Allosteric landscapes of eukaryotic cytoplasmic Hsp70s are shaped by evolutionary tuning of key interfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 11970-11975	11.5	21
146	Local and non-local topological information in the denatured state ensemble of a β barrel protein. <i>Protein Science</i> , 2018 , 27, 2062-2072	6.3	0
145	Ligand-promoted protein folding by biased kinetic partitioning. <i>Nature Chemical Biology</i> , 2017 , 13, 369-371	11.7	11
144	Key features of an Hsp70 chaperone allosteric landscape revealed by ion-mobility native mass spectrometry and double electron-electron resonance. <i>Journal of Biological Chemistry</i> , 2017 , 292, 8773-8785	5.4	33

143	Expression and Purification of Active Recombinant Human Alpha-1 Antitrypsin (AAT) from <i>Escherichia coli</i> . <i>Methods in Molecular Biology</i> , 2017 , 1639, 195-209	1.4	5
142	The Hsp70 interdomain linker is a dynamic switch that enables allosteric communication between two structured domains. <i>Journal of Biological Chemistry</i> , 2017 , 292, 14765-14774	5.4	37
141	Division of Labor: ER-Resident BiP Co-Chaperones Match Substrates to Fates Based on Specific Binding Sequences. <i>Molecular Cell</i> , 2016 , 63, 721-3	17.6	1
140	Cellular folding pathway of a metastable serpin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 6484-9	11.5	14
139	A Loyal Friend of ASBMB and JBC: Howard Schachman, 1918-2016. <i>Journal of Biological Chemistry</i> , 2016 , 291, 19724	5.4	
138	Its preferential interactions with biopolymers account for diverse observed effects of trehalose. <i>Biophysical Journal</i> , 2015 , 109, 144-53	2.9	21
137	Individual and collective contributions of chaperoning and degradation to protein homeostasis in <i>E. coli</i> . <i>Cell Reports</i> , 2015 , 11, 321-33	10.6	31
136	Substrate-binding domain conformational dynamics mediate Hsp70 allostery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E2865-73	11.5	81
135	How hsp70 molecular machines interact with their substrates to mediate diverse physiological functions. <i>Journal of Molecular Biology</i> , 2015 , 427, 1575-88	6.5	206
134	Comparing protein folding in vitro and in vivo: foldability meets the fitness challenge. <i>Current Opinion in Structural Biology</i> , 2014 , 24, 81-90	8.1	67
133	Energy landscapes of functional proteins are inherently risky. <i>Nature Chemical Biology</i> , 2014 , 10, 884-91	11.7	74
132	Physicochemical properties of cells and their effects on intrinsically disordered proteins (IDPs). <i>Chemical Reviews</i> , 2014 , 114, 6661-714	68.1	301
131	ATPase subdomain IA is a mediator of interdomain allostery in Hsp70 molecular chaperones. <i>PLoS Computational Biology</i> , 2014 , 10, e1003624	5	65
130	Challenges and dreams: physics of weak interactions essential to life. <i>Molecular Biology of the Cell</i> , 2014 , 25, 3474-7	3.5	39
129	The Role of Aromatic-Aromatic Interactions in Strand-Strand Stabilization of β Sheets. <i>Journal of Molecular Biology</i> , 2013 , 425, 3522-35	6.5	22
128	Delicate balance between functionally required flexibility and aggregation risk in a β Rich protein. <i>Biochemistry</i> , 2013 , 52, 8843-54	3.2	18
127	Early folding events protect aggregation-prone regions of a β Rich protein. <i>Structure</i> , 2013 , 21, 476-85	5.2	12
126	How bacteria survive an acid trip. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 5279-80	11.5	13

125	An interdomain energetic tug-of-war creates the allosterically active state in Hsp70 molecular chaperones. <i>Cell</i> , 2012 , 151, 1296-307	56.2	192
124	FoldEco: a model for proteostasis in <i>E. coli</i> . <i>Cell Reports</i> , 2012 , 1, 265-76	10.6	61
123	You got to know when to hold (or unfold) τ m. <i>Molecular Cell</i> , 2012 , 48, 3-4	17.6	2
122	Allosteric signal transmission in the nucleotide-binding domain of 70-kDa heat shock protein (Hsp70) molecular chaperones. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 6987-92	11.5	112
121	How one bad protein spoils the barrel: structural details of β -microglobulin amyloidogenicity. <i>Molecular Cell</i> , 2011 , 41, 129-31	17.6	4
120	Conserved, disordered C terminus of DnaK enhances cellular survival upon stress and DnaK in vitro chaperone activity. <i>Journal of Biological Chemistry</i> , 2011 , 286, 31821-9	5.4	44
119	Dynamic local unfolding in the serpin β 1 antitrypsin provides a mechanism for loop insertion and polymerization. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 222-6	17.6	46
118	Protein folding in the cell: challenges and progress. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 32-418.1		123
117	A career pathway in protein folding: from model peptides to postreductionist protein science. <i>Protein Science</i> , 2011 , 20, 783-90	6.3	3
116	The Power of Physical Chemistry Unleashed on Proteins. <i>Journal of Physical Chemistry Letters</i> , 2011 , 2, 327-328	6.4	
115	Exploring weak, transient protein-protein interactions in crowded in vivo environments by in-cell nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 2011 , 50, 9225-36	3.2	125
114	Nature's molecular sponges: small heat shock proteins grow into their chaperone roles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 2727-8	11.5	78
113	Macromolecular crowding remodels the energy landscape of a protein by favoring a more compact unfolded state. <i>Journal of the American Chemical Society</i> , 2010 , 132, 10445-52	16.4	128
112	Role of Hsp70 ATPase domain intrinsic dynamics and sequence evolution in enabling its functional interactions with NEFs. <i>PLoS Computational Biology</i> , 2010 , 6, e1000931	5	48
111	Unique physical properties and interactions of the domains of methylated DNA binding protein 2. <i>Biochemistry</i> , 2010 , 49, 4395-410	3.2	77
110	An interdomain sector mediating allostery in Hsp70 molecular chaperones. <i>Molecular Systems Biology</i> , 2010 , 6, 414	12.2	104
109	Segmental isotopic labeling of the Hsp70 molecular chaperone DnaK using expressed protein ligation. <i>Biopolymers</i> , 2010 , 94, 742-52	2.2	14
108	Exploring the interactions between signal sequences and <i>E. coli</i> SRP by two distinct and complementary crosslinking methods. <i>Biopolymers</i> , 2009 , 92, 201-11	2.2	12

107	Post-reductionist protein science, or putting Humpty Dumpty back together again. <i>Nature Chemical Biology</i> , 2009 , 5, 774-7	11.7	93
106	Sending signals dynamically. <i>Science</i> , 2009 , 324, 198-203	33.3	423
105	The molecular dating game: an antibody heavy chain hangs loose with a chaperone while waiting for its life partner. <i>Molecular Cell</i> , 2009 , 34, 635-6	17.6	3
104	A method for direct measurement of protein stability in vivo. <i>Methods in Molecular Biology</i> , 2009 , 490, 165-78	1.4	3
103	Rett syndrome-causing mutations in human MeCP2 result in diverse structural changes that impact folding and DNA interactions. <i>Journal of Biological Chemistry</i> , 2008 , 283, 20523-34	5.4	48
102	Chapter 3: A fluorescent window into protein folding and aggregation in cells. <i>Methods in Cell Biology</i> , 2008 , 89, 59-70	1.8	3
101	Use of synthetic signal sequences to explore the protein export machinery. <i>Biopolymers</i> , 2008 , 90, 307-12	19.2	18
100	Roles of beta-turns in protein folding: from peptide models to protein engineering. <i>Biopolymers</i> , 2008 , 89, 380-91	2.2	141
99	Cross-strand split tetra-Cys motifs as structure sensors in a beta-sheet protein. <i>Chemistry and Biology</i> , 2008 , 15, 1104-15		45
98	From the test tube to the cell: exploring the folding and aggregation of a beta-clam protein. <i>Biopolymers</i> , 2007 , 88, 157-63	2.2	98
97	Site-specific fluorescent labeling of poly-histidine sequences using a metal-chelating cysteine. <i>Chemical Biology and Drug Design</i> , 2007 , 69, 31-40	2.9	27
96	In-cell aggregation of a polyglutamine-containing chimera is a multistep process initiated by the flanking sequence. <i>Journal of Biological Chemistry</i> , 2007 , 282, 36736-43	5.4	54
95	Hsp70 chaperone ligands control domain association via an allosteric mechanism mediated by the interdomain linker. <i>Molecular Cell</i> , 2007 , 26, 27-39	17.6	254
94	Effects of osmolytes on protein folding and aggregation in cells. <i>Methods in Enzymology</i> , 2007 , 428, 355-72	17.7	53
93	Electrophysiological studies in <i>Xenopus</i> oocytes for the opening of <i>Escherichia coli</i> SecA-dependent protein-conducting channels. <i>Journal of Membrane Biology</i> , 2006 , 214, 103-13	2.3	19
92	The changing landscape of protein allostery. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 102-8	8.1	261
91	Natural polypeptide scaffolds: beta-sheets, beta-turns, and beta-hairpins. <i>Biopolymers</i> , 2006 , 84, 13-22	2.2	39
90	Extended polyglutamine tracts cause aggregation and structural perturbation of an adjacent beta barrel protein. <i>Journal of Biological Chemistry</i> , 2006 , 281, 12959-67	5.4	50

89	Direct comparison of a stable isolated Hsp70 substrate-binding domain in the empty and substrate-bound states. <i>Journal of Biological Chemistry</i> , 2006 , 281, 1605-11	5.4	56
88	The structure of Escherichia coli signal recognition particle revealed by scanning transmission electron microscopy. <i>Molecular Biology of the Cell</i> , 2006 , 17, 5063-74	3.5	5
87	Inhibition of protein aggregation in vitro and in vivo by a natural osmoprotectant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 13357-61	11.5	248
86	Evolutionary coupling of structural and functional sequence information in the intracellular lipid-binding protein family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 373-84	4.2	29
85	A multipronged approach to the mechanism of allostery in Hsp70 chaperones. <i>FASEB Journal</i> , 2006 , 20, A964	0.9	1
84	A well-defined amphipathic conformation for the calcium-free cyclic lipopeptide antibiotic, daptomycin, in aqueous solution. <i>Biopolymers</i> , 2005 , 80, 374-85	2.2	41
83	Aggregation of a slow-folding mutant of a beta-clam protein proceeds through a monomeric nucleus. <i>Biochemistry</i> , 2005 , 44, 7266-74	3.2	57
82	Finding the fittest fold: using the evolutionary record to design new proteins. <i>Cell</i> , 2005 , 122, 832-4	56.2	5
81	First glimpses of a chaperonin-bound folding intermediate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 13715-6	11.5	6
80	The conformation of a signal peptide bound by Escherichia coli preprotein translocase SecA. <i>Journal of Biological Chemistry</i> , 2005 , 280, 32753-60	5.4	29
79	Monitoring protein stability and aggregation in vivo by real-time fluorescent labeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 523-8	11.5	202
78	Sequence and structural analysis of cellular retinoic acid-binding proteins reveals a network of conserved hydrophobic interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 179-94	4.2	32
77	Phospholipid-induced monomerization and signal-peptide-induced oligomerization of SecA. <i>Journal of Biological Chemistry</i> , 2003 , 278, 3628-38	5.4	86
76	Native structural propensity in cellular retinoic acid-binding protein I 64-88: the role of locally encoded structure in the folding of a beta-barrel protein. <i>Biophysical Chemistry</i> , 2003 , 100, 421-36	3.5	9
75	Local sequence information in cellular retinoic acid-binding protein I: specific residue roles in beta-turns. <i>Biopolymers</i> , 2003 , 71, 638-51	2.2	13
74	Role of local sequence in the folding of cellular retinoic acid-binding protein I: structural propensities of reverse turns. <i>Biochemistry</i> , 2003 , 42, 7976-85	3.2	30
73	Functionally significant mobile regions of Escherichia coli SecA ATPase identified by NMR. <i>Journal of Biological Chemistry</i> , 2002 , 277, 50985-90	5.4	22
72	Mapping the signal sequence-binding site on SRP reveals a significant role for the NG domain. <i>Journal of Biological Chemistry</i> , 2002 , 277, 46763-8	5.4	23

71	Caught in the act: how ATP binding triggers cooperative conformational changes in a molecular machine. <i>Molecular Cell</i> , 2002 , 9, 3-5	17.6	4
70	Keeping it in the family: folding studies of related proteins. <i>Current Opinion in Structural Biology</i> , 2001 , 11, 83-93	8.1	106
69	Signal peptides bind and aggregate RNA. An alternative explanation for GTPase inhibition in the signal recognition particle. <i>Journal of Biological Chemistry</i> , 2001 , 276, 12222-7	5.4	6
68	The cost of exposing a hydrophobic loop and implications for the functional role of 4.5 S RNA in the Escherichia coli signal recognition particle. <i>Journal of Biological Chemistry</i> , 2001 , 276, 19327-31	5.4	10
67	Functional signal peptides bind a soluble N-terminal fragment of SecA and inhibit its ATPase activity. <i>Journal of Biological Chemistry</i> , 2001 , 276, 19648-55	5.4	32
66	Defining the structure of the substrate-free state of the DnaK molecular chaperone. <i>Biochemical Society Symposia</i> , 2001 , 69-82		3
65	Structural insights into substrate binding by the molecular chaperone DnaK. <i>Nature Structural Biology</i> , 2000 , 7, 298-303		165
64	Multiple roles of prolyl residues in structure and folding. <i>Journal of Molecular Biology</i> , 2000 , 301, 737-476.5		77
63	GroEL-substrate interactions: molding the fold, or folding the mold?. <i>Cell</i> , 2000 , 100, 193-6	56.2	33
62	Protein Conformational Stability Probed by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2000 , 122, 495-500	16.4	76
61	Dynamics of cellular retinoic acid binding protein I on multiple time scales with implications for ligand binding. <i>Biochemistry</i> , 2000 , 39, 9119-29	3.2	44
60	Unfolding dynamics of a beta-sheet protein studied by mass spectrometry. <i>Journal of Mass Spectrometry</i> , 1999 , 34, 1289-95	2.2	41
59	Basis of substrate binding by the chaperonin GroEL. <i>Biochemistry</i> , 1999 , 38, 12537-46	3.2	58
58	Mutations in the substrate binding domain of the Escherichia coli 70 kDa molecular chaperone, DnaK, which alter substrate affinity or interdomain coupling. <i>Journal of Molecular Biology</i> , 1999 , 286, 915-32	6.5	125
57	Probing the folding pathway of a beta-clam protein with single-tryptophan constructs. <i>Folding & Design</i> , 1998 , 3, 401-12		51
56	Molecular chaperones: clamps for the Clps?. <i>Current Biology</i> , 1998 , 8, R464-7	6.3	15
55	The LDL receptor clustering motif interacts with the clathrin terminal domain in a reverse turn conformation. <i>Journal of Cell Biology</i> , 1998 , 142, 59-67	7.3	80
54	Domain interactions in E. coli SRP: stabilization of M domain by RNA is required for effective signal sequence modulation of NG domain. <i>Molecular Cell</i> , 1997 , 1, 79-87	17.6	71

53	Cavity formation before stable hydrogen bonding in the folding of a beta-clam protein. <i>Nature Structural and Molecular Biology</i> , 1997 , 4, 883-6	17.6	58
52	Local interactions in a Schellman motif dictate interhelical arrangement in a protein fragment. <i>Folding & Design</i> , 1997 , 2, 211-22		25
51	A Novel Conformation in a Highly Potent, Constrained Gonadotropin-Releasing Hormone Antagonist. <i>Journal of the American Chemical Society</i> , 1996 , 118, 970-976	16.4	14
50	Signal sequences: the same yet different. <i>Cell</i> , 1996 , 86, 849-52	56.2	91
49	Intrinsic tryptophans of CRABPI as probes of structure and folding. <i>Protein Science</i> , 1996 , 5, 1108-17	6.3	72
48	The crystal structure of the GroES co-chaperonin at 2.8 Å resolution. <i>Nature</i> , 1996 , 379, 37-45	50.4	408
47	The structure of Escherichia coli heat-stable enterotoxin b by nuclear magnetic resonance and circular dichroism. <i>Protein Science</i> , 1995 , 4, 1718-29	6.3	42
46	¹ H and ¹⁵ N resonance assignments and secondary structure of cellular retinoic acid-binding protein with and without bound ligand. <i>Journal of Biomolecular NMR</i> , 1994 , 4, 741-60	3	38
45	Molecular chaperones. Panning for chaperone-binding peptides. <i>Current Biology</i> , 1994 , 4, 173-4	6.3	3
44	Equilibrium folding studies of cellular retinoic acid binding protein, a predominantly beta-sheet protein. <i>Biochemistry</i> , 1994 , 33, 134-42	3.2	76
43	Conformational behavior of Escherichia coli OmpA signal peptides in membrane mimetic environments. <i>Biochemistry</i> , 1993 , 32, 4881-94	3.2	192
42	Membrane-bound conformation of a signal peptide: a transferred nuclear Overhauser effect analysis. <i>Biochemistry</i> , 1993 , 32, 13991-9	3.2	74
41	Conformational analysis of a highly potent dicyclic gonadotropin-releasing hormone antagonist by nuclear magnetic resonance and molecular dynamics. <i>Journal of Medicinal Chemistry</i> , 1993 , 36, 3265-73	8.3	26
40	Characterization of a functionally important mobile domain of GroES. <i>Nature</i> , 1993 , 364, 255-8	50.4	213
39	GTP binding and hydrolysis by the signal recognition particle during initiation of protein translocation. <i>Nature</i> , 1993 , 366, 351-4	50.4	165
38	Constrained peptides: models of bioactive peptides and protein substructures. <i>Annual Review of Biochemistry</i> , 1992 , 61, 387-418	29.1	337
37	Conformational analysis of a highly potent, constrained gonadotropin-releasing hormone antagonist. 1. Nuclear magnetic resonance. <i>Journal of the American Chemical Society</i> , 1992 , 114, 2852-2859	16.4	36
36	Renaturation of citrate synthase: influence of denaturant and folding assistants. <i>Protein Science</i> , 1992 , 1, 522-9	6.3	87

35	Mutating the charged residues in the binding pocket of cellular retinoic acid-binding protein simultaneously reduces its binding affinity to retinoic acid and increases its thermostability. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 13, 87-99	4.2	79
34	Biophysical studies of recognition sequences for targeting and folding. <i>Antonie Van Leeuwenhoek</i> , 1992 , 61, 93-9	2.1	1
33	Different conformations for the same polypeptide bound to chaperones DnaK and GroEL. <i>Nature</i> , 1992 , 355, 455-7	50.4	289
32	Solution conformations of two flexible cyclic pentapeptides: cyclo(Gly-Pro-D-Phe-Gly-Ala) and cyclo(Gly-Pro-D-Phe-Gly-Val). <i>Biopolymers</i> , 1992 , 32, 1713-25	2.2	13
31	Combined use of molecular dynamics simulations and NMR to explore peptide bond isomerization and multiple intramolecular hydrogen-bonding possibilities in a cyclic pentapeptide, cyclo(Gly-Pro-D-Phe-Gly-Val). <i>Biopolymers</i> , 1992 , 32, 1727-39	2.2	10
30	Impact of a micellar environment on the conformations of two cyclic pentapeptides. <i>Biopolymers</i> , 1992 , 32, 1741-54	2.2	17
29	Side chain-backbone hydrogen bonding contributes to helix stability in peptides derived from an alpha-helical region of carboxypeptidase A. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991 , 10, 130-9	4.2	129
28	Hydrophobic content and lipid interactions of wild-type and mutant OmpA signal peptides correlate with their in vivo function. <i>Biochemistry</i> , 1991 , 30, 10155-63	3.2	76
27	The chaperonin GroEL binds a polypeptide in an alpha-helical conformation. <i>Biochemistry</i> , 1991 , 30, 7359-62	3.62	169
26	The NPXY internalization signal of the LDL receptor adopts a reverse-turn conformation. <i>Cell</i> , 1991 , 67, 1195-201	56.2	250
25	Design of biologically active, conformationally constrained GnRH antagonists. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990 , 8, 295-304	4.2	46
24	Biophysical studies of signal peptides: implications for signal sequence functions and the involvement of lipid in protein export. <i>Journal of Bioenergetics and Biomembranes</i> , 1990 , 22, 213-32	3.7	53
23	Cyclic pentapeptides as models for reverse turns: determination of the equilibrium distribution between type I and type II conformations of Pro-Asn and Pro-Ala beta-turns. <i>Biopolymers</i> , 1990 , 29, 263-87	3.2	87
22	Reduced tendency to form a beta turn in peptides from the P22 tailspike protein correlates with a temperature-sensitive folding defect. <i>Biochemistry</i> , 1990 , 29, 9765-71	3.2	23
21	Ring opening of cyclic pentapeptides by electron impact mass spectrometry: correlation with peptide bond nonplanarity. <i>Journal of the American Chemical Society</i> , 1989 , 111, 5487-5488	16.4	1
20	Signal sequences. <i>Biochemistry</i> , 1989 , 28, 923-30	3.2	482
19	Helix formation and stability in a signal sequence. <i>Biochemistry</i> , 1989 , 28, 8554-61	3.2	82
18	Conformations and orientations of a signal peptide interacting with phospholipid monolayers. <i>Biochemistry</i> , 1989 , 28, 2789-97	3.2	82

17	Crystal structure of cyclo(Gly1-L-Pro2-D-Phe3-L-Ala4-L-Pro5): a cyclic pentapeptide with a Gly-L-Pro .delta. turn. <i>Journal of the American Chemical Society</i> , 1988 , 110, 5157-5161	16.4	25
16	Nuclear magnetic resonance analysis and conformational characterization of a cyclic decapeptide antagonist of gonadotropin-releasing hormone. <i>Biochemistry</i> , 1987 , 26, 2642-56	3.2	43
15	Compatibility of .beta.- and .gamma.-turn features with a peptide backbone modification: synthesis and conformational analysis of a model cyclic pseudopentapeptide. <i>Journal of the American Chemical Society</i> , 1986 , 108, 825-831	16.4	62
14	Molecular mechanisms of protein secretion: the role of the signal sequence. <i>Advances in Protein Chemistry</i> , 1986 , 38, 109-80		184
13	Conformational analysis of a cyclic pentapeptide by one- and two-dimensional nuclear Overhauser effect spectroscopy. <i>Journal of the American Chemical Society</i> , 1985 , 107, 1400-1407	16.4	41
12	Dehydrophenylalanine as the i + 2th residue of a .beta. turn: synthesis and conformational analysis of cyclo(Gly-Pro-.DELTA.z-Phe-D-Ala-Pro) and cyclo(Gly-Pro-D-Phe-D-Ala-Pro). <i>Journal of the American Chemical Society</i> , 1985 , 107, 3349-3350	16.4	37
11	Crystal and solution structures of cyclo(Ala-Pro-Gly-D-Phe-Pro): a new type of cyclic pentapeptide which undergoes cis-trans isomerization of the Ala-Pro bond. <i>Journal of the American Chemical Society</i> , 1985 , 107, 3321-3327	16.4	21
10	Conformation of a peptide solubilize in a reversed micelle water pool. <i>Journal of the American Chemical Society</i> , 1984 , 106, 3648-3652	16.4	54
9	Exploring the conformational roles of signal sequences: synthesis and conformational analysis of lambda receptor protein wild-type and mutant signal peptides. <i>Biochemistry</i> , 1984 , 23, 3111-4	3.2	115
8	Conformational comparison of cyclic peptide and pseudopeptide structures with intramolecular hydrogen bonding. <i>Biopolymers</i> , 1983 , 22, 147-151	2.2	11
7	Spectroscopic studies of a hydrophobic peptide in membranelike environments. <i>Biopolymers</i> , 1983 , 22, 381-385	2.2	4
6	Crystal structures, molecular conformations, infrared spectra, and carbon-13 NMR spectra of methylproline peptides in the solid state. <i>Journal of the American Chemical Society</i> , 1983 , 105, 6609-6614	16.4	40
5	Interior turns in globular proteins. <i>Nature</i> , 1983 , 304, 654-7	50.4	47
4	Determination of proline ring nonplanarity from proton spin-spin coupling constants: applications to two cyclic pentapeptides. <i>Journal of the American Chemical Society</i> , 1982 , 104, 572-576	16.4	13
3	Spin trapping in heterogeneous electron transfer processes. <i>Canadian Journal of Chemistry</i> , 1982 , 60, 1621-1636	0.9	49
2	Interfacial spin trapping in model membrane systems. <i>Biochemical and Biophysical Research Communications</i> , 1981 , 102, 1350-7	3.4	8
1	Conformations of (X-L-Pro-Y) ₂ cyclic hexapeptides. Preferred beta-turn conformers and implications for beta turns in proteins. <i>Biochemistry</i> , 1981 , 20, 4730-8	3.2	196