

Lila M Gierasch

List of Publications by Year in descending order

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195
papers

12,379
citations

22132

59
h-index

26591

107
g-index

203
all docs

203
docs citations

203
times ranked

9471
citing authors

#	ARTICLE	IF	CITATIONS
1	Signal sequences. <i>Biochemistry</i> , 1989, 28, 923-930.	1.2	514
2	Sending Signals Dynamically. <i>Science</i> , 2009, 324, 198-203.	6.0	471
3	The crystal structure of the GroES co-chaperonin at 2.8 Å... resolution. <i>Nature</i> , 1996, 379, 37-45.	13.7	452
4	Physicochemical Properties of Cells and Their Effects on Intrinsically Disordered Proteins (IDPs). <i>Chemical Reviews</i> , 2014, 114, 6661-6714.	23.0	391
5	Constrained Peptides: Models of Bioactive Peptides and Protein Substructures. <i>Annual Review of Biochemistry</i> , 1992, 61, 387-416.	5.0	360
6	Different conformations for the same polypeptide bound to chaperones DnaK and GroEL. <i>Nature</i> , 1992, 355, 455-457.	13.7	315
7	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, 13357-13361.	3.3	296
8	Hsp70 Chaperone Ligands Control Domain Association via an Allosteric Mechanism Mediated by the Interdomain Linker. <i>Molecular Cell</i> , 2007, 26, 27-39.	4.5	287
9	The changing landscape of protein allostery. <i>Current Opinion in Structural Biology</i> , 2006, 16, 102-108.	2.6	282
10	How Hsp70 Molecular Machines Interact with Their Substrates to Mediate Diverse Physiological Functions. <i>Journal of Molecular Biology</i> , 2015, 427, 1575-1588.	2.0	271
11	The NPXY internalization signal of the LDL receptor adopts a reverse-turn conformation. <i>Cell</i> , 1991, 67, 1195-1201.	13.5	264
12	An Interdomain Energetic Tug-of-War Creates the Allosterically Active State in Hsp70 Molecular Chaperones. <i>Cell</i> , 2012, 151, 1296-1307.	13.5	240
13	Characterization of a functionally important mobile domain of GroES. <i>Nature</i> , 1993, 364, 255-258.	13.7	234
14	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, 523-528.	3.3	226
15	Molecular Mechanisms of Protein Secretion: The Role of the Signal Sequence. <i>Advances in Protein Chemistry</i> , 1986, 38, 109-180.	4.4	213
16	Recent advances in the structural and mechanistic aspects of Hsp70 molecular chaperones. <i>Journal of Biological Chemistry</i> , 2019, 294, 2085-2097.	1.6	202
17	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, 4730-4738.	1.2	200
18	Conformational behavior of Escherichia coli OmpA signal peptides in membrane mimetic environments. <i>Biochemistry</i> , 1993, 32, 4881-4894.	1.2	200

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19	Roles of β -turns in protein folding: From peptide models to protein engineering. <i>Biopolymers</i> , 2008, 89, 380-391.	1.2	194
20	GTP binding and hydrolysis by the signal recognition particle during initiation of protein translocation. <i>Nature</i> , 1993, 366, 351-354.	13.7	187
21	The chaperonin GroEL binds a polypeptide in an α -helical conformation. <i>Biochemistry</i> , 1991, 30, 7359-7362.	1.2	186
22	Structural insights into substrate binding by the molecular chaperone DnaK. <i>Nature Structural Biology</i> , 2000, 7, 298-303.	9.7	184
23	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, 10445-10452.	6.6	144
24	Side chain-backbone hydrogen bonding contributes to helix stability in peptides derived from an α -helical region of carboxypeptidase A. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 10, 130-139.	1.5	141
25	Exploring Weak, Transient Protein-Protein Interactions in Crowded In Vivo Environments by In-Cell Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 2011, 50, 9225-9236.	1.2	140
26	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, 6987-6992.	3.3	140
27	Protein folding in the cell: challenges and progress. <i>Current Opinion in Structural Biology</i> , 2011, 21, 32-41.	2.6	140
28	Mutations in the substrate binding domain of the Escherichia coli 70 kDa molecular chaperone, DnaK, which alter substrate affinity or interdomain coupling 1 Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 1999, 286, 915-932.	2.0	135
29	Exploring the conformational roles of signal sequences: synthesis and conformational analysis of λ receptor protein wild-type and mutant signal peptides. <i>Biochemistry</i> , 1984, 23, 3111-3114.	1.2	124
30	An interdomain sector mediating allostery in Hsp70 molecular chaperones. <i>Molecular Systems Biology</i> , 2010, 6, 414.	3.2	118
31	Keeping it in the family: folding studies of related proteins. <i>Current Opinion in Structural Biology</i> , 2001, 11, 83-93.	2.6	107
32	Post-reductionist protein science, or putting Humpty Dumpty back together again. <i>Nature Chemical Biology</i> , 2009, 5, 774-777.	3.9	107
33	From the test tube to the cell: Exploring the folding and aggregation of a β -claw protein. <i>Biopolymers</i> , 2007, 88, 157-163.	1.2	103
34	Signal Sequences: The Same Yet Different. <i>Cell</i> , 1996, 86, 849-852.	13.5	102
35	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.	3.3	101
36	Renaturation of citrate synthase: Influence of denaturant and folding assistants. <i>Protein Science</i> , 1992, 1, 522-529.	3.1	98

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37	ATPase Subdomain IA Is a Mediator of Interdomain Allostery in Hsp70 Molecular Chaperones. PLoS Computational Biology, 2014, 10, e1003624.	1.5	98
38	Nature's molecular sponges: Small heat shock proteins grow into their chaperone roles. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2727-2728.	3.3	93
39	Unique Physical Properties and Interactions of the Domains of Methylated DNA Binding Protein 2. Biochemistry, 2010, 49, 4395-4410.	1.2	91
40	Conformations and orientations of a signal peptide interacting with phospholipid monolayers. Biochemistry, 1989, 28, 2789-2797.	1.2	90
41	Phospholipid-induced Monomerization and Signal-peptide-induced Oligomerization of SecA. Journal of Biological Chemistry, 2003, 278, 3628-3638.	1.6	90
42	Energy landscapes of functional proteins are inherently risky. Nature Chemical Biology, 2014, 10, 884-891.	3.9	90
43	Helix formation and stability in a signal sequence. Biochemistry, 1989, 28, 8554-8561.	1.2	89
44	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 γ -turns. Biopolymers, 1990, 29, 263-287.	1.2	89
45	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. Proteins: Structure, Function and Bioinformatics, 1992, 13, 87-99.	1.5	89
46	The LDL Receptor Clustering Motif Interacts with the Clathrin Terminal Domain in a Reverse Turn Conformation. Journal of Cell Biology, 1998, 142, 59-67.	2.3	86
47	Comparing protein folding in vitro and in vivo: foldability meets the fitness challenge. Current Opinion in Structural Biology, 2014, 24, 81-90.	2.6	85
48	Hydrophobic content and lipid interactions of wild-type and mutant OmpA signal peptides correlate with their in vivo function. Biochemistry, 1991, 30, 10155-10163.	1.2	83
49	Equilibrium folding studies of cellular retinoic acid binding protein, a predominantly β -sheet protein. Biochemistry, 1994, 33, 134-142.	1.2	81
50	Multiple roles of prolyl residues in structure and folding 1 Edited by C. Robert Matthews. Journal of Molecular Biology, 2000, 301, 737-747.	2.0	80
51	Protein Conformational Stability Probed by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Journal of the American Chemical Society, 2000, 122, 495-500.	6.6	77
52	Membrane-bound conformation of a signal peptide: A transferred nuclear Overhauser effect analysis. Biochemistry, 1993, 32, 13991-13999.	1.2	76
53	Intrinsic tryptophans of CRABPI as probes of structure and folding. Protein Science, 1996, 5, 1108-1117.	3.1	75
54	Domain Interactions in E. coli SRP: Stabilization of M Domain by RNA Is Required for Effective Signal Sequence Modulation of NG Domain. Molecular Cell, 1997, 1, 79-87.	4.5	75

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55	FoldEco: A Model for Proteostasis in E.Âcoli. Cell Reports, 2012, 1, 265-276.	2.9	72
56	Basis of Substrate Binding by the Chaperonin GroELâ€. Biochemistry, 1999, 38, 12537-12546.	1.2	66
57	Compatibility of .beta.- and .gamma.-turn features with a peptide backbone modification: synthesis and conformational analysis of a model cyclic pseudopentapeptide. Journal of the American Chemical Society, 1986, 108, 825-831.	6.6	65
58	Hsp70 molecular chaperones: multifunctional allosteric holding and unfolding machines. Biochemical Journal, 2019, 476, 1653-1677.	1.7	65
59	Direct Comparison of a Stable Isolated Hsp70 Substrate-binding Domain in the Empty and Substrate-bound States. Journal of Biological Chemistry, 2006, 281, 1605-1611.	1.6	63
60	Role of Hsp70 ATPase Domain Intrinsic Dynamics and Sequence Evolution in Enabling its Functional Interactions with NEFs. PLoS Computational Biology, 2010, 6, e1000931.	1.5	60
61	Aggregation of a Slow-Folding Mutant of a Î²-Clam Protein Proceeds through a Monomeric Nucleusâ€. Biochemistry, 2005, 44, 7266-7274.	1.2	59
62	Conserved, Disordered C Terminus of DnaK Enhances Cellular Survival upon Stress and DnaK in Vitro Chaperone Activity. Journal of Biological Chemistry, 2011, 286, 31821-31829.	1.6	59
63	Interior turns in globular proteins. Nature, 1983, 304, 654-657.	13.7	58
64	Conformation of a peptide solubilizate in a reversed micelle water pool. Journal of the American Chemical Society, 1984, 106, 3648-3652.	6.6	58
65	Cavity formation before stable hydrogen bonding in the folding of a Î²-clam protein. Nature Structural and Molecular Biology, 1997, 4, 883-886.	3.6	58
66	In-cell Aggregation of a Polyglutamine-containing Chimera Is a Multistep Process Initiated by the Flanking Sequence. Journal of Biological Chemistry, 2007, 282, 36736-36743.	1.6	58
67	Effects of Osmolytes on Protein Folding and Aggregation in Cells. Methods in Enzymology, 2007, 428, 355-372.	0.4	57
68	Rett Syndrome-causing Mutations in Human MeCP2 Result in Diverse Structural Changes That Impact Folding and DNA Interactions. Journal of Biological Chemistry, 2008, 283, 20523-20534.	1.6	57
69	Spin trapping in heterogeneous electron transfer processes. Canadian Journal of Chemistry, 1982, 60, 1621-1636.	0.6	55
70	Biophysical studies of signal peptides: Implications for signal sequence functions and the involvement of lipid in protein export. Journal of Bioenergetics and Biomembranes, 1990, 22, 213-232.	1.0	55
71	Extended Polyglutamine Tracts Cause Aggregation and Structural Perturbation of an Adjacent Î² Barrel Protein. Journal of Biological Chemistry, 2006, 281, 12959-12967.	1.6	55
72	Dynamic local unfolding in the serpin Î±1 antitrypsin provides a mechanism for loop insertion and polymerization. Nature Structural and Molecular Biology, 2011, 18, 222-226.	3.6	54

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73	Probing the folding pathway of a β^2 -clam protein with single-tryptophan constructs. <i>Folding & Design</i> , 1998, 3, 401-412.	4.5	53
74	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.	1.6	53
75	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.	1.6	51
76	The structure of <i>Escherichia coli</i> heat-stable enterotoxin b by nuclear magnetic resonance and circular dichroism. <i>Protein Science</i> , 1995, 4, 1718-1729.	3.1	50
77	Design of biologically active, conformationally constrained GnRH antagonists. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 295-304.	1.5	49
78	Challenges and dreams: physics of weak interactions essential to life. <i>Molecular Biology of the Cell</i> , 2014, 25, 3474-3477.	0.9	49
79	A well-defined amphipathic conformation for the calcium-free cyclic lipopeptide antibiotic, daptomycin, in aqueous solution. <i>Biopolymers</i> , 2005, 80, 374-385.	1.2	46
80	Cross-Strand Split Tetra-Cys Motifs as Structure Sensors in a β^2 -Sheet Protein. <i>Chemistry and Biology</i> , 2008, 15, 1104-1115.	6.2	46
81	Nuclear magnetic resonance analysis and conformational characterization of a cyclic decapeptide antagonist of gonadotropin-releasing hormone. <i>Biochemistry</i> , 1987, 26, 2642-2656.	1.2	45
82	Dynamics of Cellular Retinoic Acid Binding Protein I on Multiple Time Scales with Implications for Ligand Binding. <i>Biochemistry</i> , 2000, 39, 9119-9129.	1.2	45
83	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.	6.6	43
84	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.	6.6	43
85	Unfolding dynamics of a β^2 -sheet protein studied by mass spectrometry. <i>Journal of Mass Spectrometry</i> , 1999, 34, 1289-1295.	0.7	42
86	Natural polypeptide scaffolds: β^2 -sheets, β^2 -turns, and β^2 -hairpins. <i>Biopolymers</i> , 2006, 84, 13-22.	1.2	41
87	Dehydrophenylalanine as the i + 2th residue of a β 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.	6.6	40
88	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, 741-760.	1.6	39
89	Individual and Collective Contributions of Chaperoning and Degradation to Protein Homeostasis in <i>E. coli</i> . <i>Cell Reports</i> , 2015, 11, 321-333.	2.9	39
90	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.	6.6	38

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91	GroELâ€™Substrate Interactions. <i>Cell</i> , 2000, 100, 193-196.	13.5	38
92	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.	3.3	38
93	Functional Signal Peptides Bind a Soluble N-terminal Fragment of SecA and Inhibit Its ATPase Activity. <i>Journal of Biological Chemistry</i> , 2001, 276, 19648-19655.	1.6	36
94	Evolutionary coupling of structural and functional sequence information in the intracellular lipid-binding protein family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 373-384.	1.5	35
95	Sequence and structural analysis of cellular retinoic acid-binding proteins reveals a network of conserved hydrophobic interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 179-194.	1.5	34
96	The Conformation of a Signal Peptide Bound by Escherichia coli Preprotein Translocase SecA. <i>Journal of Biological Chemistry</i> , 2005, 280, 32753-32760.	1.6	33
97	Role of Local Sequence in the Folding of Cellular Retinoic Acid Binding Protein I:â€™% Structural Propensities of Reverse Turns. <i>Biochemistry</i> , 2003, 42, 7976-7985.	1.2	32
98	Site-specific Fluorescent Labeling of Poly-histidine Sequences Using a Metal-chelating Cysteine. <i>Chemical Biology and Drug Design</i> , 2007, 69, 31-40.	1.5	31
99	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.	6.6	28
100	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, 3265-3273.	2.9	28
101	Local interactions in a Schellman motif dictate interhelical arrangement in a protein fragment. <i>Folding & Design</i> , 1997, 2, 211-222.	4.5	27
102	Mapping the Signal Sequence-binding Site on SRP Reveals a Significant Role for the NG Domain. <i>Journal of Biological Chemistry</i> , 2002, 277, 46763-46768.	1.6	27
103	Delicate Balance between Functionally Required Flexibility and Aggregation Risk in a $\hat{1}^2$ -Rich Protein. <i>Biochemistry</i> , 2013, 52, 8843-8854.	1.2	26
104	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, 9765-9771.	1.2	25
105	The Role of Aromaticâ€™Aromatic Interactions in Strandâ€™Strand Stabilization of $\hat{1}^2$ -Sheets. <i>Journal of Molecular Biology</i> , 2013, 425, 3522-3535.	2.0	25
106	Functionally Significant Mobile Regions of Escherichia coli SecA ATPase Identified by NMR. <i>Journal of Biological Chemistry</i> , 2002, 277, 50985-50990.	1.6	24
107	Its Preferential Interactions with Biopolymers Account for Diverse Observed Effects of Trehalose. <i>Biophysical Journal</i> , 2015, 109, 144-153.	0.2	24
108	Cellular folding pathway of a metastable serpin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6484-6489.	3.3	24

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109	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.	6.6	22
110	Use of synthetic signal sequences to explore the protein export machinery. <i>Biopolymers</i> , 2008, 90, 307-319.	1.2	22
111	The Proteome Folding Problem and Cellular Proteostasis. <i>Journal of Molecular Biology</i> , 2021, 433, 167197.	2.0	22
112	Impact of a micellar environment on the conformations of two cyclic pentapeptides. <i>Biopolymers</i> , 1992, 32, 1741-1754.	1.2	20
113	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, 103-113.	1.0	19
114	Selective promiscuity in the binding of <i>E. coli</i> Hsp70 to an unfolded protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
115	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.	6.6	16
116	A Novel Conformation in a Highly Potent, Constrained Gonadotropin-Releasing Hormone Antagonist. <i>Journal of the American Chemical Society</i> , 1996, 118, 970-976.	6.6	16
117	Molecular chaperones: Clamps for the Clps?. <i>Current Biology</i> , 1998, 8, R464-R467.	1.8	16
118	Ligand-promoted protein folding by biased kinetic partitioning. <i>Nature Chemical Biology</i> , 2017, 13, 369-371.	3.9	15
119	Local sequence information in cellular retinoic acid-binding protein I: Specific residue roles in β^2 -turns*. <i>Biopolymers</i> , 2003, 71, 638-651.	1.2	14
120	Segmental isotopic labeling of the Hsp70 molecular chaperone DnaK using expressed protein ligation. <i>Biopolymers</i> , 2010, 94, 742-752.	1.2	14
121	Early Folding Events Protect Aggregation-Prone Regions of a β^2 -Rich Protein. <i>Structure</i> , 2013, 21, 476-485.	1.6	14
122	How bacteria survive an acid trip. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5279-5280.	3.3	14
123	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.	1.6	14
124	Conformational comparison of cyclic peptide and pseudopeptide structures with intramolecular hydrogen bonding. <i>Biopolymers</i> , 1983, 22, 147-151.	1.2	13
125	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, 1713-1725.	1.2	13
126	Exploring the interactions between signal sequences and <i>E. coli</i> SRP by two distinct and complementary crosslinking methods. <i>Biopolymers</i> , 2009, 92, 201-211.	1.2	13

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127	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, 19327-19331.	1.6	12
128	Expression and Purification of Active Recombinant Human Alpha-1 Antitrypsin (AAT) from Escherichia coli. <i>Methods in Molecular Biology</i> , 2017, 1639, 195-209.	0.4	12
129	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, 1727-1739.	1.2	11
130	JBC is on a mission to facilitate scientific discovery. <i>Journal of Biological Chemistry</i> , 2017, 292, 6853-6854.	1.6	11
131	On the costs of scientific publishing. <i>Journal of Biological Chemistry</i> , 2017, 292, 16395-16396.	1.6	10
132	Interfacial spin trapping in model membrane systems. <i>Biochemical and Biophysical Research Communications</i> , 1981, 102, 1350-1357.	1.0	9
133	Native structural propensity in cellular retinoic acid-binding protein I 64â€“88: the role of locally encoded structure in the folding of a Î²-barrel protein. <i>Biophysical Chemistry</i> , 2002, 100, 421-436.	1.5	9
134	Physics-based modeling provides predictive understanding of selectively promiscuous substrate binding by Hsp70 chaperones. <i>PLoS Computational Biology</i> , 2021, 17, e1009567.	1.5	9
135	Signal Peptides Bind and Aggregate RNA. <i>Journal of Biological Chemistry</i> , 2001, 276, 12222-12227.	1.6	8
136	Disorder breathes life into a DEAD motor. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 566-569.	3.6	8
137	Proper secretion of the serpin antithrombin relies strictly on thiol-dependent quality control. <i>Journal of Biological Chemistry</i> , 2019, 294, 18992-19011.	1.6	8
138	JBC's New Year's resolutions: Check them off!. <i>Journal of Biological Chemistry</i> , 2017, 292, 21705-21706.	1.6	7
139	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, 13715-13716.	3.3	6
140	Finding the Fittest Fold: Using the Evolutionary Record to Design New Proteins. <i>Cell</i> , 2005, 122, 832-834.	13.5	6
141	The Structure of Escherichia coli Signal Recognition Particle Revealed by Scanning Transmission Electron Microscopy. <i>Molecular Biology of the Cell</i> , 2006, 17, 5063-5074.	0.9	6
142	A new twist for an Hsp70 chaperone. <i>Nature Structural Biology</i> , 2002, 9, 406-408.	9.7	5
143	How One Bad Protein Spoils the Barrel: Structural Details of Î²2-Microglobulin Amyloidogenicity. <i>Molecular Cell</i> , 2011, 41, 129-131.	4.5	5
144	A career pathway in protein folding: From model peptides to postreductionist protein science. <i>Protein Science</i> , 2011, 20, 783-790.	3.1	5

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145	The Journal of Biological Chemistry: 2016 Onward. <i>Journal of Biological Chemistry</i> , 2016, 291, 15406-15407.	1.6	5
146	The Herbert Tabor Best Paper Awards: Celebrating young authors who contribute top content to JBC. <i>Journal of Biological Chemistry</i> , 2017, 292, 17576.	1.6	5
147	ASBMB and JBC: A truly synergistic relationship. <i>Journal of Biological Chemistry</i> , 2017, 292, 9857.	1.6	5
148	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.	3.1	5
149	Spectroscopic studies of a hydrophobic peptide in membranelike environments. <i>Biopolymers</i> , 1983, 22, 381-385.	1.2	4
150	Caught in the Act. <i>Molecular Cell</i> , 2002, 9, 3-5.	4.5	4
151	Chapter 3 A Fluorescent Window Into Protein Folding and Aggregation in Cells. <i>Methods in Cell Biology</i> , 2008, 89, 59-70.	0.5	4
152	A Method for Direct Measurement of Protein Stability In Vivo. <i>Methods in Molecular Biology</i> , 2009, 490, 165-178.	0.4	4
153	The Herbert Tabor Young Investigator Awards: Meet the awardees!. <i>Journal of Biological Chemistry</i> , 2018, 293, 3468-3469.	1.6	4
154	Faster publication advances your science: The three R's. <i>Journal of Biological Chemistry</i> , 2020, 295, 672.	1.6	4
155	Defining the structure of the substrate-free state of the DnaK molecular chaperone. <i>Biochemical Society Symposia</i> , 2001, 68, 69-82.	2.7	4
156	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.	4.5	4
157	Molecular Chaperones: Panning for chaperone-binding peptides. <i>Current Biology</i> , 1994, 4, 173-174.	1.8	3
158	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, 635-636.	4.5	3
159	What Happens When You Submit a Paper to JBC?. <i>Journal of Biological Chemistry</i> , 2017, 292, 1535-1537.	1.6	3
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