Lila M Gierasch

List of Publications by Citations

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160	10,783	58	101
papers	citations	h-index	g-index
203	11,614	9.5	6.49
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
160	Signal sequences. *Biochemistry*, **1989**, 28, 923-30	3.2	482
159	Sending signals dynamically. *Science*, **2009**, 324, 198-203	33.3	423
158	The crystal structure of the GroES co-chaperonin at 2.8 A resolution. *Nature*, **1996**, 379, 37-45	50.4	408
157	Constrained peptides: models of bioactive peptides and protein substructures. *Annual Review of Biochemistry*, **1992**, 61, 387-418	29.1	337
156	Physicochemical properties of cells and their effects on intrinsically disordered proteins (IDPs). *Chemical Reviews*, **2014**, 114, 6661-714	68.1	301
155	Different conformations for the same polypeptide bound to chaperones DnaK and GroEL. *Nature*, **1992**, 355, 455-7	50.4	289
154	The changing landscape of protein allostery. *Current Opinion in Structural Biology*, **2006**, 16, 102-8	8.1	261
153	Hsp70 chaperone ligands control domain association via an allosteric mechanism mediated by the interdomain linker. *Molecular Cell*, **2007**, 26, 27-39	17.6	254
152	The NPXY internalization signal of the LDL receptor adopts a reverse-turn conformation. *Cell*, **1991**, 67, 1195-201	56.2	250
151	Inhibition of protein aggregation in vitro and in vivo by a natural osmoprotectant. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 13357-61	11.5	248
150	Characterization of a functionally important mobile domain of GroES. *Nature*, **1993**, 364, 255-8	50.4	213
149	How hsp70 molecular machines interact with their substrates to mediate diverse physiological functions. *Journal of Molecular Biology*, **2015**, 427, 1575-88	6.5	206
148	Monitoring protein stability and aggregation in vivo by real-time fluorescent labeling. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 523-8	11.5	202
147	Conformations of (X-L-Pro-Y)2 cyclic hexapeptides. Preferred beta-turn conformers and implications for beta turns in proteins. *Biochemistry*, **1981**, 20, 4730-8	3.2	196
146	An interdomain energetic tug-of-war creates the allosterically active state in Hsp70 molecular chaperones. *Cell*, **2012**, 151, 1296-307	56.2	192
145	Conformational behavior of Escherichia coli OmpA signal peptides in membrane mimetic environments. *Biochemistry*, **1993**, 32, 4881-94	3.2	192
144	Molecular mechanisms of protein secretion: the role of the signal sequence. *Advances in Protein Chemistry*, **1986**, 38, 109-80		184

143	The chaperonin GroEL binds a polypeptide in an alpha-helical conformation. *Biochemistry*, **1991**, 30, 7359-62	3.2	169
142	Structural insights into substrate binding by the molecular chaperone DnaK. *Nature Structural Biology*, **2000**, 7, 298-303		165
141	GTP binding and hydrolysis by the signal recognition particle during initiation of protein translocation. *Nature*, **1993**, 366, 351-4	50.4	165
140	Roles of beta-turns in protein folding: from peptide models to protein engineering. *Biopolymers*, **2008**, 89, 380-91	2.2	141
139	Recent advances in the structural and mechanistic aspects of Hsp70 molecular chaperones. *Journal of Biological Chemistry*, **2019**, 294, 2085-2097	5.4	130
138	Side chain-backbone hydrogen bonding contributes to helix stability in peptides derived from an alpha-helical region of carboxypeptidase A. *Proteins: Structure, Function and Bioinformatics*, **1991**, 10, 130-9	4.2	129
137	Macromolecular crowding remodels the energy landscape of a protein by favoring a more compact unfolded state. *Journal of the American Chemical Society*, **2010**, 132, 10445-52	16.4	128
136	Exploring weak, transient protein--protein interactions in crowded in vivo environments by in-cell nuclear magnetic resonance spectroscopy. *Biochemistry*, **2011**, 50, 9225-36	3.2	125
135	Mutations in the substrate binding domain of the Escherichia coli 70 kDa molecular chaperone, DnaK, which alter substrate affinity or interdomain coupling. *Journal of Molecular Biology*, **1999**, 286, 915-32	6.5	125
134	Protein folding in the cell: challenges and progress. *Current Opinion in Structural Biology*, **2011**, 21, 32-41	8.1	123
133	Exploring the conformational roles of signal sequences: synthesis and conformational analysis of lambda receptor protein wild-type and mutant signal peptides. *Biochemistry*, **1984**, 23, 3111-4	3.2	115
132	Allosteric signal transmission in the nucleotide-binding domain of 70-kDa heat shock protein (Hsp70) molecular chaperones. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 6987-92	11.5	112
131	Keeping it in the family: folding studies of related proteins. *Current Opinion in Structural Biology*, **2001**, 11, 83-93	8.1	106
130	An interdomain sector mediating allostery in Hsp70 molecular chaperones. *Molecular Systems Biology*, **2010**, 6, 414	12.2	104
129	From the test tube to the cell: exploring the folding and aggregation of a beta-clam protein. *Biopolymers*, **2007**, 88, 157-63	2.2	98
128	Post-reductionist protein science, or putting Humpty Dumpty back together again. *Nature Chemical Biology*, **2009**, 5, 774-7	11.7	93
127	Signal sequences: the same yet different. *Cell*, **1996**, 86, 849-52	56.2	91
126	Renaturation of citrate synthase: influence of denaturant and folding assistants. *Protein Science*, **1992**, 1, 522-9	6.3	87

125	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. *Biopolymers*, **1990**, 29, 263-87	3.2	87
124	Phospholipid-induced monomerization and signal-peptide-induced oligomerization of SecA. *Journal of Biological Chemistry*, **2003**, 278, 3628-38	5.4	86
123	Helix formation and stability in a signal sequence. *Biochemistry*, **1989**, 28, 8554-61	3.2	82
122	Conformations and orientations of a signal peptide interacting with phospholipid monolayers. *Biochemistry*, **1989**, 28, 2789-97	3.2	82
121	Substrate-binding domain conformational dynamics mediate Hsp70 allostery. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E2865-73	11.5	81
120	The LDL receptor clustering motif interacts with the clathrin terminal domain in a reverse turn conformation. *Journal of Cell Biology*, **1998**, 142, 59-67	7.3	80
119	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	4.2	79
118	NatureTs 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, 2727-8	11.5	78
117	Unique physical properties and interactions of the domains of methylated DNA binding protein 2. *Biochemistry*, **2010**, 49, 4395-410	3.2	77
116	Multiple roles of prolyl residues in structure and folding. *Journal of Molecular Biology*, **2000**, 301, 737-47	6.5	77
115	Protein Conformational Stability Probed by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. *Journal of the American Chemical Society*, **2000**, 122, 495-500	16.4	76
114	Equilibrium folding studies of cellular retinoic acid binding protein, a predominantly beta-sheet protein. *Biochemistry*, **1994**, 33, 134-42	3.2	76
113	Hydrophobic content and lipid interactions of wild-type and mutant OmpA signal peptides correlate with their in vivo function. *Biochemistry*, **1991**, 30, 10155-63	3.2	76
112	Energy landscapes of functional proteins are inherently risky. *Nature Chemical Biology*, **2014**, 10, 884-91	11.7	74
111	Membrane-bound conformation of a signal peptide: a transferred nuclear Overhauser effect analysis. *Biochemistry*, **1993**, 32, 13991-9	3.2	74
110	Intrinsic tryptophans of CRABPI as probes of structure and folding. *Protein Science*, **1996**, 5, 1108-17	6.3	72
109	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	17.6	71
108	Comparing protein folding in vitro and in vivo: foldability meets the fitness challenge. *Current Opinion in Structural Biology*, **2014**, 24, 81-90	8.1	67

107	ATPase subdomain IA is a mediator of interdomain allostery in Hsp70 molecular chaperones. *PLoS Computational Biology*, **2014**, 10, e1003624	5	65
106	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	16.4	62
105	FoldEco: a model for proteostasis in E. coli. *Cell Reports*, **2012**, 1, 265-76	10.6	61
104	Cavity formation before stable hydrogen bonding in the folding of a beta-clam protein. *Nature Structural and Molecular Biology*, **1997**, 4, 883-6	17.6	58
103	Basis of substrate binding by the chaperonin GroEL. *Biochemistry*, **1999**, 38, 12537-46	3.2	58
102	Aggregation of a slow-folding mutant of a beta-clam protein proceeds through a monomeric nucleus. *Biochemistry*, **2005**, 44, 7266-74	3.2	57
101	Direct comparison of a stable isolated Hsp70 substrate-binding domain in the empty and substrate-bound states. *Journal of Biological Chemistry*, **2006**, 281, 1605-11	5.4	56
100	In-cell aggregation of a polyglutamine-containing chimera is a multistep process initiated by the flanking sequence. *Journal of Biological Chemistry*, **2007**, 282, 36736-43	5.4	54
99	Conformation of a peptide solubilizate in a reversed micelle water pool. *Journal of the American Chemical Society*, **1984**, 106, 3648-3652	16.4	54
98	Effects of osmolytes on protein folding and aggregation in cells. *Methods in Enzymology*, **2007**, 428, 355-72	1.7	53
97	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, 213-32	3.7	53
96	Probing the folding pathway of a beta-clam protein with single-tryptophan constructs. *Folding & Design*, **1998**, 3, 401-12		51
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90	Dynamic local unfolding in the serpin □1 antitrypsin provides a mechanism for loop insertion and polymerization. *Nature Structural and Molecular Biology*, **2011**, 18, 222-6	17.6	46

89	Design of biologically active, conformationally constrained GnRH antagonists. *Proteins: Structure, Function and Bioinformatics*, **1990**, 8, 295-304	4.2	46
88	Cross-strand split tetra-Cys motifs as structure sensors in a beta-sheet protein. *Chemistry and Biology*, **2008**, 15, 1104-15		45
87	Conserved, disordered C terminus of DnaK enhances cellular survival upon stress and DnaK in vitro chaperone activity. *Journal of Biological Chemistry*, **2011**, 286, 31821-9	5.4	44
86	Dynamics of cellular retinoic acid binding protein I on multiple time scales with implications for ligand binding. *Biochemistry*, **2000**, 39, 9119-29	3.2	44
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84	The structure of Escherichia coli heat-stable enterotoxin b by nuclear magnetic resonance and circular dichroism. *Protein Science*, **1995**, 4, 1718-29	6.3	42
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82	Unfolding dynamics of a beta-sheet protein studied by mass spectrometry. *Journal of Mass Spectrometry*, **1999**, 34, 1289-95	2.2	41
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80	Crystal structures, molecular conformations, infrared spectra, and carbon-13 NMR spectra of methylproline peptides in the solid state. *Journal of the American Chemical Society*, **1983**, 105, 6609-6614	16.4	40
79	Challenges and dreams: physics of weak interactions essential to life. *Molecular Biology of the Cell*, **2014**, 25, 3474-7	3.5	39
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75	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). *Journal of the American Chemical Society*, **1985**, 107, 3349-3350	16.4	37
74	Hsp70 molecular chaperones: multifunctional allosteric holding and unfolding machines. *Biochemical Journal*, **2019**, 476, 1653-1677	3.8	36
73	Conformational analysis of a highly potent, constrained gonadotropin-releasing hormone antagonist. 1. Nuclear magnetic resonance. *Journal of the American Chemical Society*, **1992**, 114, 2852-2859	16.4	36
72	Key features of an Hsp70 chaperone allosteric landscape revealed by ion-mobility native mass spectrometry and double electron-electron resonance. *Journal of Biological Chemistry*, **2017**, 292, 8773-8785	5.4	33

71	GroEL-substrate interactions: molding the fold, or folding the mold?. *Cell*, **2000**, 100, 193-6	56.2	33
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68	Individual and collective contributions of chaperoning and degradation to protein homeostasis in E. coli. *Cell Reports*, **2015**, 11, 321-33	10.6	31
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66	Evolutionary coupling of structural and functional sequence information in the intracellular lipid-binding protein family. *Proteins: Structure, Function and Bioinformatics*, **2006**, 63, 373-84	4.2	29
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64	Site-specific fluorescent labeling of poly-histidine sequences using a metal-chelating cysteine. *Chemical Biology and Drug Design*, **2007**, 69, 31-40	2.9	27
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61	Crystal structure of cyclo(Gly1-L-Pro2-D-Phe3-L-Ala4-L-Pro5): a cyclic pentapeptide with a Gly-L-Pro .delta. turn. *Journal of the American Chemical Society*, **1988**, 110, 5157-5161	16.4	25
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56	Its preferential interactions with biopolymers account for diverse observed effects of trehalose. *Biophysical Journal*, **2015**, 109, 144-53	2.9	21
55	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. *Journal of the American Chemical Society*, **1985**, 107, 3321-3327	16.4	21
54	Allosteric landscapes of eukaryotic cytoplasmic Hsp70s are shaped by evolutionary tuning of key interfaces. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 11970-11975	11.5	21

53	Electrophysiological studies in Xenopus oocytes for the opening of Escherichia coli SecA-dependent protein-conducting channels. *Journal of Membrane Biology*, **2006**, 214, 103-13	2.3	19
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50	Impact of a micellar environment on the conformations of two cyclic pentapeptides. *Biopolymers*, **1992**, 32, 1741-54	2.2	17
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47	A Novel Conformation in a Highly Potent, Constrained Gonadotropin-Releasing Hormone Antagonist. *Journal of the American Chemical Society*, **1996**, 118, 970-976	16.4	14
46	Cellular folding pathway of a metastable serpin. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 6484-9	11.5	14
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40	Exploring the interactions between signal sequences and E. coli SRP by two distinct and complementary crosslinking methods. *Biopolymers*, **2009**, 92, 201-11	2.2	12
39	Ligand-promoted protein folding by biased kinetic partitioning. *Nature Chemical Biology*, **2017**, 13, 369-371	11.7	11
38	Conformational comparison of cyclic peptide and pseudopeptide structures with intramolecular hydrogen bonding. *Biopolymers*, **1983**, 22, 147-151	2.2	11
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33	First glimpses of a chaperonin-bound folding intermediate. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 13715-6	11.5	6
32	Signal peptides bind and aggregate RNA. An alternative explanation for GTPase inhibition in the signal recognition particle. *Journal of Biological Chemistry*, **2001**, 276, 12222-7	5.4	6
31	Expression and Purification of Active Recombinant Human Alpha-1 Antitrypsin (AAT) from Escherichia coli. *Methods in Molecular Biology*, **2017**, 1639, 195-209	1.4	5
30	The structure of Escherichia coli signal recognition particle revealed by scanning transmission electron microscopy. *Molecular Biology of the Cell*, **2006**, 17, 5063-74	3.5	5
29	Finding the fittest fold: using the evolutionary record to design new proteins. *Cell*, **2005**, 122, 832-4	56.2	5
28	How the Protein Data Bank changed biology: An introduction to the JBC Reviews thematic series, part 1. *Journal of Biological Chemistry*, **2021**, 296, 100608	5.4	5
27	Kinetic versus thermodynamic control of mutational effects on protein homeostasis: A perspective from computational modeling and experiment. *Protein Science*, **2019**, 28, 1324-1339	6.3	4
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22	Proper secretion of the serpin antithrombin relies strictly on thiol-dependent quality control. *Journal of Biological Chemistry*, **2019**, 294, 18992-19011	5.4	3
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15	Defining the structure of the substrate-free state of the DnaK molecular chaperone. *Biochemical Society Symposia*, **2001**, 69-82		3
14	You got to know when to hold (or unfold) Tem *Molecular Cell*, **2012**, 48, 3-4	17.6	2
13	There are more Hsp90 chaperone mechanisms in heaven and earth, dear reader, than are dreamt of in your philosophy.. *Molecular Cell*, **2022**, 82, 1403-1404	17.6	2
12	Celebrating the scientific legacy of Herbert Tabor. *Journal of Biological Chemistry*, **2019**, 294, 1635-1637	5.4	1
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8	Physics-based modeling provides predictive understanding of selectively promiscuous substrate binding by Hsp70 chaperones. *PLoS Computational Biology*, **2021**, 17, e1009567	5	1
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6	Opening ASBMB publications freely to all. *Journal of Biological Chemistry*, **2020**, 295, 7814-7815	5.4	0
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3	2021 JBC Herbert Tabor Early Career Investigator Awards: Call for nominations. *Journal of Biological Chemistry*, **2020**, 295, 13697	5.4	
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1	How the Protein Data Bank changed biology: An introduction to the JBC Reviews thematic series, part 2. *Journal of Biological Chemistry*, **2021**, 296, 100748	5.4	