

# Gary J Pielak

## List of Publications by Year in descending order

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148  
papers

9,472  
citations

29994

54  
h-index

43802

91  
g-index

153  
all docs

153  
docs citations

153  
times ranked

6327  
citing authors

#	ARTICLE	IF	CITATIONS
1	Physicochemical Properties of Cells and Their Effects on Intrinsically Disordered Proteins (IDPs). <i>Chemical Reviews</i> , 2014, 114, 6661-6714.	23.0	391
2	Tardigrades Use Intrinsically Disordered Proteins to Survive Desiccation. <i>Molecular Cell</i> , 2017, 65, 975-984.e5.	4.5	302
3	FlgM gains structure in living cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12681-12684.	3.3	290
4	Impact of Protein Denaturants and Stabilizers on Water Structure. <i>Journal of the American Chemical Society</i> , 2004, 126, 1958-1961.	6.6	289
5	Macromolecular Crowding and Protein Stability. <i>Journal of the American Chemical Society</i> , 2012, 134, 16614-16618.	6.6	289
6	Interpreting the Effects of Small Uncharged Solutes on Protein-Folding Equilibria. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2001, 30, 271-306.	18.3	264
7	Protein Crowding Tunes Protein Stability. <i>Journal of the American Chemical Society</i> , 2011, 133, 7116-7120.	6.6	255
8	Effects of Proteins on Protein Diffusion. <i>Journal of the American Chemical Society</i> , 2010, 132, 9392-9397.	6.6	223
9	Soft interactions and crowding. <i>Biophysical Reviews</i> , 2013, 5, 187-194.	1.5	205
10	Protein <sup>19</sup> F NMR in <i>Escherichia coli</i> . <i>Journal of the American Chemical Society</i> , 2010, 132, 321-327.	6.6	196
11	Unexpected Effects of Macromolecular Crowding on Protein Stability. <i>Biochemistry</i> , 2012, 51, 9773-9775.	1.2	191
12	Quinary structure modulates protein stability in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1739-1742.	3.3	186
13	Site-directed mutagenesis of cytochrome c shows that an invariant Phe is not essential for function. <i>Nature</i> , 1985, 313, 152-154.	13.7	175
14	Impact of reconstituted cytosol on protein stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19342-19347.	3.3	172
15	Solvent-induced collapse of $\alpha$ -synuclein and acid-denatured cytochrome c. <i>Protein Science</i> , 2008, 10, 2195-2199.	3.1	169
16	Macromolecular Crowding in the <i>Escherichia coli</i> Periplasm Maintains $\alpha$ -Synuclein Disorder. <i>Journal of Molecular Biology</i> , 2006, 355, 893-897.	2.0	164
17	Osmolyte-induced changes in protein conformational equilibria. <i>Biopolymers</i> , 2000, 53, 293-307.	1.2	159
18	Volume Exclusion and Soft Interaction Effects on Protein Stability under Crowded Conditions. <i>Biochemistry</i> , 2010, 49, 6984-6991.	1.2	148

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19	In-cell thermodynamics and a new role for protein surfaces. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1725-1730.	3.3	147
20	Macromolecular Crowding Fails To Fold a Globular Protein in Cells. Journal of the American Chemical Society, 2011, 133, 8082-8085.	6.6	132
21	Differential Dynamical Effects of Macromolecular Crowding on an Intrinsically Disordered Protein and a Globular Protein: Implications for In-Cell NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 6310-6311.	6.6	119
22	A cell is more than the sum of its (dilute) parts: A brief history of quinary structure. Protein Science, 2017, 26, 403-413.	3.1	111
23	Protein Crowder Charge and Protein Stability. Biochemistry, 2014, 53, 1601-1606.	1.2	106
24	Residue level quantification of protein stability in living cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11335-11340.	3.3	106
25	The Cellular Environment Stabilizes Adenine Riboswitch RNA Structure. Biochemistry, 2013, 52, 8777-8785.	1.2	104
26	Elimination of the negative Soret Cotton effect of cytochrome c by replacement of the invariant phenylalanine using site-directed mutagenesis. Journal of the American Chemical Society, 1986, 108, 2724-2727.	6.6	95
27	Design of a Ruthenium-Cytochrome c Derivative to Measure Electron Transfer to the Initial Acceptor in Cytochrome c Oxidase. Journal of Biological Chemistry, 1995, 270, 2466-2472.	1.6	92
28	Residue-Level Interrogation of Macromolecular Crowding Effects on Protein Stability. Journal of the American Chemical Society, 2008, 130, 6826-6830.	6.6	88
29	Osmotic Shock Induced Protein Destabilization in Living Cells and Its Reversal by Glycine Betaine. Journal of Molecular Biology, 2017, 429, 1155-1161.	2.0	86
30	Interaction of $\alpha$ -synuclein with vesicles that mimic mitochondrial membranes. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 512-519.	1.4	85
31	Stability of yeast iso-1-cytochrome c as a function of pH and temperature. Protein Science, 1994, 3, 1253-1260.	3.1	83
32	In Situ Structural Characterization of a Recombinant Protein in Native Escherichia coli Membranes with Solid-State Magic-Angle-Spinning NMR. Journal of the American Chemical Society, 2011, 133, 12370-12373.	6.6	83
33	<sup>19</sup> F-NMR Spectroscopy as a Probe of Cytoplasmic Viscosity and Weak Protein Interactions in Living Cells. Chemistry - A European Journal, 2013, 19, 12705-12710.	1.7	83
34	Translational and Rotational Diffusion of a Small Globular Protein under Crowded Conditions. Journal of Physical Chemistry B, 2009, 113, 13390-13392.	1.2	82
35	Assignment of proton resonances, identification of secondary structural elements, and analysis of backbone chemical shifts for the C102T variant of yeast iso-1-cytochrome c and horse cytochrome c. Biochemistry, 1990, 29, 6994-7003.	1.2	81
36	Sugar-Induced Molten-Globule Model. Biochemistry, 1998, 37, 17048-17053.	1.2	81

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37	Introduction of a disulfide bond into cytochrome c stabilizes a compact denatured state. <i>Biochemistry</i> , 1992, 31, 12337-12344.	1.2	79
38	Native tertiary structure in an A-state 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 275, 379-388.	2.0	77
39	<sup>19</sup> F NMR Studies of Î±-Synuclein Conformation and Fibrillation. <i>Biochemistry</i> , 2009, 48, 8578-8584.	1.2	76
40	Protein Nuclear Magnetic Resonance under Physiological Conditions. <i>Biochemistry</i> , 2009, 48, 226-234.	1.2	75
41	Comparison of reduced and oxidized yeast iso-1-cytochrome c using proton paramagnetic shifts. <i>Biochemistry</i> , 1991, 30, 1928-1934.	1.2	74
42	Entropic Stabilization of Cytochrome c upon Reduction. <i>Journal of the American Chemical Society</i> , 1995, 117, 1675-1677.	6.6	72
43	Electrostatic Contributions to Protein Quinary Structure. <i>Journal of the American Chemical Society</i> , 2016, 138, 13139-13142.	6.6	72
44	Protein shape modulates crowding effects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10965-10970.	3.3	72
45	Role of Configurational Gating in Intracomplex Electron Transfer from Cytochrome c to the Radical Cation in Cytochrome c Peroxidase. <i>Biochemistry</i> , 1999, 38, 6846-6854.	1.2	70
46	Stability and apoptotic activity of recombinant human cytochrome c. <i>Biochemical and Biophysical Research Communications</i> , 2003, 312, 733-740.	1.0	66
47	Design of a Ruthenium <sup>II</sup> -CytochromecDerivative To Measure Electron Transfer to the Radical Cation and Oxyferryl Heme in CytochromecPeroxidase. <i>Biochemistry</i> , 1996, 35, 15107-15119.	1.2	64
48	In-cell protein NMR and protein leakage. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 347-351.	1.5	63
49	Intrinsically Disordered Proteins and Desiccation Tolerance: Elucidating Functional and Mechanistic Underpinnings of Anhydrobiosis. <i>BioEssays</i> , 2017, 39, 1700119.	1.2	62
50	Using NMR to Distinguish Viscosity Effects from Nonspecific Protein Binding under Crowded Conditions. <i>Journal of the American Chemical Society</i> , 2009, 131, 1368-1369.	6.6	61
51	Osmolytes and Protein-Protein Interactions. <i>Journal of the American Chemical Society</i> , 2018, 140, 7441-7444.	6.6	61
52	<sup>19</sup> F NMR studies of Î±-synuclein-membrane interactions. <i>Protein Science</i> , 2010, 19, 1686-1691.	3.1	58
53	NMR studies of protein folding and binding in cells and cell-like environments. <i>Current Opinion in Structural Biology</i> , 2015, 30, 7-16.	2.6	58
54	Amide proton exchange rates of oxidized and reduced <i>saccharomyces cerevisiae</i> iso-1-cytochrome c. <i>Protein Science</i> , 1993, 2, 1966-1974.	3.1	56

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55	A bioreactor for in-cell protein NMR. <i>Journal of Magnetic Resonance</i> , 2010, 202, 140-146.	1.2	56
56	Challenge of Mimicking the Influences of the Cellular Environment on RNA Structure by PEG-Induced Macromolecular Crowding. <i>Biochemistry</i> , 2015, 54, 6447-6453.	1.2	56
57	Surface Charge Modulates Protein-Protein Interactions in Physiologically Relevant Environments. <i>Biochemistry</i> , 2018, 57, 1681-1684.	1.2	56
58	Disordered Protein Diffusion under Crowded Conditions. <i>Journal of Physical Chemistry Letters</i> , 2012, 3, 2703-2706.	2.1	53
59	Protein thermal denaturation, side-chain models, and evolution: amino acid substitutions at a conserved helix-helix interface. <i>Biochemistry</i> , 1995, 34, 3268-3276.	1.2	51
60	Effects of molecular crowding by saccharides on $\alpha$ -chymotrypsin dimerization. <i>Protein Science</i> , 2002, 11, 997-1003.	3.1	51
61	Protecting activity of desiccated enzymes. <i>Protein Science</i> , 2019, 28, 941-951.	3.1	51
62	Macromolecular Crowding Is More than Hard-Core Repulsions. <i>Annual Review of Biophysics</i> , 2022, 51, 267-300.	4.5	51
63	Baseline length and automated fitting of denaturation data. <i>Protein Science</i> , 1998, 7, 1262-1263.	3.1	49
64	Cosolutes, Crowding, and Protein Folding Kinetics. <i>Journal of Physical Chemistry B</i> , 2017, 121, 6527-6537.	1.2	49
65	The intracellular environment affects protein-protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	49
66	Intracellular p <sub>H</sub> modulates quinary structure. <i>Protein Science</i> , 2015, 24, 1748-1755.	3.1	48
67	Characterization of Horse Cytochrome c Expressed in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2001, 22, 220-224.	0.6	47
68	Probing the Cytochrome c Peroxidase <sup>+</sup> Cytochrome c Electron Transfer Reaction Using Site Specific Cross-Linking. <i>Biochemistry</i> , 1996, 35, 4837-4845.	1.2	46
69	Control of Formation and Dissociation of the High-Affinity Complex between Cytochrome c and Cytochrome c Peroxidase by Ionic Strength and the Low-Affinity Binding Site. <i>Biochemistry</i> , 1996, 35, 15800-15806.	1.2	46
70	Temperature-induced reversible conformational change in the first 100 residues of $\alpha$ -synuclein. <i>Protein Science</i> , 2006, 15, 602-608.	3.1	46
71	Protein Dynamics in Living Cells. <i>Biochemistry</i> , 2005, 44, 9275-9279.	1.2	45
72	Identifying the Physiological Electron Transfer Site of Cytochrome c Peroxidase by Structure-Based Engineering. <i>Biochemistry</i> , 1996, 35, 667-673.	1.2	44

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73	Protein Stability in Reverse Micelles. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 3586-3589.	7.2	43
74	Internal and Global Protein Motion Assessed with a Fusion Construct and In-Cell NMR Spectroscopy. <i>ChemBioChem</i> , 2011, 12, 390-391.	1.3	42
75	Cosolute and Crowding Effects on a Side-By-Side Protein Dimer. <i>Biochemistry</i> , 2017, 56, 971-976.	1.2	42
76	Macromolecular and Small Molecular Crowding Have Similar Effects on $\beta$ -Synuclein Structure. <i>ChemPhysChem</i> , 2017, 18, 55-58.	1.0	41
77	Second virial coefficients as a measure of protein-osmolyte interactions. <i>Protein Science</i> , 2001, 10, 12-16.	3.1	40
78	Protecting Enzymes from Stress-Induced Inactivation. <i>Biochemistry</i> , 2019, 58, 3825-3833.	1.2	37
79	Protein-complex stability in cells and in vitro under crowded conditions. <i>Current Opinion in Structural Biology</i> , 2021, 66, 183-192.	2.6	37
80	Hydrogen exchange of disordered proteins in <i>Escherichia coli</i> . <i>Protein Science</i> , 2015, 24, 706-713.	3.1	36
81	A model of intracellular organization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5901-5902.	3.3	35
82	Magnetic Resonance Spectroscopy as a Tool for Assessing Macromolecular Structure and Function in Living Cells. <i>Annual Review of Analytical Chemistry</i> , 2017, 10, 157-182.	2.8	35
83	Rapid Quantification of Protein-Ligand Binding via $^{19}\text{F}$ NMR Lineshape Analysis. <i>Biophysical Journal</i> , 2020, 118, 2537-2548.	0.2	34
84	$\beta$ -Synuclein Conformation Affects Its Tyrosine-Dependent Oxidative Aggregation. <i>Biochemistry</i> , 2008, 47, 13604-13609.	1.2	33
85	The structure of cytochrome c and its relation to recent studies of long-range electron transfer. <i>Protein Engineering, Design and Selection</i> , 1987, 1, 83-88.	1.0	31
86	Emergence of life: Physical chemistry changes the paradigm. <i>Biology Direct</i> , 2015, 10, 33.	1.9	31
87	Effects of Recombinant Protein Expression on Green Fluorescent Protein Diffusion in <i>Escherichia coli</i> . <i>Biochemistry</i> , 2009, 48, 5083-5089.	1.2	29
88	An upper limit for macromolecular crowding effects. <i>BMC Biophysics</i> , 2011, 4, 13.	4.4	29
89	Large cosolutes, small cosolutes, and dihydrofolate reductase activity. <i>Protein Science</i> , 2017, 26, 2417-2425.	3.1	29
90	$^1\text{H}$ and $^{15}\text{N}$ Hyperfine Shifts of Cytochrome c. <i>Journal of the American Chemical Society</i> , 1999, 121, 9247-9248.	6.6	28

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91	Effects of Crowding by Mono-, Di-, and Tetrasaccharides on Cytochrome c~Cytochrome c Peroxidase Binding:~ Comparing Experiment to Theory. <i>Biochemistry</i> , 2001, 40, 281-285.	1.2	28
92	Using NMR-Detected Backbone Amide 1H Exchange to Assess Macromolecular Crowding Effects on Globular-Protein Stability. <i>Methods in Enzymology</i> , 2009, 466, 1-18.	0.4	28
93	Positively Charged Tags Impede Protein Mobility in Cells as Quantified by <sup>19</sup> F NMR. <i>Journal of Physical Chemistry B</i> , 2019, 123, 4527-4533.	1.2	28
94	Proton nuclear magnetic resonance as a probe of differences in structure between the C102T and F82S,C102T variants of iso-1-cytochrome c from the yeast <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 1991, 30, 7033-7040.	1.2	27
95	Quinary interactions with an unfolded state ensemble. <i>Protein Science</i> , 2017, 26, 1698-1703.	3.1	26
96	An osmolyte mitigates the destabilizing effect of protein crowding. <i>Protein Science</i> , 2014, 23, 1161-1164.	3.1	25
97	Polarity of disulfide bonds. <i>Protein Science</i> , 1993, 2, 1183-1184.	3.1	24
98	Equilibrium Thermodynamics of a Physiologically-Relevant Heme~Protein Complex. <i>Biochemistry</i> , 1999, 38, 16876-16881.	1.2	24
99	Strategies for Protein NMR in <i>Escherichia coli</i> . <i>Biochemistry</i> , 2014, 53, 1971-1981.	1.2	24
100	Two-dimensional NMR as a probe of structural similarity applied to mutants of cytochrome c. <i>FEBS Journal</i> , 1988, 177, 179-185.	0.2	23
101	Interactions between Yeast Iso-1-cytochromecand Its Peroxidase~. <i>Biochemistry</i> , 2001, 40, 422-428.	1.2	22
102	Enthalpic stabilization of an SH3 domain by D<sub>2</sub>O. <i>Protein Science</i> , 2018, 27, 1710-1716.	3.1	22
103	Crowding and function reunite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17457-17458.	3.3	21
104	Quantification of size effect on protein rotational mobility in cells by <sup>19</sup> F NMR spectroscopy. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 869-874.	1.9	21
105	Changing the Transition State for Protein (Un)~folding~. <i>Biochemistry</i> , 1996, 35, 7403-7411.	1.2	20
106	Peroxidative aggregation of ~synuclein requires tyrosines. <i>Protein Science</i> , 2008, 13, 2852-2856.	3.1	20
107	Quantifying Green Fluorescent Protein Diffusion in <i>Escherichia coli</i> by Using Continuous Photobleaching with Evanescent Illumination. <i>Journal of Physical Chemistry B</i> , 2009, 113, 4837-4845.	1.2	20
108	Probing the Micelle~Bound Aggregation~Prone State of ~Synuclein with <sup>19</sup> F NMR Spectroscopy. <i>ChemBioChem</i> , 2010, 11, 1993-1996.	1.3	20

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109	Interaction of $\alpha$ -Synuclein and a Cell Penetrating Fusion Peptide with Higher Eukaryotic Cell Membranes Assessed by $^{19}\text{F}$ NMR. <i>Molecular Pharmaceutics</i> , 2012, 9, 1024-1029.	2.3	20
110	Crowding and Confinement Can Oppositely Affect Protein Stability. <i>ChemPhysChem</i> , 2018, 19, 3350-3355.	1.0	19
111	Proteinâ€™s Peptide Binding Energetics under Crowded Conditions. <i>Journal of Physical Chemistry B</i> , 2020, 124, 9297-9309.	1.2	19
112	Dynamical spectroscopy and microscopy of proteins in cells. <i>Current Opinion in Structural Biology</i> , 2021, 70, 1-7.	2.6	19
113	Nonideality and protein thermal denaturation. , 1999, 49, 471-479.		16
114	Searching for quantitative entropy-enthalpy compensation among protein variants. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 398-402.	1.5	16
115	Amide proton exchange of a dynamic loop in cell extracts. <i>Protein Science</i> , 2013, 22, 1313-1319.	3.1	16
116	Buffers, Especially the Good Kind. <i>Biochemistry</i> , 2021, 60, 3436-3440.	1.2	15
117	Crowding by Trisaccharides and the 2:1 Cytochrome <i>c</i> Cytochrome <i>c</i> Peroxidase Complex. <i>Biochemistry</i> , 2002, 41, 547-551.	1.2	14
118	Peeking into living eukaryotic cells with high-resolution NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11817-11818.	3.3	14
119	Roles of structural plasticity in chaperone HdeA activity are revealed by $^{19}\text{F}$ NMR. <i>Chemical Science</i> , 2016, 7, 2222-2228.	3.7	14
120	Protection by desiccationâ€™tolerance proteins probed at the residue level. <i>Protein Science</i> , 2022, 31, 396-406.	3.1	14
121	Dried Protein Structure Revealed at the Residue Level by Liquid-Observed Vapor Exchange NMR. <i>Biochemistry</i> , 2021, 60, 152-159.	1.2	13
122	Cytosol Has a Small Effect on Protein Backbone Dynamicsâ€™. <i>Biochemistry</i> , 2006, 45, 10085-10091.	1.2	12
123	Testing Hypotheses about Determinants of Protein Structure with High-Precision, High-Throughput Stability Measurements and Statistical Modeling. <i>Biochemistry</i> , 2003, 42, 7594-7603.	1.2	11
124	Pressure perturbation calorimetry of helical peptides. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 63, 322-326.	1.5	11
125	<i>Danio rerio</i> Oocytes for Eukaryotic In-Cell NMR. <i>Biochemistry</i> , 2021, 60, 451-459.	1.2	11
126	Waterâ€™s Variable Role in Protein Stability Uncovered by Liquid-Observed Vapor Exchange NMR. <i>Biochemistry</i> , 2021, 60, 3041-3045.	1.2	11



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127	Controlling and quantifying protein concentration in <i>Escherichia coli</i> . <i>Protein Science</i> , 2019, 28, 1307-1311.	3.1	10
128	Azo protein analogs: synthesis and characterization of arsanilazo and sulfanilazo derivatives of tyrosine and histidine. <i>Biochemistry</i> , 1984, 23, 589-596.	1.2	9
129	Preparation and characterization of sulfanilazo and arsanilazo proteins. <i>Biochemistry</i> , 1984, 23, 596-603.	1.2	9
130	Reconsideration of sedimentation equilibrium distributions reflecting the effects of small inert cosolutes on the dimerization of $\beta$ -chymotrypsin. <i>Biophysical Chemistry</i> , 2007, 130, 89-92.	1.5	9
131	The Expanding Zoo of In-Cell Protein NMR. <i>Biophysical Journal</i> , 2018, 115, 1628-1629.	0.2	9
132	Toxicity and Immunogenicity of a Tardigrade Cytosolic Abundant Heat Soluble Protein in Mice. <i>Frontiers in Pharmacology</i> , 2020, 11, 565969.	1.6	9
133	Membrane proteins, magic-angle spinning, and in-cell NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4715-4716.	3.3	8
134	Protein Stability in Reverse Micelles. <i>Angewandte Chemie</i> , 2016, 128, 3650-3653.	1.6	8
135	Membrane-mediated disorder-to-order transition of SNAP25 flexible linker facilitates its interaction with syntaxin-1 and SNARE complex assembly. <i>FASEB Journal</i> , 2019, 33, 7985-7994.	0.2	8
136	Temperature-sensitive variants of <i>Saccharomyces cerevisiae</i> iso-1-cytochrome c produced by random mutagenesis of codons 43 to 54. <i>Journal of Molecular Biology</i> , 1991, 221, 97-105.	2.0	7
137	Rheostatic Control of Protein Expression Using Tuner Cells. <i>Biochemistry</i> , 2020, 59, 733-735.	1.2	7
138	Chapter 12. Protein Stability and Weak Intracellular Interactions. <i>New Developments in NMR</i> , 2019, , 188-206.	0.1	6
139	Requirements for perpendicular helix pairing. , 1996, 26, 95-107.		4
140	Woes of proline: A cautionary kinetic tale. <i>Protein Science</i> , 2006, 15, 393-394.	3.1	3
141	A Difference between <i>In Vitro</i> and In-Cell Protein Dimer Formation. <i>Biochemistry</i> , 2022, 61, 409-412.	1.2	3
142	Design, synthesis, expression, and characterization of the genes for mouse Fc $\gamma$ RIIb1 and Fc $\gamma$ RIIb2 cytoplasmic regions. <i>Protein Science</i> , 1997, 6, 1038-1046.	3.1	2
143	Osmolyte-induced changes in protein conformational equilibria. <i>Biopolymers</i> , 2000, 53, 293.	1.2	2
144	Desiccation tolerance and globular proteins adsorb similar amounts of water. <i>Protein Science</i> , 2022, 31, e4288.	3.1	2

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145	Glycine Betaine Reverses Osmotic Shock Induced Protein Destabilization in Living Cells. Biophysical Journal, 2017, 112, 57a.	0.2	1
146	Osmolyte-induced changes in protein conformational equilibria. , 2000, 53, 293.		1
147	Physiologically-Relevant Crowding Effects on the SH3-Son of Sevenless Interaction. Biophysical Journal, 2019, 116, 158a.	0.2	0
148	Jan Hermans (1933-2018): Red-blooded biophysicists study hemoglobin. Proteins: Structure, Function and Bioinformatics, 2019, 87, 171-173.	1.5	0