Gary J Pielak

List of Publications by Citations

145 papers	7,723 citations	50 h-index	83 g-index
153 ext. papers	8,651 ext. citations	6.9 avg, IF	6.27 L-index

#	Paper	IF	Citations
145	Physicochemical properties of cells and their effects on intrinsically disordered proteins (IDPs). *Chemical Reviews*, **2014**, 114, 6661-714	68.1	301
144	Impact of protein denaturants and stabilizers on water structure. *Journal of the American Chemical Society*, **2004**, 126, 1958-61	16.4	272
143	FlgM gains structure in living cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 12681-4	11.5	265
142	Macromolecular crowding and protein stability. *Journal of the American Chemical Society*, **2012**, 134, 16614-8	16.4	247
141	Interpreting the effects of small uncharged solutes on protein-folding equilibria. *Annual Review of Biophysics and Biomolecular Structure*, **2001**, 30, 271-306		245
140	Protein crowding tunes protein stability. *Journal of the American Chemical Society*, **2011**, 133, 7116-20	16.4	214
139	Effects of proteins on protein diffusion. *Journal of the American Chemical Society*, **2010**, 132, 9392-7	16.4	197
138	Tardigrades Use Intrinsically Disordered Proteins to Survive Desiccation. *Molecular Cell*, **2017**, 65, 975-984.e5	14.5	176
137	Unexpected effects of macromolecular crowding on protein stability. *Biochemistry*, **2012**, 51, 9773-5	3.2	169
136	Protein (19)F NMR in Escherichia coli. *Journal of the American Chemical Society*, **2010**, 132, 321-7	16.4	166
135	Site-directed mutagenesis of cytochrome c shows that an invariant Phe is not essential for function. *Nature*, **1985**, 313, 152-4	50.4	156
134	Soft interactions and crowding. *Biophysical Reviews*, **2013**, 5, 187-194	3.7	150
133	Osmolyte-induced changes in protein conformational equilibria. *Biopolymers*, **2000**, 53, 293-307	2.2	147
132	Solvent-induced collapse of alpha-synuclein and acid-denatured cytochrome c. *Protein Science*, **2001**, 10, 2195-9	6.3	145
131	Quinary structure modulates protein stability in cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 1739-42	11.5	144
130	Impact of reconstituted cytosol on protein stability. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 19342-7	11.5	144
129	Macromolecular crowding in the Escherichia coli periplasm maintains alpha-synuclein disorder. *Journal of Molecular Biology*, **2006**, 355, 893-7	6.5	143

128	Volume exclusion and soft interaction effects on protein stability under crowded conditions. *Biochemistry*, **2010**, 49, 6984-91	3.2	117
127	Macromolecular crowding fails to fold a globular protein in cells. *Journal of the American Chemical Society*, **2011**, 133, 8082-5	16.4	115
126	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, 1725-30	11.5	111
125	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, 6310-1	16.4	110
124	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	16.4	87
123	The cellular environment stabilizes adenine riboswitch RNA structure. *Biochemistry*, **2013**, 52, 8777-85	3.2	86
122	Protein crowder charge and protein stability. *Biochemistry*, **2014**, 53, 1601-6	3.2	84
121	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, 2466-72	5.4	83
120	Residue level quantification of protein stability in living cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 11335-40	11.5	82
119	A cell is more than the sum of its (dilute) parts: A brief history of quinary structure. *Protein Science*, **2017**, 26, 403-413	6.3	81
118	Sugar-induced molten-globule model. *Biochemistry*, **1998**, 37, 17048-53	3.2	77
117	Stability of yeast iso-1-ferricytochrome c as a function of pH and temperature. *Protein Science*, **1994**, 3, 1253-60	6.3	76
116	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	3.2	75
115	Introduction of a disulfide bond into cytochrome c stabilizes a compact denatured state. *Biochemistry*, **1992**, 31, 12337-44	3.2	74
114	Translational and rotational diffusion of a small globular protein under crowded conditions. *Journal of Physical Chemistry B*, **2009**, 113, 13390-2	3.4	73
113	Residue-level interrogation of macromolecular crowding effects on protein stability. *Journal of the American Chemical Society*, **2008**, 130, 6826-30	16.4	73
112	Interaction of □synuclein with vesicles that mimic mitochondrial membranes. *Biochimica Et Biophysica Acta - Biomembranes*, **2012**, 1818, 512-9	3.8	72
111	Native tertiary structure in an A-state. *Journal of Molecular Biology*, **1998**, 275, 379-88	6.5	72

110	Entropic Stabilization of Cytochrome c upon Reduction. *Journal of the American Chemical Society*, **1995**, 117, 1675-1677	16.4	71
109	Comparison of reduced and oxidized yeast iso-1-cytochrome c using proton paramagnetic shifts. *Biochemistry*, **1991**, 30, 1928-34	3.2	71
108	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, 12370-3	16.4	70
107	Protein nuclear magnetic resonance under physiological conditions. *Biochemistry*, **2009**, 48, 226-34	3.2	70
106	Role of configurational gating in intracomplex electron transfer from cytochrome c to the radical cation in cytochrome c peroxidase. *Biochemistry*, **1999**, 38, 6846-54	3.2	66
105	(19) F NMR spectroscopy as a probe of cytoplasmic viscosity and weak protein interactions in living cells. *Chemistry - A European Journal*, **2013**, 19, 12705-10	4.8	65
104	19F NMR studies of alpha-synuclein conformation and fibrillation. *Biochemistry*, **2009**, 48, 8578-84	3.2	64
103	Osmotic Shock Induced Protein Destabilization in Living Cells and Its Reversal by Glycine Betaine. *Journal of Molecular Biology*, **2017**, 429, 1155-1161	6.5	60
102	Design of a ruthenium-cytochrome c derivative to measure electron transfer to the radical cation and oxyferryl heme in cytochrome c peroxidase. *Biochemistry*, **1996**, 35, 15107-19	3.2	59
101	Using NMR to distinguish viscosity effects from nonspecific protein binding under crowded conditions. *Journal of the American Chemical Society*, **2009**, 131, 1368-9	16.4	55
100	Stability and apoptotic activity of recombinant human cytochrome c. *Biochemical and Biophysical Research Communications*, **2003**, 312, 733-40	3.4	55
99	In-cell protein NMR and protein leakage. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 347-54	4.2	54
98	Natively Disordered Proteins275-357		54
97	Amide proton exchange rates of oxidized and reduced Saccharomyces cerevisiae iso-1-cytochrome c. *Protein Science*, **1993**, 2, 1966-74	6.3	52
96	Electrostatic Contributions to Protein Quinary Structure. *Journal of the American Chemical Society*, **2016**, 138, 13139-13142	16.4	52
95	NMR studies of protein folding and binding in cells and cell-like environments. *Current Opinion in Structural Biology*, **2015**, 30, 7-16	8.1	49
94	Baseline length and automated fitting of denaturation data. *Protein Science*, **1998**, 7, 1262-3	6.3	48
93	Protein thermal denaturation, side-chain models, and evolution: amino acid substitutions at a conserved helix-helix interface. *Biochemistry*, **1995**, 34, 3268-76	3.2	47

92	19F NMR studies of □synuclein-membrane interactions. *Protein Science*, **2010**, 19, 1686-91	6.3	45
91	Effects of molecular crowding by saccharides on alpha-chymotrypsin dimerization. *Protein Science*, **2002**, 11, 997-1003	6.3	45
90	Protein shape modulates crowding effects. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 10965-10970	11.5	45
89	Characterization of horse cytochrome c expressed in Escherichia coli. *Protein Expression and Purification*, **2001**, 22, 220-4	2	44
88	Probing the cytochrome c peroxidase-cytochrome c electron transfer reaction using site specific cross-linking. *Biochemistry*, **1996**, 35, 4837-45	3.2	44
87	A bioreactor for in-cell protein NMR. *Journal of Magnetic Resonance*, **2010**, 202, 140-6	3	43
86	Challenge of mimicking the influences of the cellular environment on RNA structure by PEG-induced macromolecular crowding. *Biochemistry*, **2015**, 54, 6447-53	3.2	42
85	Surface Charge Modulates Protein-Protein Interactions in Physiologically Relevant Environments. *Biochemistry*, **2018**, 57, 1681-1684	3.2	42
84	Disordered Protein Diffusion under Crowded Conditions. *Journal of Physical Chemistry Letters*, **2012** , 3, 2703-2706	6.4	42
83	Protein dynamics in living cells. *Biochemistry*, **2005**, 44, 9275-9	3.2	41
82	Temperature-induced reversible conformational change in the first 100 residues of alpha-synuclein. *Protein Science*, **2006**, 15, 602-8	6.3	41
81	Identifying the physiological electron transfer site of cytochrome c peroxidase by structure-based engineering. *Biochemistry*, **1996**, 35, 667-73	3.2	41
80	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. *Biochemistry*, **1996**, 35, 15800-6	3.2	41
79	Intracellular pH modulates quinary structure. *Protein Science*, **2015**, 24, 1748-55	6.3	39
78	Second virial coefficients as a measure of protein--osmolyte interactions. *Protein Science*, **2001**, 10, 12-6	6.3	39
77	Cosolutes, Crowding, and Protein Folding Kinetics. *Journal of Physical Chemistry B*, **2017**, 121, 6527-6537	3.4	38
76	Internal and global protein motion assessed with a fusion construct and in-cell NMR spectroscopy. *ChemBioChem*, **2011**, 12, 390-1	3.8	38
75	Intrinsically Disordered Proteins and Desiccation Tolerance: Elucidating Functional and Mechanistic Underpinnings of Anhydrobiosis. *BioEssays*, **2017**, 39, 1700119	4.1	37

74	Osmolytes and Protein-Protein Interactions. *Journal of the American Chemical Society*, **2018**, 140, 7441-7444	14.4	35
73	Cosolute and Crowding Effects on a Side-By-Side Protein Dimer. *Biochemistry*, **2017**, 56, 971-976	3.2	31
72	A model of intracellular organization. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 5901-2	11.5	31
71	Macromolecular and Small Molecular Crowding Have Similar Effects on α-Synuclein Structure. *ChemPhysChem*, **2017**, 18, 55-58	3.2	30
70	Alpha-Synuclein conformation affects its tyrosine-dependent oxidative aggregation. *Biochemistry*, **2008**, 47, 13604-9	3.2	29
69	Protein Stability in Reverse Micelles. *Angewandte Chemie - International Edition*, **2016**, 55, 3586-9	16.4	29
68	Hydrogen exchange of disordered proteins in Escherichia coli. *Protein Science*, **2015**, 24, 706-13	6.3	28
67	The structure of cytochrome c and its relation to recent studies of long-range electron transfer. *Protein Engineering, Design and Selection*, **1987**, 1, 83-8	1.9	28
66	Effects of crowding by mono-, di-, and tetrasaccharides on cytochrome c-cytochrome c peroxidase binding: comparing experiment to theory. *Biochemistry*, **2001**, 40, 281-5	3.2	27
65	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 Saccharomyces cerevisiae. *Biochemistry*, **1991**, 30, 7033-40	3.2	27
64	Effects of recombinant protein expression on green fluorescent protein diffusion in Escherichia coli. *Biochemistry*, **2009**, 48, 5083-9	3.2	25
63	1H and 15N Hyperfine Shifts of Cytochrome c. *Journal of the American Chemical Society*, **1999**, 121, 9247-9248	14.4	25
62	Magnetic Resonance Spectroscopy as a Tool for Assessing Macromolecular Structure and Function in Living Cells. *Annual Review of Analytical Chemistry*, **2017**, 10, 157-182	12.5	24
61	Using NMR-detected backbone amide 1H exchange to assess macromolecular crowding effects on globular-protein stability. *Methods in Enzymology*, **2009**, 466, 1-18	1.7	24
60	Emergence of life: Physical chemistry changes the paradigm. *Biology Direct*, **2015**, 10, 33	7.2	23
59	Equilibrium thermodynamics of a physiologically-relevant heme-protein complex. *Biochemistry*, **1999**, 38, 16876-81	3.2	23
58	Two-dimensional NMR as a probe of structural similarity applied to mutants of cytochrome c. *FEBS Journal*, **1988**, 177, 179-85		23
57	Protecting Enzymes from Stress-Induced Inactivation. *Biochemistry*, **2019**, 58, 3825-3833	3.2	22

56	Polarity of disulfide bonds. *Protein Science*, **1993**, 2, 1183-4	6.3	22
55	An osmolyte mitigates the destabilizing effect of protein crowding. *Protein Science*, **2014**, 23, 1161-4	6.3	21
54	Protecting activity of desiccated enzymes. *Protein Science*, **2019**, 28, 941-951	6.3	20
53	Strategies for protein NMR in Escherichia coli. *Biochemistry*, **2014**, 53, 1971-81	3.2	20
52	An upper limit for macromolecular crowding effects. *BMC Biophysics*, **2011**, 4, 13	0	20
51	Quantifying green fluorescent protein diffusion in Escherichia coli by using continuous photobleaching with evanescent illumination. *Journal of Physical Chemistry B*, **2009**, 113, 4837-45	3.4	19
50	Probing the micelle-bound aggregation-prone state of □synuclein with (19)F NMR spectroscopy. *ChemBioChem*, **2010**, 11, 1993-6	3.8	19
49	Interactions between yeast iso-1-cytochrome c and its peroxidase. *Biochemistry*, **2001**, 40, 422-8	3.2	19
48	Changing the transition state for protein (Un) folding. *Biochemistry*, **1996**, 35, 7403-11	3.2	19
47	Quinary interactions with an unfolded state ensemble. *Protein Science*, **2017**, 26, 1698-1703	6.3	18
46	Large cosolutes, small cosolutes, and dihydrofolate reductase activity. *Protein Science*, **2017**, 26, 2417-2425	6.3	18
45	Crowding and function reunite. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 17457-8	11.5	18
44	Peroxidative aggregation of alpha-synuclein requires tyrosines. *Protein Science*, **2004**, 13, 2852-6	6.3	18
43	Protein-complex stability in cells and in vitro under crowded conditions. *Current Opinion in Structural Biology*, **2021**, 66, 183-192	8.1	18
42	Rapid Quantification of Protein-Ligand Binding via F NMR Lineshape Analysis. *Biophysical Journal*, **2020**, 118, 2537-2548	2.9	17
41	Interaction of □synuclein and a cell penetrating fusion peptide with higher eukaryotic cell membranes assessed by □□F NMR. *Molecular Pharmaceutics*, **2012**, 9, 1024-9	5.6	16
40	Quantification of size effect on protein rotational mobility in cells by F NMR spectroscopy. *Analytical and Bioanalytical Chemistry*, **2018**, 410, 869-874	4.4	16
39	Amide proton exchange of a dynamic loop in cell extracts. *Protein Science*, **2013**, 22, 1313-9	6.3	15

38	Searching for quantitative entropy-enthalpy compensation among protein variants. *Proteins: Structure, Function and Bioinformatics*, **2002**, 49, 398-402	4.2	15
37	Peeking into living eukaryotic cells with high-resolution NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 11817-8	11.5	14
36	Crowding by trisaccharides and the 2:1 cytochrome c-cytochrome c peroxidase complex. *Biochemistry*, **2002**, 41, 547-51	3.2	14
35	Nonideality and protein thermal denaturation. *Biopolymers*, **1999**, 49, 471-9	2.2	14
34	The intracellular environment affects protein-protein interactions. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	13
33	Cytosol has a small effect on protein backbone dynamics. *Biochemistry*, **2006**, 45, 10085-91	3.2	12
32	Crowding and Confinement Can Oppositely Affect Protein Stability. *ChemPhysChem*, **2018**, 19, 3350-3355	3.2	12
31	Positively Charged Tags Impede Protein Mobility in Cells as Quantified by F NMR. *Journal of Physical Chemistry B*, **2019**, 123, 4527-4533	3.4	11
30	Pressure perturbation calorimetry of helical peptides. *Proteins: Structure, Function and Bioinformatics*, **2006**, 63, 322-6	4.2	11
29	Enthalpic stabilization of an SH3 domain by D O. *Protein Science*, **2018**, 27, 1710-1716	6.3	10
28	Testing hypotheses about determinants of protein structure with high-precision, high-throughput stability measurements and statistical modeling. *Biochemistry*, **2003**, 42, 7594-603	3.2	9
27	Reconsideration of sedimentation equilibrium distributions reflecting the effects of small inert cosolutes on the dimerization of alpha-chymotrypsin. *Biophysical Chemistry*, **2007**, 130, 89-92	3.5	8
26	Preparation and characterization of sulfanilazo and arsanilazo proteins. *Biochemistry*, **1984**, 23, 596-603	3.2	8
25	Roles of structural plasticity in chaperone HdeA activity are revealed by F NMR. *Chemical Science*, **2016**, 7, 2222-2228	9.4	7
24	Membrane proteins, magic-angle spinning, and in-cell NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 4715-6	11.5	7
23	Azo protein analogs: synthesis and characterization of arsanilazo and sulfanilazo derivatives of tyrosine and histidine. *Biochemistry*, **1984**, 23, 589-596	3.2	7
22	The Expanding Zoo of In-Cell Protein NMR. *Biophysical Journal*, **2018**, 115, 1628-1629	2.9	7
21	Controlling and quantifying protein concentration in Escherichia coli. *Protein Science*, **2019**, 28, 1307-1316	6.3	6

20	Protein Stability in Reverse Micelles. *Angewandte Chemie*, **2016**, 128, 3650-3653	3.6	6
19	Temperature-sensitive variants of Saccharomyces cerevisiae iso-1-cytochrome c produced by random mutagenesis of codons 43 to 54. *Journal of Molecular Biology*, **1991**, 221, 97-105	6.5	6
18	Dynamical spectroscopy and microscopy of proteins in cells. *Current Opinion in Structural Biology*, **2021**, 70, 1-7	8.1	6
17	Protein-Peptide Binding Energetics under Crowded Conditions. *Journal of Physical Chemistry B*, **2020**, 124, 9297-9309	3.4	5
16	Dried Protein Structure Revealed at the Residue Level by Liquid-Observed Vapor Exchange NMR. *Biochemistry*, **2021**, 60, 152-159	3.2	5
15	Requirements for perpendicular helix pairing. *Proteins: Structure, Function and Bioinformatics*, **1996**, 26, 95-107	4.2	4
14	Protection by desiccation-tolerance proteins probed at the residue level. *Protein Science*, **2021**,	6.3	4
13	Rheostatic Control of Protein Expression Using Tuner Cells. *Biochemistry*, **2020**, 59, 733-735	3.2	4
12	Chapter 12. Protein Stability and Weak Intracellular Interactions. *New Developments in NMR*, **2019**, 188-206	0.9	4
11	Buffers, Especially the Good Kind. *Biochemistry*, **2021**, 60, 3436-3440	3.2	4
10	Membrane-mediated disorder-to-order transition of SNAP25 flexible linker facilitates its interaction with syntaxin-1 and SNARE-complex assembly. *FASEB Journal*, **2019**, 33, 7985-7994	0.9	3
9	Woes of proline: a cautionary kinetic tale. *Protein Science*, **2006**, 15, 393-4	6.3	3
8	Water's Variable Role in Protein Stability Uncovered by Liquid-Observed Vapor Exchange NMR. *Biochemistry*, **2021**, 60, 3041-3045	3.2	3
7	Design, synthesis, expression, and characterization of the genes for mouse Fc gamma RIIb1 and Fc gamma RIIb2 cytoplasmic regions. *Protein Science*, **1997**, 6, 1038-46	6.3	2
6	Toxicity and Immunogenicity of a Tardigrade Cytosolic Abundant Heat Soluble Protein in Mice. *Frontiers in Pharmacology*, **2020**, 11, 565969	5.6	2
5	Oocytes for Eukaryotic In-Cell NMR. *Biochemistry*, **2021**, 60, 451-459	3.2	2
4	Osmolyte-induced changes in protein conformational equilibria **2000**, 53, 293		2
3	Osmolyte-induced changes in protein conformational equilibria **2000**, 53, 293		1

2	Desiccation-tolerance and globular proteins adsorb similar amounts of water.. *Protein Science*, **2022**, 31, e4288	6.3	1
1	Jan Hermans (1933-2018): Red-blooded biophysicists study hemoglobin. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 171-173	4.2	