

Gary J Pielak

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/625736/gary-j-pielak-publications-by-year.pdf>
Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Desiccation-tolerance and globular proteins adsorb similar amounts of water.. <i>Protein Science</i> , 2022 , 31, e4288	6.3	1
144	Protection by desiccation-tolerance proteins probed at the residue level. <i>Protein Science</i> , 2021 ,	6.3	4
143	The intracellular environment affects protein-protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	13
142	Buffers, Especially the Good Kind. <i>Biochemistry</i> , 2021 , 60, 3436-3440	3.2	4
141	Protein-complex stability in cells and in vitro under crowded conditions. <i>Current Opinion in Structural Biology</i> , 2021 , 66, 183-192	8.1	18
140	Oocytes for Eukaryotic In-Cell NMR. <i>Biochemistry</i> , 2021 , 60, 451-459	3.2	2
139	Water's Variable Role in Protein Stability Uncovered by Liquid-Observed Vapor Exchange NMR. <i>Biochemistry</i> , 2021 , 60, 3041-3045	3.2	3
138	Dynamical spectroscopy and microscopy of proteins in cells. <i>Current Opinion in Structural Biology</i> , 2021 , 70, 1-7	8.1	6
137	Dried Protein Structure Revealed at the Residue Level by Liquid-Observed Vapor Exchange NMR. <i>Biochemistry</i> , 2021 , 60, 152-159	3.2	5
136	Rapid Quantification of Protein-Ligand Binding via F NMR Lineshape Analysis. <i>Biophysical Journal</i> , 2020 , 118, 2537-2548	2.9	17
135	Rheostatic Control of Protein Expression Using Tuner Cells. <i>Biochemistry</i> , 2020 , 59, 733-735	3.2	4
134	Toxicity and Immunogenicity of a Tardigrade Cytosolic Abundant Heat Soluble Protein in Mice. <i>Frontiers in Pharmacology</i> , 2020 , 11, 565969	5.6	2
133	Protein-Peptide Binding Energetics under Crowded Conditions. <i>Journal of Physical Chemistry B</i> , 2020 , 124, 9297-9309	3.4	5
132	Protecting Enzymes from Stress-Induced Inactivation. <i>Biochemistry</i> , 2019 , 58, 3825-3833	3.2	22
131	Positively Charged Tags Impede Protein Mobility in Cells as Quantified by F NMR. <i>Journal of Physical Chemistry B</i> , 2019 , 123, 4527-4533	3.4	11
130	Controlling and quantifying protein concentration in Escherichia coli. <i>Protein Science</i> , 2019 , 28, 1307-1316	6.3	6
129	Jan Hermans (1933-2018): Red-blooded biophysicists study hemoglobin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 171-173	4.2	

128	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	0.9	3
127	Protecting activity of desiccated enzymes. <i>Protein Science</i> , 2019 , 28, 941-951	6.3	20
126	Chapter 12. Protein Stability and Weak Intracellular Interactions. <i>New Developments in NMR</i> , 2019 , 188-206		4
125	Surface Charge Modulates Protein-Protein Interactions in Physiologically Relevant Environments. <i>Biochemistry</i> , 2018 , 57, 1681-1684	3.2	42
124	Enthalpic stabilization of an SH3 domain by D O. <i>Protein Science</i> , 2018 , 27, 1710-1716	6.3	10
123	Quantification of size effect on protein rotational mobility in cells by F NMR spectroscopy. <i>Analytical and Bioanalytical Chemistry</i> , 2018 , 410, 869-874	4.4	16
122	Protein shape modulates crowding effects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 10965-10970	11.5	45
121	Crowding and Confinement Can Oppositely Affect Protein Stability. <i>ChemPhysChem</i> , 2018 , 19, 3350-3355	5.2	12
120	The Expanding Zoo of In-Cell Protein NMR. <i>Biophysical Journal</i> , 2018 , 115, 1628-1629	2.9	7
119	Osmolytes and Protein-Protein Interactions. <i>Journal of the American Chemical Society</i> , 2018 , 140, 7441-7444	16.4	35
118	Cosolute and Crowding Effects on a Side-By-Side Protein Dimer. <i>Biochemistry</i> , 2017 , 56, 971-976	3.2	31
117	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	12.5	24
116	Osmotic Shock Induced Protein Destabilization in Living Cells and Its Reversal by Glycine Betaine. <i>Journal of Molecular Biology</i> , 2017 , 429, 1155-1161	6.5	60
115	Quinary interactions with an unfolded state ensemble. <i>Protein Science</i> , 2017 , 26, 1698-1703	6.3	18
114	Cosolutes, Crowding, and Protein Folding Kinetics. <i>Journal of Physical Chemistry B</i> , 2017 , 121, 6527-6537	3.4	38
113	Tardigrades Use Intrinsically Disordered Proteins to Survive Desiccation. <i>Molecular Cell</i> , 2017 , 65, 975-984	17.6	176
112	A cell is more than the sum of its (dilute) parts: A brief history of quinary structure. <i>Protein Science</i> , 2017 , 26, 403-413	6.3	81
111	Intrinsically Disordered Proteins and Desiccation Tolerance: Elucidating Functional and Mechanistic Underpinnings of Anhydrobiosis. <i>BioEssays</i> , 2017 , 39, 1700119	4.1	37

110	Large cosolutes, small cosolutes, and dihydrofolate reductase activity. <i>Protein Science</i> , 2017 , 26, 2417-2425	4.5	18
109	Macromolecular and Small Molecular Crowding Have Similar Effects on E-Synuclein Structure. <i>ChemPhysChem</i> , 2017 , 18, 55-58	3.2	30
108	Protein Stability in Reverse Micelles. <i>Angewandte Chemie</i> , 2016 , 128, 3650-3653	3.6	6
107	In-cell thermodynamics and a new role for protein surfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 1725-30	11.5	111
106	Roles of structural plasticity in chaperone HdeA activity are revealed by F NMR. <i>Chemical Science</i> , 2016 , 7, 2222-2228	9.4	7
105	Protein Stability in Reverse Micelles. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 3586-9	16.4	29
104	Electrostatic Contributions to Protein Quinary Structure. <i>Journal of the American Chemical Society</i> , 2016 , 138, 13139-13142	16.4	52
103	Challenge of mimicking the influences of the cellular environment on RNA structure by PEG-induced macromolecular crowding. <i>Biochemistry</i> , 2015 , 54, 6447-53	3.2	42
102	NMR studies of protein folding and binding in cells and cell-like environments. <i>Current Opinion in Structural Biology</i> , 2015 , 30, 7-16	8.1	49
101	Intracellular pH modulates quinary structure. <i>Protein Science</i> , 2015 , 24, 1748-55	6.3	39
100	Emergence of life: Physical chemistry changes the paradigm. <i>Biology Direct</i> , 2015 , 10, 33	7.2	23
99	Quinary structure modulates protein stability in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 1739-42	11.5	144
98	Hydrogen exchange of disordered proteins in Escherichia coli. <i>Protein Science</i> , 2015 , 24, 706-13	6.3	28
97	Protein crowder charge and protein stability. <i>Biochemistry</i> , 2014 , 53, 1601-6	3.2	84
96	Strategies for protein NMR in Escherichia coli. <i>Biochemistry</i> , 2014 , 53, 1971-81	3.2	20
95	Residue level quantification of protein stability in living cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 11335-40	11.5	82
94	Physicochemical properties of cells and their effects on intrinsically disordered proteins (IDPs). <i>Chemical Reviews</i> , 2014 , 114, 6661-714	68.1	301
93	An osmolyte mitigates the destabilizing effect of protein crowding. <i>Protein Science</i> , 2014 , 23, 1161-4	6.3	21

92	Soft interactions and crowding. <i>Biophysical Reviews</i> , 2013 , 5, 187-194	3.7	150
91	The cellular environment stabilizes adenine riboswitch RNA structure. <i>Biochemistry</i> , 2013 , 52, 8777-85	3.2	86
90	Amide proton exchange of a dynamic loop in cell extracts. <i>Protein Science</i> , 2013 , 22, 1313-9	6.3	15
89	Impact of reconstituted cytosol on protein stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 19342-7	11.5	144
88	(19) F NMR spectroscopy as a probe of cytoplasmic viscosity and weak protein interactions in living cells. <i>Chemistry - A European Journal</i> , 2013 , 19, 12705-10	4.8	65
87	Unexpected effects of macromolecular crowding on protein stability. <i>Biochemistry</i> , 2012 , 51, 9773-5	3.2	169
86	Disordered Protein Diffusion under Crowded Conditions. <i>Journal of Physical Chemistry Letters</i> , 2012 , 3, 2703-2706	6.4	42
85	Interaction of β -synuclein and a cell penetrating fusion peptide with higher eukaryotic cell membranes assessed by ^{19}F NMR. <i>Molecular Pharmaceutics</i> , 2012 , 9, 1024-9	5.6	16
84	Interaction of β -synuclein with vesicles that mimic mitochondrial membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 512-9	3.8	72
83	Macromolecular crowding and protein stability. <i>Journal of the American Chemical Society</i> , 2012 , 134, 16614-8	16.4	247
82	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, 4715-6	11.5	7
81	Macromolecular crowding fails to fold a globular protein in cells. <i>Journal of the American Chemical Society</i> , 2011 , 133, 8082-5	16.4	115
80	Protein crowding tunes protein stability. <i>Journal of the American Chemical Society</i> , 2011 , 133, 7116-20	16.4	214
79	An upper limit for macromolecular crowding effects. <i>BMC Biophysics</i> , 2011 , 4, 13	0	20
78	In-cell protein NMR and protein leakage. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 347-54	4.2	54
77	Internal and global protein motion assessed with a fusion construct and in-cell NMR spectroscopy. <i>ChemBioChem</i> , 2011 , 12, 390-1	3.8	38
76	In situ structural characterization of a recombinant protein in native Escherichia coli membranes with solid-state magic-angle-spinning NMR. <i>Journal of the American Chemical Society</i> , 2011 , 133, 12370-3	16.4	70
75	Crowding and function reunite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 17457-8	11.5	18

74	Effects of proteins on protein diffusion. <i>Journal of the American Chemical Society</i> , 2010 , 132, 9392-7	16.4	197
73	Volume exclusion and soft interaction effects on protein stability under crowded conditions. <i>Biochemistry</i> , 2010 , 49, 6984-91	3.2	117
72	Protein (19)F NMR in Escherichia coli. <i>Journal of the American Chemical Society</i> , 2010 , 132, 321-7	16.4	166
71	Probing the micelle-bound aggregation-prone state of β -synuclein with (19)F NMR spectroscopy. <i>ChemBioChem</i> , 2010 , 11, 1993-6	3.8	19
70	A bioreactor for in-cell protein NMR. <i>Journal of Magnetic Resonance</i> , 2010 , 202, 140-6	3	43
69	¹⁹ F NMR studies of β -synuclein-membrane interactions. <i>Protein Science</i> , 2010 , 19, 1686-91	6.3	45
68	Using NMR-detected backbone amide ¹ H exchange to assess macromolecular crowding effects on globular-protein stability. <i>Methods in Enzymology</i> , 2009 , 466, 1-18	1.7	24
67	Protein nuclear magnetic resonance under physiological conditions. <i>Biochemistry</i> , 2009 , 48, 226-34	3.2	70
66	Effects of recombinant protein expression on green fluorescent protein diffusion in Escherichia coli. <i>Biochemistry</i> , 2009 , 48, 5083-9	3.2	25
65	Using NMR to distinguish viscosity effects from nonspecific protein binding under crowded conditions. <i>Journal of the American Chemical Society</i> , 2009 , 131, 1368-9	16.4	55
64	Quantifying green fluorescent protein diffusion in Escherichia coli by using continuous photobleaching with evanescent illumination. <i>Journal of Physical Chemistry B</i> , 2009 , 113, 4837-45	3.4	19
63	Translational and rotational diffusion of a small globular protein under crowded conditions. <i>Journal of Physical Chemistry B</i> , 2009 , 113, 13390-2	3.4	73
62	¹⁹ F NMR studies of alpha-synuclein conformation and fibrillation. <i>Biochemistry</i> , 2009 , 48, 8578-84	3.2	64
61	Differential dynamical effects of macromolecular crowding on an intrinsically disordered protein and a globular protein: implications for in-cell NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2008 , 130, 6310-1	16.4	110
60	Residue-level interrogation of macromolecular crowding effects on protein stability. <i>Journal of the American Chemical Society</i> , 2008 , 130, 6826-30	16.4	73
59	Alpha-Synuclein conformation affects its tyrosine-dependent oxidative aggregation. <i>Biochemistry</i> , 2008 , 47, 13604-9	3.2	29
58	Reconsideration of sedimentation equilibrium distributions reflecting the effects of small inert cosolutes on the dimerization of alpha-chymotrypsin. <i>Biophysical Chemistry</i> , 2007 , 130, 89-92	3.5	8
57	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, 11817-8	11.5	14

56	Temperature-induced reversible conformational change in the first 100 residues of alpha-synuclein. <i>Protein Science</i> , 2006 , 15, 602-8	6.3	41
55	Cytosol has a small effect on protein backbone dynamics. <i>Biochemistry</i> , 2006 , 45, 10085-91	3.2	12
54	Macromolecular crowding in the Escherichia coli periplasm maintains alpha-synuclein disorder. <i>Journal of Molecular Biology</i> , 2006 , 355, 893-7	6.5	143
53	Woes of proline: a cautionary kinetic tale. <i>Protein Science</i> , 2006 , 15, 393-4	6.3	3
52	Pressure perturbation calorimetry of helical peptides. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 322-6	4.2	11
51	Protein dynamics in living cells. <i>Biochemistry</i> , 2005 , 44, 9275-9	3.2	41
50	A model of intracellular organization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 5901-2	11.5	31
49	Peroxidative aggregation of alpha-synuclein requires tyrosines. <i>Protein Science</i> , 2004 , 13, 2852-6	6.3	18
48	Impact of protein denaturants and stabilizers on water structure. <i>Journal of the American Chemical Society</i> , 2004 , 126, 1958-61	16.4	272
47	Testing hypotheses about determinants of protein structure with high-precision, high-throughput stability measurements and statistical modeling. <i>Biochemistry</i> , 2003 , 42, 7594-603	3.2	9
46	Stability and apoptotic activity of recombinant human cytochrome c. <i>Biochemical and Biophysical Research Communications</i> , 2003 , 312, 733-40	3.4	55
45	Searching for quantitative entropy-enthalpy compensation among protein variants. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 49, 398-402	4.2	15
44	Effects of molecular crowding by saccharides on alpha-chymotrypsin dimerization. <i>Protein Science</i> , 2002 , 11, 997-1003	6.3	45
43	FlgM gains structure in living cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 12681-4	11.5	265
42	Crowding by trisaccharides and the 2:1 cytochrome c-cytochrome c peroxidase complex. <i>Biochemistry</i> , 2002 , 41, 547-51	3.2	14
41	Solvent-induced collapse of alpha-synuclein and acid-denatured cytochrome c. <i>Protein Science</i> , 2001 , 10, 2195-9	6.3	145
40	Second virial coefficients as a measure of protein--osmolyte interactions. <i>Protein Science</i> , 2001 , 10, 12-6	6.3	39
39	Characterization of horse cytochrome c expressed in Escherichia coli. <i>Protein Expression and Purification</i> , 2001 , 22, 220-4	2	44

38	Interpreting the effects of small uncharged solutes on protein-folding equilibria. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2001 , 30, 271-306		245
37	Interactions between yeast iso-1-cytochrome c and its peroxidase. <i>Biochemistry</i> , 2001 , 40, 422-8	3.2	19
36	Effects of crowding by mono-, di-, and tetrasaccharides on cytochrome c-cytochrome c peroxidase binding: comparing experiment to theory. <i>Biochemistry</i> , 2001 , 40, 281-5	3.2	27
35	Osmolyte-induced changes in protein conformational equilibria. <i>Biopolymers</i> , 2000 , 53, 293-307	2.2	147
34	Osmolyte-induced changes in protein conformational equilibria 2000 , 53, 293		1
33	Osmolyte-induced changes in protein conformational equilibria 2000 , 53, 293		2
32	Nonideality and protein thermal denaturation. <i>Biopolymers</i> , 1999 , 49, 471-9	2.2	14
31	¹ H and ¹⁵ N Hyperfine Shifts of Cytochrome c. <i>Journal of the American Chemical Society</i> , 1999 , 121, 9247-9248	6.4	25
30	Role of configurational gating in intracomplex electron transfer from cytochrome c to the radical cation in cytochrome c peroxidase. <i>Biochemistry</i> , 1999 , 38, 6846-54	3.2	66
29	Equilibrium thermodynamics of a physiologically-relevant heme-protein complex. <i>Biochemistry</i> , 1999 , 38, 16876-81	3.2	23
28	Baseline length and automated fitting of denaturation data. <i>Protein Science</i> , 1998 , 7, 1262-3	6.3	48
27	Sugar-induced molten-globule model. <i>Biochemistry</i> , 1998 , 37, 17048-53	3.2	77
26	Native tertiary structure in an A-state. <i>Journal of Molecular Biology</i> , 1998 , 275, 379-88	6.5	72
25	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, 1038-46	6.3	2
24	Identifying the physiological electron transfer site of cytochrome c peroxidase by structure-based engineering. <i>Biochemistry</i> , 1996 , 35, 667-73	3.2	41
23	Probing the cytochrome c peroxidase-cytochrome c electron transfer reaction using site specific cross-linking. <i>Biochemistry</i> , 1996 , 35, 4837-45	3.2	44
22	Changing the transition state for protein (Un) folding. <i>Biochemistry</i> , 1996 , 35, 7403-11	3.2	19
21	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, 15800-6	3.2	41

20	Design of a ruthenium-cytochrome c derivative to measure electron transfer to the radical cation and oxyferryl heme in cytochrome c peroxidase. <i>Biochemistry</i> , 1996 , 35, 15107-19	3.2	59
19	Requirements for perpendicular helix pairing. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 26, 95-107	4.2	4
18	Protein thermal denaturation, side-chain models, and evolution: amino acid substitutions at a conserved helix-helix interface. <i>Biochemistry</i> , 1995 , 34, 3268-76	3.2	47
17	Design of a ruthenium-cytochrome c derivative to measure electron transfer to the initial acceptor in cytochrome c oxidase. <i>Journal of Biological Chemistry</i> , 1995 , 270, 2466-72	5.4	83
16	Entropic Stabilization of Cytochrome c upon Reduction. <i>Journal of the American Chemical Society</i> , 1995 , 117, 1675-1677	16.4	71
15	Stability of yeast iso-1-ferricytochrome c as a function of pH and temperature. <i>Protein Science</i> , 1994 , 3, 1253-60	6.3	76
14	Polarity of disulfide bonds. <i>Protein Science</i> , 1993 , 2, 1183-4	6.3	22
13	Amide proton exchange rates of oxidized and reduced <i>Saccharomyces cerevisiae</i> iso-1-cytochrome c. <i>Protein Science</i> , 1993 , 2, 1966-74	6.3	52
12	Introduction of a disulfide bond into cytochrome c stabilizes a compact denatured state. <i>Biochemistry</i> , 1992 , 31, 12337-44	3.2	74
11	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, 7033-40	3.2	27
10	Comparison of reduced and oxidized yeast iso-1-cytochrome c using proton paramagnetic shifts. <i>Biochemistry</i> , 1991 , 30, 1928-34	3.2	71
9	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	6.5	6
8	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. <i>Biochemistry</i> , 1990 , 29, 6994-7003	3.2	75
7	Two-dimensional NMR as a probe of structural similarity applied to mutants of cytochrome c. <i>FEBS Journal</i> , 1988 , 177, 179-85		23
6	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, 83-8	1.9	28
5	Elimination of the negative Soret Cotton effect of cytochrome c by replacement of the invariant phenylalanine using site-directed mutagenesis. <i>Journal of the American Chemical Society</i> , 1986 , 108, 2724-2727	16.4	87
4	Site-directed mutagenesis of cytochrome c shows that an invariant Phe is not essential for function. <i>Nature</i> , 1985 , 313, 152-4	50.4	156
3	Azo protein analogs: synthesis and characterization of arsanilazo and sulfanilazo derivatives of tyrosine and histidine. <i>Biochemistry</i> , 1984 , 23, 589-596	3.2	7

2 Preparation and characterization of sulfanilazo and arsanilazo proteins. *Biochemistry*, **1984**, 23, 596-603 3.2 8

1 Natively Disordered Proteins 275-357 54