

# Gary J Pielak

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/625736/publications.pdf>

Version: 2024-02-01

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	Protection by desiccation-tolerance proteins probed at the residue level. <i>Protein Science</i> , 2022, 31, 396-406.	3.1	14
2	A Difference between <i>In Vitro</i> and In-Cell Protein Dimer Formation. <i>Biochemistry</i> , 2022, 61, 409-412.	1.2	3
3	Macromolecular Crowding Is More than Hard-Core Repulsions. <i>Annual Review of Biophysics</i> , 2022, 51, 267-300.	4.5	51
4	Desiccation-tolerance and globular proteins adsorb similar amounts of water. <i>Protein Science</i> , 2022, 31, e4288.	3.1	2
5	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
6	<i>Danio rerio</i> Oocytes for Eukaryotic In-Cell NMR. <i>Biochemistry</i> , 2021, 60, 451-459.	1.2	11
7	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
8	Buffers, Especially the Good Kind. <i>Biochemistry</i> , 2021, 60, 3436-3440.	1.2	15
9	Water's Variable Role in Protein Stability Uncovered by Liquid-Observed Vapor Exchange NMR. <i>Biochemistry</i> , 2021, 60, 3041-3045.	1.2	11
10	Dynamical spectroscopy and microscopy of proteins in cells. <i>Current Opinion in Structural Biology</i> , 2021, 70, 1-7.	2.6	19
11	Dried Protein Structure Revealed at the Residue Level by Liquid-Observed Vapor Exchange NMR. <i>Biochemistry</i> , 2021, 60, 152-159.	1.2	13
12	Toxicity and Immunogenicity of a Tardigrade Cytosolic Abundant Heat Soluble Protein in Mice. <i>Frontiers in Pharmacology</i> , 2020, 11, 565969.	1.6	9
13	Protein's Peptide Binding Energetics under Crowded Conditions. <i>Journal of Physical Chemistry B</i> , 2020, 124, 9297-9309.	1.2	19
14	Rapid Quantification of Protein-Ligand Binding via <sup>19</sup> F NMR Lineshape Analysis. <i>Biophysical Journal</i> , 2020, 118, 2537-2548.	0.2	34
15	Rheostatic Control of Protein Expression Using Tuner Cells. <i>Biochemistry</i> , 2020, 59, 733-735.	1.2	7
16	Protecting Enzymes from Stress-Induced Inactivation. <i>Biochemistry</i> , 2019, 58, 3825-3833.	1.2	37
17	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
18	Controlling and quantifying protein concentration in <i>Escherichia coli</i> . <i>Protein Science</i> , 2019, 28, 1307-1311.	3.1	10

#	ARTICLE	IF	CITATIONS
19	Physiologically-Relevant Crowding Effects on the SH3-Son of Sevenless Interaction. <i>Biophysical Journal</i> , 2019, 116, 158a.	0.2	0
20	Jan Hermans (1933-2018): Red-blooded biophysicists study hemoglobin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 171-173.	1.5	0
21	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
22	Protecting activity of desiccated enzymes. <i>Protein Science</i> , 2019, 28, 941-951.	3.1	51
23	Chapter 12. Protein Stability and Weak Intracellular Interactions. <i>New Developments in NMR</i> , 2019, , 188-206.	0.1	6
24	Surface Charge Modulates Protein-Protein Interactions in Physiologically Relevant Environments. <i>Biochemistry</i> , 2018, 57, 1681-1684.	1.2	56
25	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
26	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
27	Crowding and Confinement Can Oppositely Affect Protein Stability. <i>ChemPhysChem</i> , 2018, 19, 3350-3355.	1.0	19
28	The Expanding Zoo of In-Cell Protein NMR. <i>Biophysical Journal</i> , 2018, 115, 1628-1629.	0.2	9
29	Osmolytes and Protein-Protein Interactions. <i>Journal of the American Chemical Society</i> , 2018, 140, 7441-7444.	6.6	61
30	Enthalpic stabilization of an SH3 domain by D <sub>2</sub> O. <i>Protein Science</i> , 2018, 27, 1710-1716.	3.1	22
31	Cosolute and Crowding Effects on a Side-By-Side Protein Dimer. <i>Biochemistry</i> , 2017, 56, 971-976.	1.2	42
32	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
33	Osmotic Shock Induced Protein Destabilization in Living Cells and Its Reversal by Glycine Betaine. <i>Journal of Molecular Biology</i> , 2017, 429, 1155-1161.	2.0	86
34	Quinary interactions with an unfolded state ensemble. <i>Protein Science</i> , 2017, 26, 1698-1703.	3.1	26
35	Cosolutes, Crowding, and Protein Folding Kinetics. <i>Journal of Physical Chemistry B</i> , 2017, 121, 6527-6537.	1.2	49
36	Glycine Betaine Reverses Osmotic Shock Induced Protein Destabilization in Living Cells. <i>Biophysical Journal</i> , 2017, 112, 57a.	0.2	1

#	ARTICLE	IF	CITATIONS
37	Tardigrades Use Intrinsically Disordered Proteins to Survive Desiccation. <i>Molecular Cell</i> , 2017, 65, 975-984.e5.	4.5	302
38	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.	3.1	111
39	Intrinsically Disordered Proteins and Desiccation Tolerance: Elucidating Functional and Mechanistic Underpinnings of Anhydrobiosis. <i>BioEssays</i> , 2017, 39, 1700119.	1.2	62
40	Large cosolutes, small cosolutes, and dihydrofolate reductase activity. <i>Protein Science</i> , 2017, 26, 2417-2425.	3.1	29
41	Macromolecular and Small Molecular Crowding Have Similar Effects on $\alpha$ -Synuclein Structure. <i>ChemPhysChem</i> , 2017, 18, 55-58.	1.0	41
42	Protein Stability in Reverse Micelles. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 3586-3589.	7.2	43
43	Electrostatic Contributions to Protein Quinary Structure. <i>Journal of the American Chemical Society</i> , 2016, 138, 13139-13142.	6.6	72
44	Protein Stability in Reverse Micelles. <i>Angewandte Chemie</i> , 2016, 128, 3650-3653.	1.6	8
45	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, 1725-1730.	3.3	147
46	Roles of structural plasticity in chaperone HdeA activity are revealed by 19F NMR. <i>Chemical Science</i> , 2016, 7, 2222-2228.	3.7	14
47	Intracellular $pH$ modulates quinary structure. <i>Protein Science</i> , 2015, 24, 1748-1755.	3.1	48
48	Emergence of life: Physical chemistry changes the paradigm. <i>Biology Direct</i> , 2015, 10, 33.	1.9	31
49	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
50	Hydrogen exchange of disordered proteins in <i>Escherichia coli</i> . <i>Protein Science</i> , 2015, 24, 706-713.	3.1	36
51	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
52	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
53	An osmolyte mitigates the destabilizing effect of protein crowding. <i>Protein Science</i> , 2014, 23, 1161-1164.	3.1	25
54	Protein Crowder Charge and Protein Stability. <i>Biochemistry</i> , 2014, 53, 1601-1606.	1.2	106

#	ARTICLE	IF	CITATIONS
55	Strategies for Protein NMR in <i>Escherichia coli</i> . <i>Biochemistry</i> , 2014, 53, 1971-1981.	1.2	24
56	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, 11335-11340.	3.3	106
57	Physicochemical Properties of Cells and Their Effects on Intrinsically Disordered Proteins (IDPs). <i>Chemical Reviews</i> , 2014, 114, 6661-6714.	23.0	391
58	Soft interactions and crowding. <i>Biophysical Reviews</i> , 2013, 5, 187-194.	1.5	205
59	The Cellular Environment Stabilizes Adenine Riboswitch RNA Structure. <i>Biochemistry</i> , 2013, 52, 8777-8785.	1.2	104
60	Amide proton exchange of a dynamic loop in cell extracts. <i>Protein Science</i> , 2013, 22, 1313-1319.	3.1	16
61	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
62	<sup>19</sup> F NMR Spectroscopy as a Probe of Cytoplasmic Viscosity and Weak Protein Interactions in Living Cells. <i>Chemistry - A European Journal</i> , 2013, 19, 12705-12710.	1.7	83
63	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
64	Unexpected Effects of Macromolecular Crowding on Protein Stability. <i>Biochemistry</i> , 2012, 51, 9773-9775.	1.2	191
65	Disordered Protein Diffusion under Crowded Conditions. <i>Journal of Physical Chemistry Letters</i> , 2012, 3, 2703-2706.	2.1	53
66	Interaction of $\alpha$ -Synuclein and a Cell Penetrating Fusion Peptide with Higher Eukaryotic Cell Membranes Assessed by <sup>19</sup> F NMR. <i>Molecular Pharmaceutics</i> , 2012, 9, 1024-1029.	2.3	20
67	Interaction of $\alpha$ -synuclein with vesicles that mimic mitochondrial membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 512-519.	1.4	85
68	Macromolecular Crowding and Protein Stability. <i>Journal of the American Chemical Society</i> , 2012, 134, 16614-16618.	6.6	289
69	In Situ Structural Characterization of a Recombinant Protein in Native <i>Escherichia coli</i> Membranes with Solid-State Magic-Angle-Spinning NMR. <i>Journal of the American Chemical Society</i> , 2011, 133, 12370-12373.	6.6	83
70	Macromolecular Crowding Fails To Fold a Globular Protein in Cells. <i>Journal of the American Chemical Society</i> , 2011, 133, 8082-8085.	6.6	132
71	Protein Crowding Tunes Protein Stability. <i>Journal of the American Chemical Society</i> , 2011, 133, 7116-7120.	6.6	255
72	An upper limit for macromolecular crowding effects. <i>BMC Biophysics</i> , 2011, 4, 13.	4.4	29

#	ARTICLE	IF	CITATIONS
73	In-cell protein NMR and protein leakage. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 347-351.	1.5	63
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	Probing the Micelle-bound Aggregation-prone State of $\alpha$ -Synuclein with <sup>19</sup> F NMR Spectroscopy. <i>ChemBioChem</i> , 2010, 11, 1993-1996.	1.3	20
76	A bioreactor for in-cell protein NMR. <i>Journal of Magnetic Resonance</i> , 2010, 202, 140-146.	1.2	56
77	<sup>19</sup> F NMR studies of $\alpha$ -synuclein-membrane interactions. <i>Protein Science</i> , 2010, 19, 1686-1691.	3.1	58
78	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
79	Effects of Proteins on Protein Diffusion. <i>Journal of the American Chemical Society</i> , 2010, 132, 9392-9397.	6.6	223
80	Volume Exclusion and Soft Interaction Effects on Protein Stability under Crowded Conditions. <i>Biochemistry</i> , 2010, 49, 6984-6991.	1.2	148
81	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
82	Using NMR-Detected Backbone Amide <sup>1</sup> H Exchange to Assess Macromolecular Crowding Effects on Globular-Protein Stability. <i>Methods in Enzymology</i> , 2009, 466, 1-18.	0.4	28
83	Protein Nuclear Magnetic Resonance under Physiological Conditions. <i>Biochemistry</i> , 2009, 48, 226-234.	1.2	75
84	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
85	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
86	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
87	Translational and Rotational Diffusion of a Small Globular Protein under Crowded Conditions. <i>Journal of Physical Chemistry B</i> , 2009, 113, 13390-13392.	1.2	82
88	<sup>19</sup> F NMR Studies of $\alpha$ -Synuclein Conformation and Fibrillation. <i>Biochemistry</i> , 2009, 48, 8578-8584.	1.2	76
89	Solvent-induced collapse of $\alpha$ -synuclein and acid-denatured cytochrome c. <i>Protein Science</i> , 2008, 10, 2195-2199.	3.1	169
90	Peroxidative aggregation of $\alpha$ -synuclein requires tyrosines. <i>Protein Science</i> , 2008, 13, 2852-2856.	3.1	20

#	ARTICLE	IF	CITATIONS
91	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, 6310-6311.	6.6	119
92	Residue-Level Interrogation of Macromolecular Crowding Effects on Protein Stability. <i>Journal of the American Chemical Society</i> , 2008, 130, 6826-6830.	6.6	88
93	$\hat{\alpha}$ -Synuclein Conformation Affects Its Tyrosine-Dependent Oxidative Aggregation. <i>Biochemistry</i> , 2008, 47, 13604-13609.	1.2	33
94	Reconsideration of sedimentation equilibrium distributions reflecting the effects of small inert cosolutes on the dimerization of $\hat{\alpha}$ -chymotrypsin. <i>Biophysical Chemistry</i> , 2007, 130, 89-92.	1.5	9
95	Temperature-induced reversible conformational change in the first 100 residues of $\hat{\alpha}$ -synuclein. <i>Protein Science</i> , 2006, 15, 602-608.	3.1	46
96	Cytosol Has a Small Effect on Protein Backbone Dynamics. <i>Biochemistry</i> , 2006, 45, 10085-10091.	1.2	12
97	Macromolecular Crowding in the Escherichia coli Periplasm Maintains $\hat{\alpha}$ -Synuclein Disorder. <i>Journal of Molecular Biology</i> , 2006, 355, 893-897.	2.0	164
98	Woes of proline: A cautionary kinetic tale. <i>Protein Science</i> , 2006, 15, 393-394.	3.1	3
99	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
100	Pressure perturbation calorimetry of helical peptides. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 63, 322-326.	1.5	11
101	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
102	Protein Dynamics in Living Cells. <i>Biochemistry</i> , 2005, 44, 9275-9279.	1.2	45
103	Impact of Protein Denaturants and Stabilizers on Water Structure. <i>Journal of the American Chemical Society</i> , 2004, 126, 1958-1961.	6.6	289
104	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
105	Stability and apoptotic activity of recombinant human cytochrome c. <i>Biochemical and Biophysical Research Communications</i> , 2003, 312, 733-740.	1.0	66
106	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
107	Crowding by Trisaccharides and the 2:1 Cytochrome c <sup>+</sup> Cytochrome c Peroxidase Complex. <i>Biochemistry</i> , 2002, 41, 547-551.	1.2	14
108	Searching for quantitative entropy-enthalpy compensation among protein variants. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 398-402.	1.5	16

#	ARTICLE	IF	CITATIONS
109	Effects of molecular crowding by saccharides on $\hat{I}$ -chymotrypsin dimerization. <i>Protein Science</i> , 2002, 11, 997-1003.	3.1	51
110	Second virial coefficients as a measure of protein-osmolyte interactions. <i>Protein Science</i> , 2001, 10, 12-16.	3.1	40
111	Characterization of Horse Cytochrome c Expressed in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2001, 22, 220-224.	0.6	47
112	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
113	Interactions between Yeast Iso-1-cytochromecand Its Peroxidaseâ€. <i>Biochemistry</i> , 2001, 40, 422-428.	1.2	22
114	Effects of Crowding by Mono-, Di-, and Tetrasaccharides on Cytochrome câ~Cytochrome c Peroxidase Binding:â€% Comparing Experiment to Theory. <i>Biochemistry</i> , 2001, 40, 281-285.	1.2	28
115	Osmolyte-induced changes in protein conformational equilibria. <i>Biopolymers</i> , 2000, 53, 293-307.	1.2	159
116	Osmolyte-induced changes in protein conformational equilibria. , 2000, 53, 293.		1
117	Osmolyte-induced changes in protein conformational equilibria. <i>Biopolymers</i> , 2000, 53, 293.	1.2	2
118	Nonideality and protein thermal denaturation. , 1999, 49, 471-479.		16
119	$1\text{H}$ and $15\text{N}$ Hyperfine Shifts of Cytochromec. <i>Journal of the American Chemical Society</i> , 1999, 121, 9247-9248.	6.6	28
120	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
121	Equilibrium Thermodynamics of a Physiologically-Relevant Hemeâ~Protein Complex. <i>Biochemistry</i> , 1999, 38, 16876-16881.	1.2	24
122	Baseline length and automated fitting of denaturation data. <i>Protein Science</i> , 1998, 7, 1262-1263.	3.1	49
123	Sugar-Induced Molten-Globule Model. <i>Biochemistry</i> , 1998, 37, 17048-17053.	1.2	81
124	Native tertiary structure in an A-state 1 1Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 275, 379-388.	2.0	77
125	Design, synthesis, expression, and characterization of the genes for mouse $\text{Fc}\hat{I}^3\text{RIIb}1$ and $\text{Fc}\hat{I}^3\text{RIIb}2$ cytoplasmic regions. <i>Protein Science</i> , 1997, 6, 1038-1046.	3.1	2
126	Identifying the Physiological Electron Transfer Site of CytochromecPeroxidase by Structure-Based Engineeringâ€. <i>Biochemistry</i> , 1996, 35, 667-673.	1.2	44



#	ARTICLE	IF	CITATIONS
127	Probing the Cytochrome Peroxidase <sup>h</sup> Cytochrome Electron Transfer Reaction Using Site Specific Cross-Linking. <i>Biochemistry</i> , 1996, 35, 4837-4845.	1.2	46
128	Changing the Transition State for Protein (Un)Folding. <i>Biochemistry</i> , 1996, 35, 7403-7411.	1.2	20
129	Control of Formation and Dissociation of the High-Affinity Complex between Cytochrome and Cytochrome Peroxidase by Ionic Strength and the Low-Affinity Binding Site. <i>Biochemistry</i> , 1996, 35, 15800-15806.	1.2	46
130	Design of a Ruthenium <sup>h</sup> Cytochrome Derivative To Measure Electron Transfer to the Radical Cation and Oxyferryl Heme in Cytochrome Peroxidase. <i>Biochemistry</i> , 1996, 35, 15107-15119.	1.2	64
131	Requirements for perpendicular helix pairing. , 1996, 26, 95-107.		4
132	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
133	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, 2466-2472.	1.6	92
134	Entropic Stabilization of Cytochrome c upon Reduction. <i>Journal of the American Chemical Society</i> , 1995, 117, 1675-1677.	6.6	72
135	Stability of yeast iso-1 <sup>h</sup> ferricytochrome c as a function of pH and temperature. <i>Protein Science</i> , 1994, 3, 1253-1260.	3.1	83
136	Polarity of disulfide bonds. <i>Protein Science</i> , 1993, 2, 1183-1184.	3.1	24
137	Amide proton exchange rates of oxidized and reduced <i>Saccharomyces cerevisiae</i> iso-1 <sup>h</sup> cytochrome c. <i>Protein Science</i> , 1993, 2, 1966-1974.	3.1	56
138	Introduction of a disulfide bond into cytochrome c stabilizes a compact denatured state. <i>Biochemistry</i> , 1992, 31, 12337-12344.	1.2	79
139	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
140	Comparison of reduced and oxidized yeast iso-1-cytochrome c using proton paramagnetic shifts. <i>Biochemistry</i> , 1991, 30, 1928-1934.	1.2	74
141	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
142	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.	1.2	81
143	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
144	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

#	ARTICLE	IF	CITATIONS
145	Elimination of the negative soer 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.	6.6	95
146	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
147	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
148	Preparation and characterization of sulfanilazo and arsanilazo proteins. <i>Biochemistry</i> , 1984, 23, 596-603.	1.2	9