

# Bruce E Bowler

## List of Publications by Year in descending order

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71  
papers

1,864  
citations

218381

26  
h-index

301761

39  
g-index

71  
all docs

71  
docs citations

71  
times ranked

960  
citing authors

#	ARTICLE	IF	CITATIONS
1	Destabilizing effects of replacing a surface lysine of cytochrome c with aromatic amino acids: implications for the denatured state. <i>Biochemistry</i> , 1993, 32, 183-190.	1.2	114
2	Structure of a mitochondrial cytochrome <i>c</i> conformer competent for peroxidase activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6648-6653.	3.3	96
3	Residual structure in unfolded proteins. <i>Current Opinion in Structural Biology</i> , 2012, 22, 4-13.	2.6	72
4	Cytochrome c folding traps are not due solely to histidine-heme ligation: direct demonstration of a role for N-terminal amino group-heme ligation 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 275, 719-724.	2.0	69
5	Thermodynamics of protein denatured states. <i>Molecular BioSystems</i> , 2007, 3, 88-99.	2.9	68
6	Denatured state thermodynamics: residual structure, chain stiffness and scaling factors 1 Edited by C. R. Matthews. <i>Journal of Molecular Biology</i> , 2001, 311, 1091-1104.	2.0	64
7	A Lysine 73 → Histidine Variant of Yeast Iso-1-cytochrome <i>c</i> : Evidence for a Native-like Intermediate in the Unfolding Pathway and Implications for m Value Effects. <i>Biochemistry</i> , 1997, 36, 119-126.	1.2	58
8	Measuring denatured state energetics: deviations from random coil behavior and implications for the folding of iso-1-cytochrome <i>c</i> 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 296, 217-228.	2.0	54
9	pH Dependence of Formation of a Partially Unfolded State of a Lys 73 → His Variant of Iso-1-cytochrome <i>c</i> : Implications for the Alkaline Conformational Transition of Cytochrome <i>c</i> . <i>Biochemistry</i> , 2000, 39, 13584-13594.	1.2	53
10	Long-Range Electron Transfer in Donor (Spacer) Acceptor Molecules and Proteins. <i>Progress in Inorganic Chemistry</i> , 0, , 259-322.	3.0	51
11	Protein dynamics and function: Making new strides with an old warhorse, the alkaline conformational transition of cytochrome <i>c</i> . <i>Coordination Chemistry Reviews</i> , 2011, 255, 664-677.	9.5	48
12	Characterization of the guanidine-hydrochloride-denatured state of iso-1-cytochrome <i>c</i> by infrared spectroscopy. <i>Biochemistry</i> , 1994, 33, 2402-2408.	1.2	45
13	Effect of pH on Formation of a Native-like Intermediate on the Unfolding Pathway of a Lys 73 → His Variant of Yeast Iso-1-cytochrome <i>c</i> . <i>Biochemistry</i> , 1999, 38, 487-495.	1.2	43
14	The Effects of Hydrophilic to Hydrophobic Surface Mutations on the Denatured State of Iso-1-cytochrome <i>c</i> : Investigation of Aliphatic Residues. <i>Biochemistry</i> , 1995, 34, 3040-3047.	1.2	37
15	Cytochrome <i>c</i> Can Form a Well-Defined Binding Pocket for Hydrocarbons. <i>Journal of the American Chemical Society</i> , 2016, 138, 16770-16778.	6.6	37
16	Evaluation of Cooperative Interactions between Substructures of Iso-1-Cytochrome <i>c</i> Using Double Mutant Cycles. <i>Biochemistry</i> , 2003, 42, 10659-10666.	1.2	36
17	Proton-Mediated Dynamics of the Alkaline Conformational Transition of Yeast Iso-1-Cytochrome <i>c</i> . <i>Journal of the American Chemical Society</i> , 2004, 126, 6751-6758.	6.6	36
18	Communication of Stabilizing Energy between Substructures of a Protein. <i>Biochemistry</i> , 2005, 44, 2349-2359.	1.2	35

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19	Kinetics of Loop Formation and Breakage in the Denatured State of Iso-1-cytochrome c. <i>Journal of Molecular Biology</i> , 2005, 353, 730-743.	2.0	35
20	Compressing the free energy range of substructure stabilities in iso-1-cytochrome c. <i>Protein Science</i> , 2009, 18, 1155-1164.	3.1	35
21	A histidine variant of yeast iso-1-cytochrome c that strongly affects the energetics of the denatured state. <i>Journal of Molecular Biology</i> , 1997, 268, 816-821.	2.0	33
22	Thermodynamics and Kinetics of Formation of the Alkaline State of a Lys 79 $\rightarrow$ Ala/Lys 73 $\rightarrow$ His Variant of Iso-1-cytochrome c. <i>Biochemistry</i> , 2005, 44, 14956-14968.	1.2	33
23	Effects of Topology and Excluded Volume on Protein Denatured State Conformational Properties. <i>Biochemistry</i> , 2002, 41, 10173-10181.	1.2	31
24	Role of Hydrogen Bond Networks and Dynamics in Positive and Negative Cooperative Stabilization of a Protein. <i>Biochemistry</i> , 2005, 44, 2900-2908.	1.2	31
25	Conformationally Gated Electron Transfer in Iso-1-cytochrome c: Engineering the Rate of a Conformational Switch. <i>Journal of the American Chemical Society</i> , 2005, 127, 9702-9703.	6.6	30
26	Effect of a K72A Mutation on the Structure, Stability, Dynamics, and Peroxidase Activity of Human Cytochrome c. <i>Biochemistry</i> , 2017, 56, 3358-3368.	1.2	29
27	Conformational Properties of the Iso-1-Cytochrome c Denatured State: Dependence on Guanidine Hydrochloride Concentration. <i>Journal of Molecular Biology</i> , 2004, 339, 185-197.	2.0	27
28	Mutation of Asparagine 52 to Glycine Promotes the Alkaline Form of Iso-1-cytochrome c and Causes Loss of Cooperativity in Acid Unfolding. <i>Biochemistry</i> , 2006, 45, 4611-4619.	1.2	26
29	Mutation of Trimethyllysine 72 to Alanine Enhances His79 $\rightarrow$ Heme-Mediated Dynamics of Iso-1-cytochrome c. <i>Biochemistry</i> , 2013, 52, 837-846.	1.2	26
30	Alkaline Conformational Transition and Gated Electron Transfer with a Lys 79 $\rightarrow$ His Variant of Iso-1-cytochrome c. <i>Biochemistry</i> , 2007, 46, 10643-10654.	1.2	25
31	Naturally Occurring A51V Variant of Human Cytochrome c Destabilizes the Native State and Enhances Peroxidase Activity. <i>Journal of Physical Chemistry B</i> , 2019, 123, 8939-8953.	1.2	25
32	Thermal denaturation of iso-1-cytochrome c variants: Comparison with solvent denaturation. <i>Protein Science</i> , 1997, 6, 657-665.	3.1	22
33	Disruption of a hydrogen bond network in human versus spider monkey cytochrome c affects heme crevice stability. <i>Journal of Inorganic Biochemistry</i> , 2016, 158, 62-69.	1.5	22
34	Probing the Bottom of a Folding Funnel Using Conformationally Gated Electron Transfer Reactions. <i>Journal of the American Chemical Society</i> , 2008, 130, 7540-7541.	6.6	21
35	Electrostatic Constituents of the Interaction of Cardiolipin with Site A of Cytochrome c. <i>Biochemistry</i> , 2018, 57, 5683-5695.	1.2	21
36	Direct Detection of Heat and Cold Denaturation for Partial Unfolding of a Protein. <i>Journal of the American Chemical Society</i> , 2001, 123, 7453-7454.	6.6	20

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37	Curvature-Dependent Binding of Cytochrome <i>c</i> to Cardiolipin. <i>Journal of the American Chemical Society</i> , 2020, 142, 19532-19539.	6.6	20
38	Manifestations of Native Topology in the Denatured State Ensemble of <i>Rhodospseudomonas palustris</i> Cytochrome <i>c</i> . <i>Biochemistry</i> , 2011, 50, 1029-1041.	1.2	19
39	Effect of pH on the Iso-1-cytochrome Denatured State: Changing Constraints Due to Heme Ligation. <i>Biochemistry</i> , 2003, 42, 2174-2184.	1.2	18
40	Probing the Dynamics of a His73 Heme Alkaline Transition in a Destabilized Variant of Yeast Iso-1-cytochrome <i>c</i> with Conformationally Gated Electron Transfer Methods. <i>Biochemistry</i> , 2011, 50, 10027-10040.	1.2	18
41	Tuning the Rate and pH Accessibility of a Conformational Electron Transfer Gate. <i>Inorganic Chemistry</i> , 2006, 45, 6338-6346.	1.9	17
42	Site A-Mediated Partial Unfolding of Cytochrome <i>c</i> on Cardiolipin Vesicles Is Species-Dependent and Does Not Require Lys72. <i>Biochemistry</i> , 2017, 56, 4830-4839.	1.2	17
43	Cardiolipin Preferentially Partitions to the Inner Leaflet of Mixed Lipid Large Unilamellar Vesicles. <i>Journal of Physical Chemistry B</i> , 2019, 123, 9111-9122.	1.2	15
44	Effect of V83G and I81A Substitutions to Human Cytochrome <i>c</i> on Acid Unfolding and Peroxidase Activity below a Neutral pH. <i>Biochemistry</i> , 2019, 58, 2921-2933.	1.2	15
45	Sequence Composition Effects on Denatured State Loop Formation in Iso-1-cytochrome <i>c</i> Variants: Polyalanine versus Polyglycine Inserts. <i>Journal of Molecular Biology</i> , 2007, 371, 577-584.	2.0	14
46	Denatured states of low-complexity polypeptide sequences differ dramatically from those of foldable sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11364-11369.	3.3	14
47	Thermodynamics of Loop Formation in the Denatured State of <i>Rhodospseudomonas palustris</i> Cytochrome <i>c</i> : Scaling Exponents and the Reconciliation Problem. <i>Journal of Molecular Biology</i> , 2009, 392, 1315-1325.	2.0	13
48	Effect of an Ala81His Mutation on the Met80 Loop Dynamics of Iso-1-cytochrome <i>c</i> . <i>Biochemistry</i> , 2015, 54, 1729-1742.	1.2	13
49	The response of $\alpha$ -loop D dynamics to truncation of trimethyllysine 72 of yeast iso-1-cytochrome <i>c</i> depends on the nature of loop deformation. <i>Journal of Biological Inorganic Chemistry</i> , 2015, 20, 805-819.	1.1	13
50	Induction of Helical Structure in a Heptapeptide with a Metal Cross-Link: Modification of the Lifson-Roig Helix-Coil Theory to Account for Covalent Cross-Links. <i>Biochemistry</i> , 2002, 41, 15826-15837.	1.2	12
51	Dynamics of the His79-Heme Alkaline Transition of Yeast Iso-1-cytochrome <i>c</i> Probed by Conformationally Gated Electron Transfer with Co(II)bis(terpyridine). <i>Journal of the American Chemical Society</i> , 2013, 135, 12772-12782.	6.6	12
52	The magnitude of changes in guanidine-HCl unfolding $m$ values in the protein, iso-1-cytochrome <i>c</i> , depends upon the substructure containing the mutation. <i>Protein Science</i> , 1998, 7, 1789-1795.	3.1	11
53	Propensities of Aromatic Amino Acids versus Leucine and Proline to Induce Residual Structure in the Denatured-State Ensemble of Iso-1-cytochrome <i>c</i> . <i>Journal of Molecular Biology</i> , 2010, 403, 495-504.	2.0	11
54	Scaling Properties of Glycine-Rich Sequences in Guanidine Hydrochloride Solutions. <i>Biophysical Journal</i> , 2012, 102, 1969-1978.	0.2	10

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55	A cytochrome <i>c</i> electron transfer switch modulated by heme ligation and isomerization of a peptidyl-prolyl bond. <i>Biopolymers</i> , 2013, 100, 114-124.	1.2	10
56	Structure and Unfolding of the Third Type III Domain from Human Fibronectin. <i>Biochemistry</i> , 2015, 54, 6724-6733.	1.2	10
57	Lower Protein Stability Does Not Necessarily Increase Local Dynamics. <i>Biochemistry</i> , 2016, 55, 2681-2693.	1.2	10
58	Importance of Contact Persistence in Denatured State Loop Formation: Kinetic Insights into Sequence Effects on Nucleation Early in Folding. <i>Journal of Molecular Biology</i> , 2009, 390, 124-134.	2.0	8
59	Rapid quantification of cardiolipin and DOPC lipid and vesicle concentration. <i>Analytical Biochemistry</i> , 2017, 520, 58-61.	1.1	8
60	Humanlike substitutions to $\alpha$ -loop D of yeast iso-1-cytochrome c only modestly affect dynamics and peroxidase activity. <i>Journal of Inorganic Biochemistry</i> , 2018, 183, 146-156.	1.5	8
61	The Human Cytochrome <i>c</i> Domain-Swapped Dimer Facilitates Tight Regulation of Intrinsic Apoptosis. <i>Biochemistry</i> , 2020, 59, 2055-2068.	1.2	6
62	Competition between Reversible Aggregation and Loop Formation in Denatured Iso-1-cytochrome <i>c</i> . <i>Biochemistry</i> , 2009, 48, 481-491.	1.2	5
63	Tryptophan Stabilizes His-Heme Loops in the Denatured State Only When It Is Near a Loop End. <i>Biochemistry</i> , 2012, 51, 3586-3595.	1.2	5
64	Probing Denatured State Conformational Bias in a Three-Helix Bundle, UBA(2), Using a Cytochrome <i>c</i> Fusion Protein. <i>Biochemistry</i> , 2018, 57, 1711-1721.	1.2	4
65	Rapid quantification of vesicle concentration for DOPG/DOPC and Cardiolipin/DOPC mixed lipid systems of variable composition. <i>Analytical Biochemistry</i> , 2018, 553, 12-14.	1.1	4
66	Denatured State Conformational Biases in Three-Helix Bundles Containing Divergent Sequences Localize near Turns and Helix Capping Residues. <i>Biochemistry</i> , 2021, 60, 3071-3085.	1.2	4
67	Conformational Properties of Polyglutamine Sequences in Guanidine Hydrochloride Solutions. <i>Biophysical Journal</i> , 2012, 103, 1989-1999.	0.2	3
68	Effect on intrinsic peroxidase activity of substituting coevolved residues from $\alpha$ -loop C of human cytochrome c into yeast iso-1-cytochrome c. <i>Journal of Inorganic Biochemistry</i> , 2022, 232, 111819.	1.5	3
69	Residual Structure in the Denatured State of the Fast-Folding UBA(1) Domain from the Human DNA Excision Repair Protein HHR23A. <i>Biochemistry</i> , 2022, , .	1.2	3
70	Effect of an Imposed Contact on Secondary Structure in the Denatured State of Yeast Iso-1-cytochrome c. <i>Biochemistry</i> , 2017, 56, 6662-6676.	1.2	2
71	Helical Propensity Affects the Conformational Properties of the Denatured State of Cytochrome <i>c</i> <sup>2</sup> . <i>Biophysical Journal</i> , 2018, 114, 311-322.	0.2	1