

David J Brockwell

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

4,119
citations

125106

35
h-index

145109

60
g-index

97
all docs

97
docs citations

97
times ranked

4404
citing authors

#	ARTICLE	IF	CITATIONS
1	High-throughput directed evolution: a golden era for protein science. Trends in Chemistry, 2022, 4, 378-391.	4.4	12
2	The effect of mutation on an aggregation-prone protein: An in vivo, in vitro, and in silico analysis. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	5
3	Dynamic interplay between the periplasmic chaperone SurA and the BAM complex in outer membrane protein folding. Communications Biology, 2022, 5, .	2.0	12
4	Tuning Protein Hydrogel Mechanics through Modulation of Nanoscale Unfolding and Entanglement in Postgelation Relaxation. ACS Nano, 2022, 16, 10667-10678.	7.3	15
5	De novo design of transmembrane β^2 barrels. Science, 2021, 371, .	6.0	83
6	The role of membrane destabilisation and protein dynamics in BAM catalysed OMP folding. Nature Communications, 2021, 12, 4174.	5.8	22
7	Control of Nanoscale <i>In Situ</i> Protein Unfolding Defines Network Architecture and Mechanics of Protein Hydrogels. ACS Nano, 2021, 15, 11296-11308.	7.3	24
8	Looking Beyond the Core: The Role of Flanking Regions in the Aggregation of Amyloidogenic Peptides and Proteins. Frontiers in Neuroscience, 2020, 14, 611285.	1.4	52
9	Single molecule protein stabilisation translates to macromolecular mechanics of a protein network. Soft Matter, 2020, 16, 6389-6399.	1.2	23
10	Reaction Rate Governs the Viscoelasticity and Nanostructure of Folded Protein Hydrogels. Biomacromolecules, 2020, 21, 4253-4260.	2.6	18
11	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. Communications Biology, 2020, 3, 766.	2.0	32
12	The uniqueness of flow in probing the aggregation behavior of clinically relevant antibodies. Engineering Reports, 2020, 2, e12147.	0.9	5
13	<code><sc>PyXlinkViewer</sc></code> : A flexible tool for visualization of protein chemical crosslinking data within the <code><sc>PyMOL</sc></code> molecular graphics system. Protein Science, 2020, 29, 1851-1857.	3.1	56
14	A short motif in the N-terminal region of β^2 -synuclein is critical for both aggregation and function. Nature Structural and Molecular Biology, 2020, 27, 249-259.	3.6	116
15	Role of the lipid bilayer in outer membrane protein folding in Gram-negative bacteria. Journal of Biological Chemistry, 2020, 295, 10340-10367.	1.6	88
16	Using protein engineering to understand and modulate aggregation. Current Opinion in Structural Biology, 2020, 60, 157-166.	2.6	27
17	Inter-domain dynamics in the chaperone SurA and multi-site binding to its outer membrane protein clients. Nature Communications, 2020, 11, 2155.	5.8	48
18	An in vivo platform to select and evolve aggregation-resistant proteins. Nature Communications, 2020, 11, 1816.	5.8	22

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19	The Role of SurA PPlase Domains in Preventing Aggregation of the Outer-Membrane Proteins tOmpA and OmpT. <i>Journal of Molecular Biology</i> , 2019, 431, 1267-1283.	2.0	22
20	A peptide- α -display protein scaffold to facilitate single molecule force studies of aggregation-prone peptides. <i>Protein Science</i> , 2018, 27, 1205-1217.	3.1	6
21	Using extensional flow to reveal diverse aggregation landscapes for three IgG1 molecules. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1216-1225.	1.7	15
22	Phosphorylation-induced unfolding regulates p19 ^{INK4d} during the human cell cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3344-3349.	3.3	28
23	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 16688-16692.	7.2	48
24	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. <i>Angewandte Chemie</i> , 2018, 130, 16930-16934.	1.6	6
25	Inducing protein aggregation by extensional flow. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4673-4678.	3.3	77
26	Gating of TonB-dependent transporters by substrate-specific forced remodelling. <i>Nature Communications</i> , 2017, 8, 14804.	5.8	64
27	Assessing the Potential of Folded Globular Polyproteins As Hydrogel Building Blocks. <i>Biomacromolecules</i> , 2017, 18, 636-646.	2.6	35
28	Effects of Periplasmic Chaperones and Membrane Thickness on BamA-Catalyzed Outer-Membrane Protein Folding. <i>Journal of Molecular Biology</i> , 2017, 429, 3776-3792.	2.0	63
29	Outer membrane protein folding from an energy landscape perspective. <i>BMC Biology</i> , 2017, 15, 123.	1.7	62
30	Skp is a multivalent chaperone of outer-membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 786-793.	3.6	82
31	Lateral opening in the intact β^2 -barrel assembly machinery captured by cryo-EM. <i>Nature Communications</i> , 2016, 7, 12865.	5.8	157
32	Differential Effects of Hydrophobic Core Packing Residues for Thermodynamic and Mechanical Stability of a Hyperthermophilic Protein. <i>Langmuir</i> , 2016, 32, 7392-7402.	1.6	24
33	Tuning protein mechanics through an ionic cluster graft from an extremophilic protein. <i>Soft Matter</i> , 2016, 12, 2688-2699.	1.2	10
34	An in vivo platform for identifying inhibitors of protein aggregation. <i>Nature Chemical Biology</i> , 2016, 12, 94-101.	3.9	75
35	Life in extreme environments: single molecule force spectroscopy as a tool to explore proteins from extremophilic organisms. <i>Biochemical Society Transactions</i> , 2015, 43, 179-185.	1.6	7
36	Optimizing the calculation of energy landscape parameters from single-molecule protein unfolding experiments. <i>Physical Review E</i> , 2015, 91, 012710.	0.8	13

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37	Extraction of Accurate Biomolecular Parameters from Single-Molecule Force Spectroscopy Experiments. <i>ACS Nano</i> , 2015, 9, 1315-1324.	7.3	14
38	Force-induced remodelling of proteins and their complexes. <i>Current Opinion in Structural Biology</i> , 2015, 30, 89-99.	2.6	42
39	The Folding of SasG: A Long and Remarkably Strong Monomeric Protein Responsible for Biofilm Formation is a Highly Cooperative System. <i>Biophysical Journal</i> , 2015, 108, 346a.	0.2	0
40	Rapid and Robust Polyprotein Production Facilitates Single-Molecule Mechanical Characterization of β -Barrel Assembly Machinery Polypeptide Transport Associated Domains. <i>ACS Nano</i> , 2015, 9, 8811-8821.	7.3	26
41	Cooperative folding of intrinsically disordered domains drives assembly of a strong elongated protein. <i>Nature Communications</i> , 2015, 6, 7271.	5.8	52
42	Mechanistic studies of the biogenesis and folding of outer membrane proteins in vitro and in vivo: What have we learned to date?. <i>Archives of Biochemistry and Biophysics</i> , 2014, 564, 265-280.	1.4	46
43	Single molecule force spectroscopy reveals the temperature-dependent robustness and malleability of a hyperthermophilic protein. <i>Soft Matter</i> , 2013, 9, 9016.	1.2	18
44	Towards design principles for determining the mechanical stability of proteins. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 15767.	1.3	57
45	Dissecting the Effects of Periplasmic Chaperones on the In Vitro Folding of the Outer Membrane Protein PagP. <i>Journal of Molecular Biology</i> , 2013, 425, 3178-3191.	2.0	45
46	Single-Molecule Force Spectroscopy Identifies a Small Cold Shock Protein as Being Mechanically Robust. <i>Journal of Physical Chemistry B</i> , 2013, 117, 1819-1826.	1.2	23
47	A Force-Activated Trip Switch Triggers Rapid Dissociation of a Colicin from Its Immunity Protein. <i>PLoS Biology</i> , 2013, 11, e1001489.	2.6	26
48	Malleability of the Folding Mechanism of the Outer Membrane Protein PagP: Parallel Pathways and the Effect of Membrane Elasticity. <i>Journal of Molecular Biology</i> , 2012, 416, 453-464.	2.0	24
49	Prying Open Single GroES Ring Complexes by Force Reveals Cooperativity across Domains. <i>Biophysical Journal</i> , 2012, 102, 1961-1968.	0.2	1
50	Mechanically Unfolding Protein L Using a Laser-Feedback-Controlled Cantilever. <i>Biophysical Journal</i> , 2011, 100, 1800-1809.	0.2	4
51	Unravelling the design principles for single protein mechanical strength. <i>Current Opinion in Structural Biology</i> , 2010, 20, 508-517.	2.6	61
52	The transition state for folding of an outer membrane protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4099-4104.	3.3	129
53	Dynamics of the Coiled-Coil Unfolding Transition of Myosin Rod Probed by Δ Dissipation Force Spectrum. <i>Biophysical Journal</i> , 2010, 99, 257-262.	0.2	18
54	Single-Molecule Studies of the Im7 Folding Landscape. <i>Journal of Molecular Biology</i> , 2010, 398, 132-145.	2.0	18

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55	Identification of a Mechanical Rheostat in the Hydrophobic Core of Protein L. <i>Journal of Molecular Biology</i> , 2009, 393, 237-248.	2.0	55
56	Tuning the Elastic Modulus of Hydrated Collagen Fibrils. <i>Biophysical Journal</i> , 2009, 97, 2985-2992.	0.2	143
57	Mechanically unfolding proteins: The effect of unfolding history and the supramolecular scaffold. <i>Protein Science</i> , 2009, 11, 2759-2765.	3.1	75
58	The Effect of Temperature on Mechanical Resistance of the Native and Intermediate States of I27. <i>Biophysical Journal</i> , 2008, 95, 5296-5305.	0.2	29
59	Internal friction of single polypeptide chains at high stretch. <i>Faraday Discussions</i> , 2008, 139, 35.	1.6	36
60	Effects of hydration on the mechanical response of individual collagen fibrils. <i>Applied Physics Letters</i> , 2008, 92, .	1.5	111
61	The Dynamical Response of Proteins Under Force. , 2008, , 205-249.		1
62	The N-terminal Helix Is a Post-assembly Clamp in the Bacterial Outer Membrane Protein PagP. <i>Journal of Molecular Biology</i> , 2007, 373, 529-540.	2.0	55
63	Probing the mechanical stability of proteins using the atomic force microscope. <i>Biochemical Society Transactions</i> , 2007, 35, 1564-1568.	1.6	30
64	The Effect of Protein Complexation on the Mechanical Stability of Im9. <i>Biophysical Journal</i> , 2007, 92, L79-L81.	0.2	31
65	Intermediates: ubiquitous species on folding energy landscapes?. <i>Current Opinion in Structural Biology</i> , 2007, 17, 30-37.	2.6	196
66	Force Denaturation of Proteins - an Unfolding Story. <i>Current Nanoscience</i> , 2007, 3, 3-15.	0.7	29
67	Mechanical Resistance of Proteins Explained Using Simple Molecular Models. <i>Biophysical Journal</i> , 2006, 90, 287-297.	0.2	106
68	Viscoelastic Study of the Mechanical Unfolding of a Protein by AFM. <i>Biophysical Journal</i> , 2006, 91, L16-L18.	0.2	49
69	Urea-Induced Unfolding of the Immunity Protein Im9 Monitored by spFRET. <i>Biophysical Journal</i> , 2006, 91, L42-L44.	0.2	50
70	Prediction of the Translocation Kinetics of a Protein from Its Mechanical Properties. <i>Biophysical Journal</i> , 2006, 91, L51-L53.	0.2	34
71	Mechanically Unfolding the Small, Topologically Simple Protein L. <i>Biophysical Journal</i> , 2005, 89, 506-519.	0.2	154
72	Force mode atomic force microscopy as a tool for protein folding studies. <i>Analytica Chimica Acta</i> , 2003, 479, 87-105.	2.6	120

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73	Improved methods of cultivation and production of deuteriated proteins from E. coli strains grown on fully deuteriated minimal medium. <i>Journal of Applied Microbiology</i> , 2003, 94, 580-586.	1.4	39
74	Pulling geometry defines the mechanical resistance of a β -sheet protein. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 731-737.	3.6	356
75	Unfolding dynamics of proteins under applied force. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2003, 361, 713-730.	1.6	25
76	The Effect of Core Destabilization on the Mechanical Resistance of I27. <i>Biophysical Journal</i> , 2002, 83, 458-472.	0.2	132
77	Physicochemical consequences of the perdeuteration of glutathione S-transferase from <i>S. japonicum</i> . <i>Protein Science</i> , 2001, 10, 572-580.	3.1	31
78	Accurate Use of Single Molecule Fluorescence Correlation Spectroscopy to Determine Molecular Diffusion Times. <i>Single Molecules</i> , 2001, 2, 177-181.	1.7	31
79	Towards single molecule unfolding of proteins using AFM and its observation using fluorescence. <i>Biochemical Society Transactions</i> , 2000, 28, A69-A69.	1.6	0
80	Protein folding mechanisms: new methods and emerging ideas. <i>Current Opinion in Structural Biology</i> , 2000, 10, 16-25.	2.6	125
81	The X-ray crystal structures of perdeuteriated and protiated enzyme elongation factor Tu are very similar. <i>Chemical Communications</i> , 1998, , 1063-1064.	2.2	8
82	77 Structural investigations of kirromycin bound to bacterial elongation factor Tu by NMR and molecular dynamics. <i>Biochemical Society Transactions</i> , 1997, 25, S612-S612.	1.6	1