

James C A Bardwell

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

2,108
citations

279798

23
h-index

243625

44
g-index

54
all docs

54
docs citations

54
times ranked

2712
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>SERF</scp>, a family of tiny highly conserved, highly charged proteins with enigmatic functions. FEBS Journal, 2023, 290, 4150-4162.	4.7	6
2	Microreactor equipped with naturally acid-resistant histidine ammonia lyase from an extremophile. Materials Advances, 2022, 3, 3649-3662.	5.4	1
3	ATP-Independent Chaperones. Annual Review of Biophysics, 2022, 51, 409-429.	10.0	16
4	Trigger factor both holds and folds its client proteins. Nature Communications, 2022, 13, .	12.8	8
5	Mechanism of the small ATP-independent chaperone Spy is substrate specific. Nature Communications, 2021, 12, 851.	12.8	20
6	A cytochrome c is the natural electron acceptor for nicotine oxidoreductase. Nature Chemical Biology, 2021, 17, 344-350.	8.0	11
7	Polyphosphate drives bacterial heterochromatin formation. Science Advances, 2021, 7, eabk0233.	10.3	27
8	A metabolite binding protein moonlights as a bile-responsive chaperone. EMBO Journal, 2020, 39, e104231.	7.8	6
9	Yeast Tripartite Biosensors Sensitive to Protein Stability and Aggregation Propensity. ACS Chemical Biology, 2020, 15, 1078-1088.	3.4	4
10	Chaperone OsmY facilitates the biogenesis of a major family of autotransporters. Molecular Microbiology, 2019, 112, 1373-1387.	2.5	16
11	Protein folding while chaperone bound is dependent on weak interactions. Nature Communications, 2019, 10, 4833.	12.8	28
12	SERF engages in a fuzzy complex that accelerates primary nucleation of amyloid proteins. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23040-23049.	7.1	25
13	Identifying dynamic, partially occupied residues using anomalous scattering. Acta Crystallographica Section D: Structural Biology, 2019, 75, 1084-1095.	2.3	5
14	Folding against the wind. Nature Chemical Biology, 2018, 14, 329-330.	8.0	1
15	Selecting Conformational Ensembles Using Residual Electron and Anomalous Density (READ). Methods in Molecular Biology, 2018, 1764, 491-504.	0.9	5
16	Directed evolution to improve protein folding in vivo. Current Opinion in Structural Biology, 2018, 48, 117-123.	5.7	32
17	Folding while bound to chaperones. Current Opinion in Structural Biology, 2018, 48, 1-5.	5.7	42
18	Reply to "Misreading chaperone" substrate complexes from random noise™. Nature Structural and Molecular Biology, 2018, 25, 990-991.	8.2	2

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19	In vivo chloride concentrations surge to proteotoxic levels during acid stress. <i>Nature Chemical Biology</i> , 2018, 14, 1051-1058.	8.0	16
20	Periplasmic Chaperones and Prolyl Isomerases. <i>EcoSal Plus</i> , 2018, 8, .	5.4	29
21	Elaborating a coiled-coil-assembled octahedral protein cage with additional protein domains. <i>Protein Science</i> , 2018, 27, 1893-1900.	7.6	13
22	Electrostatic interactions are important for chaperone-client interaction in vivo. <i>Microbiology (United Kingdom)</i> , 2018, 164, 992-997.	1.8	11
23	Evaluation of de novo-designed coiled coils as off-the-shelf components for protein assembly. <i>Molecular Systems Design and Engineering</i> , 2017, 2, 140-148.	3.4	22
24	Symmetry-Directed Self-Assembly of a Tetrahedral Protein Cage Mediated by de Novo-Designed Coiled Coils. <i>ChemBioChem</i> , 2017, 18, 1888-1892.	2.6	42
25	Capturing a Dynamic Chaperone-Substrate Interaction Using NMR-Informed Molecular Modeling. <i>Journal of the American Chemical Society</i> , 2016, 138, 9826-9839.	13.7	25
26	Flexible, symmetry-directed approach to assembling protein cages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8681-8686.	7.1	91
27	Determining crystal structures through crowdsourcing and coursework. <i>Nature Communications</i> , 2016, 7, 12549.	12.8	47
28	RNAs as chaperones. <i>RNA Biology</i> , 2016, 13, 1228-1231.	3.1	35
29	Detection of the pH-dependent Activity of <i>Escherichia coli</i> Chaperone HdeB <i>In Vitro</i> and <i>In Vivo</i> . <i>Journal of Visualized Experiments</i> , 2016, , .	0.3	0
30	Forces Driving Chaperone Action. <i>Cell</i> , 2016, 166, 369-379.	28.9	89
31	Visualizing chaperone-assisted protein folding. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 691-697.	8.2	52
32	Protein unfolding as a switch from self-recognition to high-affinity client binding. <i>Nature Communications</i> , 2016, 7, 10357.	12.8	48
33	Substrate protein folds while it is bound to the ATP-independent chaperone Spy. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 53-58.	8.2	68
34	Folding Optimization In Vivo Uncovers New Chaperones. <i>Journal of Molecular Biology</i> , 2015, 427, 2983-2994.	4.2	26
35	Converting a Sulfenic Acid Reductase into a Disulfide Bond Isomerase. <i>Antioxidants and Redox Signaling</i> , 2015, 23, 945-957.	5.4	4
36	Polyphosphate Is a Primordial Chaperone. <i>Molecular Cell</i> , 2014, 53, 689-699.	9.7	291

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37	Cytosolic Selection Systems To Study Protein Stability. <i>Journal of Bacteriology</i> , 2014, 196, 4333-4343.	2.2	11
38	Isolation of Bacteria Envelope Proteins. <i>Methods in Molecular Biology</i> , 2013, 966, 359-366.	0.9	77
39	Conditional disorder in chaperone action. <i>Trends in Biochemical Sciences</i> , 2012, 37, 517-525.	7.5	122
40	Genetic Selection for Enhanced Folding <i>In Vivo</i> Targets the Cys14-Cys38 Disulfide Bond in Bovine Pancreatic Trypsin Inhibitor. <i>Antioxidants and Redox Signaling</i> , 2011, 14, 973-984.	5.4	6
41	Genetic selection designed to stabilize proteins uncovers a chaperone called Spy. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 262-269.	8.2	138
42	<i>E. coli</i> chaperones DnaK, Hsp33 and Spy inhibit bacterial functional amyloid assembly. <i>Prion</i> , 2011, 5, 323-334.	1.8	31
43	Engineered Pathways for Correct Disulfide Bond Oxidation. <i>Antioxidants and Redox Signaling</i> , 2011, 14, 2399-2412.	5.4	18
44	<i>E. coli</i> chaperones DnaK, Hsp33 and Spy inhibit bacterial functional amyloid assembly. <i>Prion</i> , 2011, 5, 323-334.	1.8	18
45	Protein refolding by pH-triggered chaperone binding and release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1071-1076.	7.1	89
46	Optimizing Protein Stability <i>In Vivo</i> . <i>Molecular Cell</i> , 2009, 36, 861-871.	9.7	147
47	The origami of thioredoxin-like folds. <i>Protein Science</i> , 2006, 15, 2217-2227.	7.6	93
48	The crystal structure of TrxA(CACA): Insights into the formation of a [2Fe-2S] iron-sulfur cluster in an <i>Escherichia coli</i> thioredoxin mutant. <i>Protein Science</i> , 2005, 14, 1863-1869.	7.6	21
49	Disulfides out of thin air. <i>Nature Structural Biology</i> , 2002, 9, 2-3.	9.7	6
50	The uncharged surface features surrounding the active site of <i>Escherichia coli</i> DsbA are conserved and are implicated in peptide binding. <i>Protein Science</i> , 1997, 6, 1148-1156.	7.6	78
51	Structural analysis of three His32 mutants of DsbA: Support for an electrostatic role of His32 in DsbA stability. <i>Protein Science</i> , 1997, 6, 1893-1900.	7.6	82