

Karen G Fleming

List of Publications by Year in descending order

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77
papers

4,663
citations

81743

39
h-index

106150

65
g-index

86
all docs

86
docs citations

86
times ranked

4286
citing authors

#	ARTICLE	IF	CITATIONS
1	Local Bilayer Hydrophobicity Modulates Membrane Protein Stability. <i>Journal of the American Chemical Society</i> , 2021, 143, 764-772.	6.6	21
2	De novo design of transmembrane β^2 barrels. <i>Science</i> , 2021, 371, .	6.0	83
3	Membrane proteins enter the fold. <i>Current Opinion in Structural Biology</i> , 2021, 69, 124-130.	2.6	8
4	Domain interactions determine the conformational ensemble of the periplasmic chaperone SurA. <i>Protein Science</i> , 2020, 29, 2043-2053.	3.1	11
5	SurA is a cryptically grooved chaperone that expands unfolded outer membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28026-28035.	3.3	25
6	Backbone Hydrogen Bond Energies in Membrane Proteins Are Insensitive to Large Changes in Local Water Concentration. <i>Journal of the American Chemical Society</i> , 2020, 142, 6227-6235.	6.6	9
7	Protein Structure Prediction and Design in a Biologically Realistic Implicit Membrane. <i>Biophysical Journal</i> , 2020, 118, 2042-2055.	0.2	59
8	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. <i>Angewandte Chemie</i> , 2020, 132, 11201-11207.	1.6	3
9	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 11108-11114.	7.2	21
10	Determining the Free Energies of Outer Membrane Proteins in Lipid Bilayers. <i>Methods in Molecular Biology</i> , 2020, 2168, 217-232.	0.4	1
11	Plasticity and transient binding are key ingredients of the periplasmic chaperone network. <i>Protein Science</i> , 2019, 28, 1340-1349.	3.1	11
12	A Thermodynamically-Rigorous, Biologically-Driven Energy Function for Membrane Protein Modeling and Design. <i>Biophysical Journal</i> , 2019, 116, 58a.	0.2	0
13	HullRad: Fast Calculations of Folded and Disordered Protein and Nucleic Acid Hydrodynamic Properties. <i>Biophysical Journal</i> , 2018, 114, 856-869.	0.2	130
14	Taking deterministic control of membrane protein monomer-dimer measurements. <i>Journal of General Physiology</i> , 2018, 150, 181-183.	0.9	0
15	Building Blocks of the Outer Membrane: Calculating a General Elastic Energy Model for β^2 -Barrel Membrane Proteins. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 4487-4497.	2.3	22
16	Genetically encoded biosensors for visualizing live-cell biochemical activity at super-resolution. <i>Nature Methods</i> , 2017, 14, 427-434.	9.0	138
17	Novel Kinetic Intermediates Populated along the Folding Pathway of the Transmembrane β^2 -Barrel OmpA. <i>Biochemistry</i> , 2017, 56, 47-60.	1.2	30
18	Selective pressure for rapid membrane integration constrains the sequence of bacterial outer membrane proteins. <i>Molecular Microbiology</i> , 2017, 106, 777-792.	1.2	16

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19	Influence of Protein Scaffold on Side-Chain Transfer Free Energies. <i>Biophysical Journal</i> , 2017, 113, 597-604.	0.2	26
20	Periplasmic Chaperones Play Hot Potato With Unfolded Outer Membrane Proteins. <i>FASEB Journal</i> , 2017, 31, 604.8.	0.2	1
21	Negative Charge Neutralization in the Loops and Turns of Outer Membrane Phospholipase A Impacts Folding Hysteresis at Neutral pH. <i>Biochemistry</i> , 2016, 55, 6133-6137.	1.2	5
22	Dynamic periplasmic chaperone reservoir facilitates biogenesis of outer membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4794-800.	3.3	45
23	From Chaperones to the Membrane with a BAM!. <i>Trends in Biochemical Sciences</i> , 2016, 41, 872-882.	3.7	72
24	BamA POTRA Domain Interacts with a Native Lipid Membrane Surface. <i>Biophysical Journal</i> , 2016, 110, 2698-2709.	0.2	65
25	Aromatic Side Chain Water-to-Lipid Transfer Free Energies Show a Depth Dependence across the Membrane Normal. <i>Journal of the American Chemical Society</i> , 2016, 138, 7946-7950.	6.6	44
26	Deuterium Labeling Together with Contrast Variation Small-Angle Neutron Scattering Suggests How Skp Captures and Releases Unfolded Outer Membrane Proteins. <i>Methods in Enzymology</i> , 2016, 566, 159-210.	0.4	46
27	Applications of Analytical Ultracentrifugation to Membrane Proteins. , 2016, , 311-327.		1
28	Aqueous, Unfolded OmpA Forms Amyloid-Like Fibrils upon Self-Association. <i>PLoS ONE</i> , 2015, 10, e0132301.	1.1	32
29	Membrane Defects Accelerate Outer Membrane β -Barrel Protein Folding. <i>Biochemistry</i> , 2015, 54, 97-99.	1.2	53
30	BamA Alone Accelerates Outer Membrane Protein Folding In Vitro through a Catalytic Mechanism. <i>Biochemistry</i> , 2015, 54, 6009-6011.	1.2	32
31	A combined kinetic push and thermodynamic pull as driving forces for outer membrane protein sorting and folding in bacteria. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20150026.	1.8	42
32	The Role of a Destabilized Membrane for OMP Insertion. <i>Methods in Molecular Biology</i> , 2015, 1329, 57-65.	0.4	3
33	Skp Trimer Formation Is Insensitive to Salts in the Physiological Range. <i>Biochemistry</i> , 2015, 54, 7059-7062.	1.2	20
34	Outer membrane β -barrel protein folding is physically controlled by periplasmic lipid head groups and BamA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5878-5883.	3.3	164
35	Energetics of Membrane Protein Folding. <i>Annual Review of Biophysics</i> , 2014, 43, 233-255.	4.5	66
36	E.Âcoli Outer Membrane and Interactions with OmpLA. <i>Biophysical Journal</i> , 2014, 106, 2493-2502.	0.2	128

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37	Membrane protein thermodynamic stability may serve as the energy sink for sorting in the periplasm. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4285-4290.	3.3	104
38	Induced fit on heme binding to the <i>Pseudomonas aeruginosa</i> cytoplasmic protein (PhuS) drives interaction with heme oxygenase (HemO). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5639-5644.	3.3	46
39	Outer membrane phospholipase A in phospholipid bilayers: A model system for concerted computational and experimental investigations of amino acid side chain partitioning into lipid bilayers. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 126-134.	1.4	39
40	A Designed Point Mutant in Fis1 Disrupts Dimerization and Mitochondrial Fission. Journal of Molecular Biology, 2012, 423, 143-158.	2.0	13
41	Overcoming Hysteresis to Attain Reversible Equilibrium Folding for Outer Membrane Phospholipase A in Phospholipid Bilayers. Journal of Molecular Biology, 2011, 413, 484-494.	2.0	49
42	The soluble, periplasmic domain of OmpA folds as an independent unit and displays chaperone activity by reducing the self-association propensity of the unfolded OmpA transmembrane β^2 -barrel. Biophysical Chemistry, 2011, 159, 194-204.	1.5	49
43	Using Tryptophan Fluorescence to Measure the Stability of Membrane Proteins Folded in Liposomes. Methods in Enzymology, 2011, 492, 189-211.	0.4	70
44	Side-chain hydrophobicity scale derived from transmembrane protein folding into lipid bilayers. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10174-10177.	3.3	272
45	Self-Association of Unfolded Outer Membrane Proteins. Macromolecular Bioscience, 2010, 10, 763-767.	2.1	39
46	Structure of the lethal phage pinhole. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18966-18971.	3.3	74
47	Association energetics of membrane spanning β -helices. Current Opinion in Structural Biology, 2008, 18, 412-419.	2.6	79
48	Determination of Membrane Protein Molecular Weight Using Sedimentation Equilibrium Analytical Ultracentrifugation. Current Protocols in Protein Science, 2008, 53, Unit 7.12.1-7.12.13.	2.8	20
49	The process of folding proteins into membranes: Challenges and progress. Archives of Biochemistry and Biophysics, 2008, 469, 46-66.	1.4	84
50	Outer Membrane Phospholipase A Dimer Stability Does Not Correlate to Occluded Surface Area. Biochemistry, 2008, 47, 12095-12103.	1.2	4
51	β^2 -Barrel Proteins That Reside in the Escherichia coli Outer Membrane in Vivo Demonstrate Varied Folding Behavior in Vitro. Journal of Biological Chemistry, 2008, 283, 26748-26758.	1.6	209
52	Determination of Membrane Protein Molecular Weights and Association Equilibrium Constants Using Sedimentation Equilibrium and Sedimentation Velocity. Methods in Cell Biology, 2008, 84, 181-211.	0.5	24
53	Lipid Chain Selectivity by Outer Membrane Phospholipase A. Journal of Molecular Biology, 2007, 366, 461-468.	2.0	15
54	Dimerization of the Erythropoietin Receptor Transmembrane Domain in Micelles. Journal of Molecular Biology, 2007, 366, 517-524.	2.0	44

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55	The Role of a Hydrogen Bonding Network in the Transmembrane \hat{I}^2 -Barrel OMPLA. <i>Journal of Molecular Biology</i> , 2007, 370, 912-924.	2.0	32
56	Changes in Apparent Free Energy of Helix-Helix Dimerization in a Biological Membrane Due to Point Mutations. <i>Journal of Molecular Biology</i> , 2007, 371, 422-434.	2.0	70
57	Alternate Interfaces May Mediate Homomeric and Heteromeric Assembly in the Transmembrane Domains of SNARE Proteins. <i>Journal of Molecular Biology</i> , 2006, 357, 184-194.	2.0	26
58	Energetics of Outer Membrane Phospholipase A (OMPLA) Dimerization. <i>Journal of Molecular Biology</i> , 2006, 358, 120-131.	2.0	30
59	The Transmembrane Domains of ErbB Receptors do not Dimerize Strongly in Micelles. <i>Journal of Molecular Biology</i> , 2005, 347, 759-772.	2.0	57
60	The GxxxG-Containing Transmembrane Domain of the CCK4 Oncogene Does Not Encode Preferential Self-Interactions. <i>Biochemistry</i> , 2005, 44, 1464-1470.	1.2	36
61	Thermodynamics of glycoporphin A transmembrane helix dimerization in C14 betaine micelles. <i>Biophysical Chemistry</i> , 2004, 108, 43-49.	1.5	47
62	Sequence Context Modulates the Stability of a GxxxG-mediated Transmembrane Helix-Helix Dimer. <i>Journal of Molecular Biology</i> , 2004, 341, 991-998.	2.0	100
63	Binding of Polyubiquitin Chains to Ubiquitin-associated (UBA) Domains of HHR23A. <i>Journal of Molecular Biology</i> , 2004, 341, 1367-1379.	2.0	148
64	Complex Interactions at the Helix-Helix Interface Stabilize the Glycophorin A Transmembrane Dimer. <i>Journal of Molecular Biology</i> , 2004, 343, 1487-1497.	2.0	102
65	Standardizing the Free Energy Change of Transmembrane Helix-Helix Interactions. <i>Journal of Molecular Biology</i> , 2002, 323, 563-571.	2.0	125
66	Quaternary and Domain Structure of Glycoprotein Processing Glucosidase II. <i>Biochemistry</i> , 2001, 40, 10717-10722.	1.2	82
67	Computation and mutagenesis suggest a right-handed structure for the synaptobrevin transmembrane dimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 313-317.	1.5	52
68	Human 5-Aminoimidazole-4-carboxamide Ribonucleotide Transformylase/Inosine 5'-Monophosphate Cyclohydrolase. <i>Journal of Biological Chemistry</i> , 2001, 276, 7727-7733.	1.6	34
69	Specificity in transmembrane helix-helix interactions can define a hierarchy of stability for sequence variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 14340-14344.	3.3	172
70	Probing stability of helical transmembrane proteins. <i>Methods in Enzymology</i> , 2000, 323, 63-77.	0.4	22
71	Oligomerization of a MutS Mismatch Repair Protein from <i>Thermus aquaticus</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 23673-23678.	1.6	51
72	Visual Arrestin Activity May Be Regulated by Self-association. <i>Journal of Biological Chemistry</i> , 1999, 274, 21186-21190.	1.6	68

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73	The effects of salt on the TATA binding protein-DNA interaction from a hyperthermophilic archaeon 1 Edited by I. Tinoco. Journal of Molecular Biology, 1998, 279, 117-125.	2.0	119
74	A Revised Model for the Oligomeric State of the N-Ethylmaleimide-sensitive Fusion Protein, NSF. Journal of Biological Chemistry, 1998, 273, 15675-15681.	1.6	85
75	The effect of point mutations on the free energy of transmembrane α -helix dimerization. Journal of Molecular Biology, 1997, 272, 266-275.	2.0	237
76	A Zinc-binding Domain Involved in the Dimerization of RAG1. Journal of Molecular Biology, 1996, 260, 70-84.	2.0	104
77	What makes a protein a protein? Hydrophobic core designs that specify stability and structural properties. Protein Science, 1996, 5, 1584-1593.	3.1	189