

# 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	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
2	The effect of point mutations on the free energy of transmembrane $\alpha$ -helix dimerization. Journal of Molecular Biology, 1997, 272, 266-275.	2.0	237
3	$\beta$ -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
4	What makes a protein a protein? Hydrophobic core designs that specify stability and structural properties. Protein Science, 1996, 5, 1584-1593.	3.1	189
5	Specificity in transmembrane helix-helix interactions can define a hierarchy of stability for sequence variants. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 14340-14344.	3.3	172
6	Outer membrane $\beta$ -barrel protein folding is physically controlled by periplasmic lipid head groups and BamA. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5878-5883.	3.3	164
7	Binding of Polyubiquitin Chains to Ubiquitin-associated (UBA) Domains of HHR23A. Journal of Molecular Biology, 2004, 341, 1367-1379.	2.0	148
8	Genetically encoded biosensors for visualizing live-cell biochemical activity at super-resolution. Nature Methods, 2017, 14, 427-434.	9.0	138
9	HullRad: Fast Calculations of Folded and Disordered Protein and Nucleic Acid Hydrodynamic Properties. Biophysical Journal, 2018, 114, 856-869.	0.2	130
10	E. coli Outer Membrane and Interactions with OmpLA. Biophysical Journal, 2014, 106, 2493-2502.	0.2	128
11	Standardizing the Free Energy Change of Transmembrane Helix-Helix Interactions. Journal of Molecular Biology, 2002, 323, 563-571.	2.0	125
12	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
13	A Zinc-binding Domain Involved in the Dimerization of RAG1. Journal of Molecular Biology, 1996, 260, 70-84.	2.0	104
14	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
15	Complex Interactions at the Helix-Helix Interface Stabilize the Glycophorin A Transmembrane Dimer. Journal of Molecular Biology, 2004, 343, 1487-1497.	2.0	102
16	Sequence Context Modulates the Stability of a GxxxG-mediated Transmembrane Helix-Helix Dimer. Journal of Molecular Biology, 2004, 341, 991-998.	2.0	100
17	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
18	The process of folding proteins into membranes: Challenges and progress. Archives of Biochemistry and Biophysics, 2008, 469, 46-66.	1.4	84

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19	De novo design of transmembrane $\beta^2$ barrels. <i>Science</i> , 2021, 371, .	6.0	83
20	Quaternary and Domain Structure of Glycoprotein Processing Glucosidase II. <i>Biochemistry</i> , 2001, 40, 10717-10722.	1.2	82
21	Association energetics of membrane spanning $\beta$ -helices. <i>Current Opinion in Structural Biology</i> , 2008, 18, 412-419.	2.6	79
22	Structure of the lethal phage pinhole. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18966-18971.	3.3	74
23	From Chaperones to the Membrane with a BAM!. <i>Trends in Biochemical Sciences</i> , 2016, 41, 872-882.	3.7	72
24	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
25	Using Tryptophan Fluorescence to Measure the Stability of Membrane Proteins Folded in Liposomes. <i>Methods in Enzymology</i> , 2011, 492, 189-211.	0.4	70
26	Visual Arrestin Activity May Be Regulated by Self-association. <i>Journal of Biological Chemistry</i> , 1999, 274, 21186-21190.	1.6	68
27	Energetics of Membrane Protein Folding. <i>Annual Review of Biophysics</i> , 2014, 43, 233-255.	4.5	66
28	BamA POTRA Domain Interacts with a Native Lipid Membrane Surface. <i>Biophysical Journal</i> , 2016, 110, 2698-2709.	0.2	65
29	Protein Structure Prediction and Design in a Biologically Realistic Implicit Membrane. <i>Biophysical Journal</i> , 2020, 118, 2042-2055.	0.2	59
30	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
31	Membrane Defects Accelerate Outer Membrane $\beta^2$ -Barrel Protein Folding. <i>Biochemistry</i> , 2015, 54, 97-99.	1.2	53
32	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
33	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
34	Overcoming Hysteresis to Attain Reversible Equilibrium Folding for Outer Membrane Phospholipase A in Phospholipid Bilayers. <i>Journal of Molecular Biology</i> , 2011, 413, 484-494.	2.0	49
35	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 $\beta^2$ -barrel. <i>Biophysical Chemistry</i> , 2011, 159, 194-204.	1.5	49
36	Thermodynamics of glycophorin A transmembrane helix dimerization in C14 betaine micelles. <i>Biophysical Chemistry</i> , 2004, 108, 43-49.	1.5	47

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37	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
38	Deuterium Labeling Together with Contrast Variation Small-Angle Neutron Scattering Suggests How Skp Captures and Releases Unfolded Outer Membrane Proteins. Methods in Enzymology, 2016, 566, 159-210.	0.4	46
39	Dynamic periplasmic chaperone reservoir facilitates biogenesis of outer membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4794-800.	3.3	45
40	Dimerization of the Erythropoietin Receptor Transmembrane Domain in Micelles. Journal of Molecular Biology, 2007, 366, 517-524.	2.0	44
41	Aromatic Side Chain Water-to-Lipid Transfer Free Energies Show a Depth Dependence across the Membrane Normal. Journal of the American Chemical Society, 2016, 138, 7946-7950.	6.6	44
42	A combined kinetic push and thermodynamic pull as driving forces for outer membrane protein sorting and folding in bacteria. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20150026.	1.8	42
43	Self-Association of Unfolded Outer Membrane Proteins. Macromolecular Bioscience, 2010, 10, 763-767.	2.1	39
44	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
45	The GxxxG-Containing Transmembrane Domain of the CCK4 Oncogene Does Not Encode Preferential Self-Interactions. Biochemistry, 2005, 44, 1464-1470.	1.2	36
46	Human 5-Aminoimidazole-4-carboxamide Ribonucleotide Transformylase/Inosine 5'-Monophosphate Cyclohydrolase. Journal of Biological Chemistry, 2001, 276, 7727-7733.	1.6	34
47	The Role of a Hydrogen Bonding Network in the Transmembrane $\beta$ -Barrel OMPLA. Journal of Molecular Biology, 2007, 370, 912-924.	2.0	32
48	Aqueous, Unfolded OmpA Forms Amyloid-Like Fibrils upon Self-Association. PLoS ONE, 2015, 10, e0132301.	1.1	32
49	BamA Alone Accelerates Outer Membrane Protein Folding In Vitro through a Catalytic Mechanism. Biochemistry, 2015, 54, 6009-6011.	1.2	32
50	Energetics of Outer Membrane Phospholipase A (OMPLA) Dimerization. Journal of Molecular Biology, 2006, 358, 120-131.	2.0	30
51	Novel Kinetic Intermediates Populated along the Folding Pathway of the Transmembrane $\beta$ -Barrel OmpA. Biochemistry, 2017, 56, 47-60.	1.2	30
52	Alternate Interfaces May Mediate Homomeric and Heteromeric Assembly in the Transmembrane Domains of SNARE Proteins. Journal of Molecular Biology, 2006, 357, 184-194.	2.0	26
53	Influence of Protein Scaffold on Side-Chain Transfer Free Energies. Biophysical Journal, 2017, 113, 597-604.	0.2	26
54	SurA is a cryptically grooved chaperone that expands unfolded outer membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28026-28035.	3.3	25

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55	Determination of Membrane Protein Molecular Weights and Association Equilibrium Constants Using Sedimentation Equilibrium and Sedimentation Velocity. <i>Methods in Cell Biology</i> , 2008, 84, 181-211.	0.5	24
56	Probing stability of helical transmembrane proteins. <i>Methods in Enzymology</i> , 2000, 323, 63-77.	0.4	22
57	Building Blocks of the Outer Membrane: Calculating a General Elastic Energy Model for $\beta$ -Barrel Membrane Proteins. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 4487-4497.	2.3	22
58	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 11108-11114.	7.2	21
59	Local Bilayer Hydrophobicity Modulates Membrane Protein Stability. <i>Journal of the American Chemical Society</i> , 2021, 143, 764-772.	6.6	21
60	Determination of Membrane Protein Molecular Weight Using Sedimentation Equilibrium Analytical Ultracentrifugation. <i>Current Protocols in Protein Science</i> , 2008, 53, Unit 7.12.1-7.12.13.	2.8	20
61	Skp Trimer Formation Is Insensitive to Salts in the Physiological Range. <i>Biochemistry</i> , 2015, 54, 7059-7062.	1.2	20
62	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
63	Lipid Chain Selectivity by Outer Membrane Phospholipase A. <i>Journal of Molecular Biology</i> , 2007, 366, 461-468.	2.0	15
64	A Designed Point Mutant in Fis1 Disrupts Dimerization and Mitochondrial Fission. <i>Journal of Molecular Biology</i> , 2012, 423, 143-158.	2.0	13
65	Plasticity and transient binding are key ingredients of the periplasmic chaperone network. <i>Protein Science</i> , 2019, 28, 1340-1349.	3.1	11
66	Domain interactions determine the conformational ensemble of the periplasmic chaperone SurA. <i>Protein Science</i> , 2020, 29, 2043-2053.	3.1	11
67	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
68	Membrane proteins enter the fold. <i>Current Opinion in Structural Biology</i> , 2021, 69, 124-130.	2.6	8
69	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
70	Outer Membrane Phospholipase A Dimer Stability Does Not Correlate to Occluded Surface Area. <i>Biochemistry</i> , 2008, 47, 12095-12103.	1.2	4
71	The Role of a Destabilized Membrane for OMP Insertion. <i>Methods in Molecular Biology</i> , 2015, 1329, 57-65.	0.4	3
72	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. <i>Angewandte Chemie</i> , 2020, 132, 11201-11207.	1.6	3

#	ARTICLE	IF	CITATIONS
73	Applications of Analytical Ultracentrifugation to Membrane Proteins. , 2016, , 311-327.		1
74	Periplasmic Chaperones Play Hot Potato With Unfolded Outer Membrane Proteins. FASEB Journal, 2017, 31, 604.8.	0.2	1
75	Determining the Free Energies of Outer Membrane Proteins in Lipid Bilayers. Methods in Molecular Biology, 2020, 2168, 217-232.	0.4	1
76	Taking deterministic control of membrane protein monomerâ€“dimer measurements. Journal of General Physiology, 2018, 150, 181-183.	0.9	0
77	A Thermodynamically-Rigorous, Biologically-Driven Energy Function for Membrane Protein Modeling and Design. Biophysical Journal, 2019, 116, 58a.	0.2	0