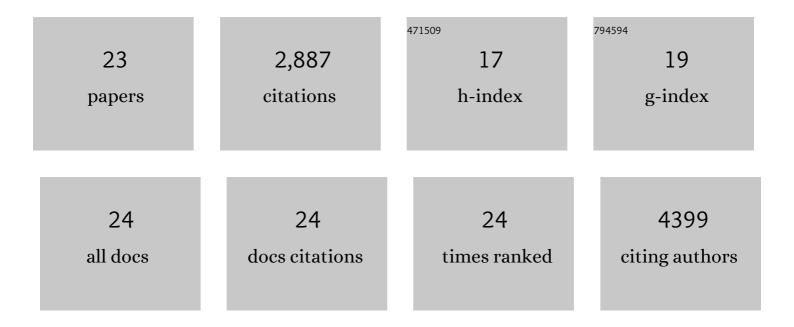
## Elizabeth H Kellogg

List of Publications by Year in descending order

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FUZABETH H KELLOCC

#	Article	IF	CITATIONS
1	Compartmentalization of telomeres through DNA-scaffolded phase separation. Developmental Cell, 2022, 57, 277-290.e9.	7.0	38
2	AAA+ regulator MuB distorts DNA to drive forward transposition. Biophysical Journal, 2022, 121, 332a.	0.5	0
3	Structural basis of target-site selection in RNA-guided DNA transposition systems. Biophysical Journal, 2022, 121, 1a.	0.5	0
4	Structural basis for target site selection in RNA-guided DNA transposition systems. Science, 2021, 373, 768-774.	12.6	45
5	What Could Go Wrong? A Practical Guide to Single-Particle Cryo-EM: From Biochemistry to Atomic Models. Journal of Chemical Information and Modeling, 2020, 60, 2458-2469.	5.4	25
6	Towards a Mechanistic Understanding of P element Transposition Using Single-Particle Cryo-EM. Microscopy and Microanalysis, 2019, 25, 1288-1289.	0.4	0
7	Structure of a P element transposase–DNA complex reveals unusual DNA structures and GTP-DNA contacts. Nature Structural and Molecular Biology, 2019, 26, 1013-1022.	8.2	30
8	Cryoâ€EM Structure of the P Element Transposase Strand Transfer Complex. FASEB Journal, 2019, 33, 89.3.	0.5	0
9	Structural and functional differences between porcine brain and budding yeast microtubules. Cell Cycle, 2018, 17, 278-287.	2.6	28
10	Near-atomic model of microtubule-tau interactions. Science, 2018, 360, 1242-1246.	12.6	285
11	Insights into the Distinct Mechanisms of Action of Taxane and Non-Taxane Microtubule Stabilizers from Cryo-EM Structures. Journal of Molecular Biology, 2017, 429, 633-646.	4.2	161
12	Challenges and opportunities in the high-resolution cryo-EM visualization of microtubules and their binding partners. Current Opinion in Structural Biology, 2017, 46, 65-70.	5.7	17
13	Structural differences between yeast and mammalian microtubules revealed by cryo-EM. Journal of Cell Biology, 2017, 216, 2669-2677.	5.2	68
14	Near-atomic cryo-EM structure of PRC1 bound to the microtubule. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9430-9439.	7.1	70
15	High-Resolution Microtubule Structures Reveal the Structural Transitions in αβ-Tubulin upon GTP Hydrolysis. Cell, 2014, 157, 1117-1129.	28.9	582
16	Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. Methods in Enzymology, 2013, 523, 109-143.	1.0	195
17	Evaluation and Optimization of Discrete State Models of Protein Folding. Journal of Physical Chemistry B, 2012, 116, 11405-11413.	2.6	44
18	Role of conformational sampling in computing mutationâ€induced changes in protein structure and stability. Proteins: Structure, Function and Bioinformatics, 2011, 79, 830-838.	2.6	550

#	Article	IF	CITATIONS
19	Insights from the crystal structure of the sixth BRCT domain of topoisomerase IIβ binding protein 1. Protein Science, 2010, 19, 162-167.	7.6	12
20	High-resolution mapping of protein sequence-function relationships. Nature Methods, 2010, 7, 741-746.	19.0	482
21	Fast Cleavage Kinetics of a Natural Hammerhead Ribozyme. Journal of the American Chemical Society, 2004, 126, 10848-10849.	13.7	181
22	The Effect of Mutation on RNA Dielsâ^'Alderases. Journal of the American Chemical Society, 2004, 126, 11843-11851.	13.7	25
23	Characteristics of an RNA Dielsâ^'Alderase Active Site. Journal of the American Chemical Society, 1999, 121, 3614-3617.	13.7	46