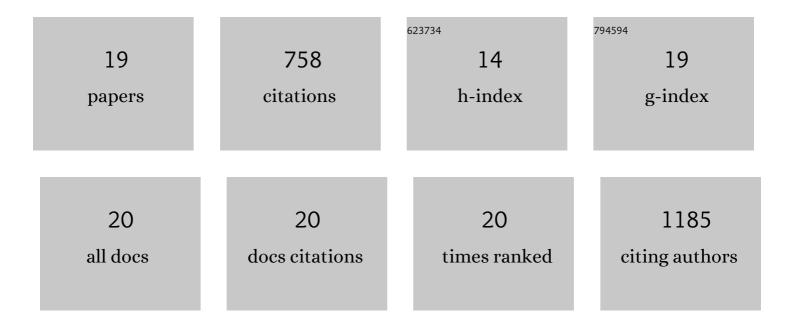
Cathleen Zeymer

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Directed Evolution of Protein Catalysts. Annual Review of Biochemistry, 2018, 87, 131-157.	11.1	330
2	Efficient laboratory evolution of computationally designed enzymes with low starting activities using fluorescence-activated droplet sorting. Protein Engineering, Design and Selection, 2016, 29, 355-366.	2.1	58
3	Lysine acylation using conjugating enzymes for site-specific modification and ubiquitination of recombinant proteins. Nature Chemistry, 2020, 12, 1008-1015.	13.6	46
4	Optimization of Enzyme Mechanism along the Evolutionary Trajectory of a Computationally Designed (Retro-)Aldolase. Journal of the American Chemical Society, 2017, 139, 12541-12549.	13.7	45
5	Emergence of a Negative Activation Heat Capacity during Evolution of a Designed Enzyme. Journal of the American Chemical Society, 2019, 141, 11745-11748.	13.7	42
6	Bap (Sil1) regulates the molecular chaperone BiP by coupling release of nucleotide and substrate. Nature Structural and Molecular Biology, 2018, 25, 90-100.	8.2	39
7	Tight and specific lanthanide binding in a de novo TIM barrel with a large internal cavity designed by symmetric domain fusion. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30362-30369.	7.1	31
8	trans-Acting Arginine Residues in the AAA+ Chaperone ClpB Allosterically Regulate the Activity through Inter- and Intradomain Communication. Journal of Biological Chemistry, 2014, 289, 32965-32976.	3.4	23
9	RNA Specificity and Regulation of Catalysis in the Eukaryotic Polynucleotide Kinase Clp1. Molecular Cell, 2014, 54, 975-986.	9.7	23
10	The Molecular Mechanism of Hsp100 Chaperone Inhibition by the Prion Curing Agent Guanidinium Chloride. Journal of Biological Chemistry, 2013, 288, 7065-7076.	3.4	19
11	Elements in nucleotide sensing and hydrolysis of the AAA+ disaggregation machine ClpB: a structure-based mechanistic dissection of a molecular motor. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 582-595.	2.5	18
12	Characterizing Active Site Conformational Heterogeneity along the Trajectory of an Enzymatic Phosphoryl Transfer Reaction. Angewandte Chemie - International Edition, 2016, 55, 11533-11537.	13.8	16
13	Americium preferred: lanmodulin, a natural lanthanide-binding protein favors an actinide over lanthanides. Chemical Science, 2021, 12, 15581-15587.	7.4	16
14	Coupling of Oligomerization and Nucleotide Binding in the AAA+ Chaperone ClpB. Biochemistry, 2011, 50, 899-909.	2.5	14
15	Design and engineering of artificial metalloproteins: from <i>de novo</i> metal coordination to catalysis. Protein Engineering, Design and Selection, 2021, 34, .	2.1	14
16	A Sterile α-Motif Domain in NafY Targets Apo-NifDK for Iron-Molybdenum Cofactor Delivery via a Tethered Domain. Journal of Biological Chemistry, 2011, 286, 6321-6328.	3.4	13
17	Analysis of electrostatic coupling throughout the laboratory evolution of a designed retroaldolase. Protein Science, 2021, 30, 1617-1627.	7.6	5
18	Efficient laboratory evolution of computationally designed enzymes with low starting activities using fluorescence-activated droplet sorting. Protein Engineering, Design and Selection, 2017, 30, 531-531.	2.1	4

#	Article	IF	CITATIONS
19	Characterizing Active Site Conformational Heterogeneity along the Trajectory of an Enzymatic Phosphoryl Transfer Reaction. Angewandte Chemie, 2016, 128, 11705-11709.	2.0	0