

Cathleen Zeymer

List of Publications by Year in descending order

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19
papers

758
citations

623734

14
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794594

19
g-index

20
all docs

20
docs citations

20
times ranked

1185
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of electrostatic coupling throughout the laboratory evolution of a designed retroaldolase. <i>Protein Science</i> , 2021, 30, 1617-1627.	7.6	5
2	Design and engineering of artificial metalloproteins: from <i>de novo</i> metal coordination to catalysis. <i>Protein Engineering, Design and Selection</i> , 2021, 34, .	2.1	14
3	Americium preferred: lanmodulin, a natural lanthanide-binding protein favors an actinide over lanthanides. <i>Chemical Science</i> , 2021, 12, 15581-15587.	7.4	16
4	Tight and specific lanthanide binding in a <i>de novo</i> TIM barrel with a large internal cavity designed by symmetric domain fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30362-30369.	7.1	31
5	Lysine acylation using conjugating enzymes for site-specific modification and ubiquitination of recombinant proteins. <i>Nature Chemistry</i> , 2020, 12, 1008-1015.	13.6	46
6	Emergence of a Negative Activation Heat Capacity during Evolution of a Designed Enzyme. <i>Journal of the American Chemical Society</i> , 2019, 141, 11745-11748.	13.7	42
7	Directed Evolution of Protein Catalysts. <i>Annual Review of Biochemistry</i> , 2018, 87, 131-157.	11.1	330
8	Bap (Sil1) regulates the molecular chaperone BiP by coupling release of nucleotide and substrate. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 90-100.	8.2	39
9	Efficient laboratory evolution of computationally designed enzymes with low starting activities using fluorescence-activated droplet sorting. <i>Protein Engineering, Design and Selection</i> , 2017, 30, 531-531.	2.1	4
10	Optimization of Enzyme Mechanism along the Evolutionary Trajectory of a Computationally Designed (Retro-)Aldolase. <i>Journal of the American Chemical Society</i> , 2017, 139, 12541-12549.	13.7	45
11	Characterizing Active Site Conformational Heterogeneity along the Trajectory of an Enzymatic Phosphoryl Transfer Reaction. <i>Angewandte Chemie</i> , 2016, 128, 11705-11709.	2.0	0
12	Efficient laboratory evolution of computationally designed enzymes with low starting activities using fluorescence-activated droplet sorting. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 355-366.	2.1	58
13	Characterizing Active Site Conformational Heterogeneity along the Trajectory of an Enzymatic Phosphoryl Transfer Reaction. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 11533-11537.	13.8	16
14	trans-Acting Arginine Residues in the AAA+ Chaperone ClpB Allosterically Regulate the Activity through Inter- and Intradomain Communication. <i>Journal of Biological Chemistry</i> , 2014, 289, 32965-32976.	3.4	23
15	RNA Specificity and Regulation of Catalysis in the Eukaryotic Polynucleotide Kinase Clp1. <i>Molecular Cell</i> , 2014, 54, 975-986.	9.7	23
16	Elements in nucleotide sensing and hydrolysis of the AAA+ disaggregation machine ClpB: a structure-based mechanistic dissection of a molecular motor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 582-595.	2.5	18
17	The Molecular Mechanism of Hsp100 Chaperone Inhibition by the Prion Curing Agent Guanidinium Chloride. <i>Journal of Biological Chemistry</i> , 2013, 288, 7065-7076.	3.4	19
18	Coupling of Oligomerization and Nucleotide Binding in the AAA+ Chaperone ClpB. <i>Biochemistry</i> , 2011, 50, 899-909.	2.5	14

#	ARTICLE	IF	CITATIONS
19	A Sterile Î±-Motif Domain in NafY Targets Apo-NifDK for Iron-Molybdenum Cofactor Delivery via a Tethered Domain. <i>Journal of Biological Chemistry</i> , 2011, 286, 6321-6328.	3.4	13