Laura S Itzhaki

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/719760/publications.pdf

Version: 2024-02-01

65 papers	1,791 citations	304743 22 h-index	302126 39 g-index
109 all docs	109 docs citations	109 times ranked	2264 citing authors

#	Article	IF	Citations
1	The Pathological G51D Mutation in Alpha-Synuclein Oligomers Confers Distinct Structural Attributes and Cellular Toxicity. Molecules, 2022, 27, 1293.	3.8	6
2	Unraveling the Mechanics of a Repeat-Protein Nanospring: From Folding of Individual Repeats to Fluctuations of the Superhelix. ACS Nano, 2022, 16, 3895-3905.	14.6	6
3	Micromechanics of soft materials using microfluidics. MRS Bulletin, 2022, 47, 119-126.	3.5	8
4	Structure-Based Discovery of Lipoteichoic Acid Synthase Inhibitors. Journal of Chemical Information and Modeling, 2022, 62, 2586-2599.	5.4	13
5	Engineering mono- and multi-valent inhibitors on a modular scaffold. Chemical Science, 2021, 12, 880-895.	7.4	7
6	Testing the length limit of loop grafting in a helical repeat protein. Current Research in Structural Biology, 2021, 3, 30-40.	2.2	5
7	Parallel and Sequential Pathways of Molecular Recognition of a Tandem-Repeat Protein and Its Intrinsically Disordered Binding Partner. Biomolecules, 2021, 11, 827.	4.0	3
8	Exploring the binding of rationally engineered tandem-repeat proteins to E3 ubiquitin ligase Keap1. Protein Engineering, Design and Selection, 2021, 34, .	2.1	1
9	Functionalized Double Strain-Promoted Stapled Peptides for Inhibiting the p53-MDM2 Interaction. ACS Omega, 2020, 5, 1157-1169.	3.5	7
10	Mapping pathogenic processes contributing to neurodegeneration in <i>Drosophila</i> models of Alzheimer's disease. FEBS Open Bio, 2020, 10, 338-350.	2.3	6
11	Probing the unfolded protein response in long-lived naked mole-rats. Biochemical and Biophysical Research Communications, 2020, 529, 1151-1157.	2.1	3
12	Diarylethene moiety as an enthalpy-entropy switch: photoisomerizable stapled peptides for modulating p53/MDM2 interaction. Organic and Biomolecular Chemistry, 2020, 18, 5359-5369.	2.8	14
13	Structural and mechanistic insights into the Keap1-Nrf2 system as a route to drug discovery. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140405.	2.3	39
14	Water-soluble, stable and azide-reactive strained dialkynes for biocompatible double strain-promoted click chemistry. Organic and Biomolecular Chemistry, 2019, 17, 8014-8018.	2.8	14
15	Editorial Overview: Biophysical and computational methods. Current Opinion in Structural Biology, 2019, 58, vii-ix.	5.7	0
16	Decoupling a tandem-repeat protein: Impact of multiple loop insertions on a modular scaffold. Scientific Reports, 2019, 9, 15439.	3.3	3
17	Bioorthogonal protein-DNA conjugation methods for force spectroscopy. Scientific Reports, 2019, 9, 13820.	3.3	34
18	Kinetic and thermodynamic effects of phosphorylation on p53 binding to MDM2. Scientific Reports, 2019, 9, 693.	3.3	25

#	Article	IF	Citations
19	Toolbox of Diverse Linkers for Navigating the Cellular Efficacy Landscape of Stapled Peptides. ACS Chemical Biology, 2019, 14, 526-533.	3.4	28
20	Targeted covalent inhibitors of MDM2 using electrophile-bearing stapled peptides. Chemical Communications, 2019, 55, 7914-7917.	4.1	23
21	Scalable Geometrically Designed Protein Cages Assembled via Genetically Encoded Split Inteins. Structure, 2019, 27, 776-784.e4.	3.3	9
22	The tetratricopeptide-repeat motif is a versatile platform that enables diverse modes of molecular recognition. Current Opinion in Structural Biology, 2019, 54, 43-49.	5.7	99
23	The AAA+ protease ClpXP can easily degrade a 31 and a 52-knotted protein. Scientific Reports, 2019, 9, 2421.	3.3	22
24	Exploring new strategies for grafting binding peptides onto protein loops using a consensusâ€designed tetratricopeptide repeat scaffold. Protein Science, 2019, 28, 738-745.	7.6	9
25	Programmed Protein Self-Assembly Driven by Genetically Encoded Intein-Mediated Native Chemical Ligation. ACS Synthetic Biology, 2018, 7, 1067-1074.	3.8	7
26	PyFolding: Open-Source Graphing, Simulation, and Analysis of the Biophysical Properties of Proteins. Biophysical Journal, 2018, 114, 516-521.	0.5	7
27	Context-Dependent Energetics of Loop Extensions in a Family of Tandem-Repeat Proteins. Biophysical Journal, 2018, 114, 2552-2562.	0.5	10
28	Folding cooperativity and allosteric function in the tandem-repeat protein class. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170188.	4.0	15
29	Macrocyclized Extended Peptides: Inhibiting the Substrate-Recognition Domain of Tankyrase. Journal of the American Chemical Society, 2017, 139, 2245-2256.	13.7	55
30	Development of Cellâ€Permeable, Nonâ€Helical Constrained Peptides to Target a Key Proteinâ€“Protein Interaction in Ovarian Cancer. Angewandte Chemie, 2017, 129, 539-544.	2.0	6
31	A New Methodology for Incorporating Chiral Linkers into Stapled Peptides. ChemBioChem, 2017, 18, 1066-1071.	2.6	23
32	Development of Cellâ€Permeable, Nonâ€Helical Constrained Peptides to Target a Key Proteinâ€“Protein Interaction in Ovarian Cancer. Angewandte Chemie - International Edition, 2017, 56, 524-529.	13.8	41
33	A method for rapid high-throughput biophysical analysis of proteins. Scientific Reports, 2017, 7, 9071.	3.3	18
34	Nanoscale click-reactive scaffolds from peptide self-assembly. Journal of Nanobiotechnology, 2017, 15, 70.	9.1	11
35	Discovery of a small-molecule binder of the oncoprotein gankyrin that modulates gankyrin activity in the cell. Scientific Reports, 2016, 6, 23732.	3.3	28
36	Dissecting and reprogramming the folding and assembly of tandem-repeat proteins. Biochemical Society Transactions, 2015, 43, 881-888.	3.4	11

#	Article	IF	Citations
37	Mapping the Topography of a Protein Energy Landscape. Journal of the American Chemical Society, 2015, 137, 14610-14625.	13.7	24
38	Single-Molecule FRET Reveals Hidden Complexity in a Protein Energy Landscape. Structure, 2015, 23, 190-198.	3.3	5
39	Functionalised staple linkages for modulating the cellular activity of stapled peptides. Chemical Science, 2014, 5, 1804-1809.	7.4	165
40	When ribosomes pick the structure. Nature Chemistry, 2014, 6, 378-379.	13.6	4
41	A Virus that Can Take the Heat. Structure, 2014, 22, 1549-1550.	3.3	0
42	Tandem-repeat proteins: regularity plus modularity equals design-ability. Current Opinion in Structural Biology, 2013, 23, 622-631.	5.7	52
43	Complex Energy Landscape of a Giant Repeat Protein. Structure, 2013, 21, 1954-1965.	3.3	33
44	The howâ€™s and whyâ€™s of protein folding intermediates. Archives of Biochemistry and Biophysics, 2013, 531, 14-23.	3.0	47
45	Subdomain Architecture and Stability of a Giant Repeat Protein. Journal of Physical Chemistry B, 2013, 117, 13029-13037.	2.6	10
46	Effects of Ligand Binding on the Mechanical Properties of Ankyrin Repeat Protein Gankyrin. PLoS Computational Biology, 2013, 9, e1002864.	3.2	18
47	Implications of 3D Domain Swapping for Protein Folding, Misfolding and Function. Advances in Experimental Medicine and Biology, 2012, 747, 137-152.	1.6	91
48	From Artificial Antibodies to Nanosprings. Advances in Experimental Medicine and Biology, 2012, 747, 153-166.	1.6	6
49	Using FlAsH To Probe Conformational Changes in a Large HEAT Repeat Protein. ChemBioChem, 2012, 13, 1199-1205.	2.6	6
50	Mechanical Unfolding of an Ankyrin Repeat Protein. Biophysical Journal, 2010, 98, 1294-1301.	0.5	56
51	Shifting transition states in the unfolding of a large ankyrin repeat protein. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9982-9987.	7.1	48
52	Rational redesign of the folding pathway of a modular protein. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2679-2684.	7.1	72
53	Probing a moving target with a plastic unfolding intermediate of an ankyrin-repeat protein. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7863-7868.	7.1	59
54	Biophysical Characterisation of the Small Ankyrin Repeat Protein Myotrophin. Journal of Molecular Biology, 2007, 365, 1245-1255.	4.2	33

#	ARTICLE	IF	CITATIONS
55	Activation of Ubiquitin Ligase SCFSkp2 by Cks1: Insights from Hydrogen Exchange Mass Spectrometry. Journal of Molecular Biology, 2006, 363, 673-686.	4.2	23
56	Binding of EMSY to HP1Î²: implications for recruitment of HP1Î² and BS69. EMBO Reports, 2005, 6, 675-680.	4.5	29
57	Role of Conformational Heterogeneity in Domain Swapping and Adapter Function of the Cks Proteins. Journal of Biological Chemistry, 2005, 280, 30448-30459.	3.4	23
58	Crystal Structure of the ENT Domain of Human EMSY. Journal of Molecular Biology, 2005, 350, 964-973.	4.2	24
59	Comparison of BRCT domains of BRCA1 and 53BP1: A biophysical analysis. Protein Science, 2004, 13, 617-625.	7.6	17
60	Sequential Unfolding of Ankyrin Repeats in Tumor Suppressor p16. Structure, 2003, 11, 67-73.	3.3	83
61	Cooperative organization in a macromolecular complex. Nature Structural and Molecular Biology, 2003, 10, 718-724.	8.2	21
62	Three Different Binding Sites of Cks1 Are Required for p27-Ubiquitin Ligation. Journal of Biological Chemistry, 2002, 277, 42233-42240.	3.4	80
63	Folding and Association of the Human Cell Cycle Regulatory Proteins ckshs1 and ckshs2. Biochemistry, 2002, 41, 1202-1210.	2.5	21
64	Stability and folding of the tumour suppressor protein p16 1 1Edited by J. Karn. Journal of Molecular Biology, 1999, 285, 1869-1886.	4.2	120
65	Multivalent Interaction of Beta-Catenin With its Intrinsically Disordered Binding Partner Adenomatous Polyposis Coli. Frontiers in Molecular Biosciences, 0, 9, .	3.5	3