Laura S Itzhaki

List of Publications by Year
in descending order

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	Functionalised staple linkages for modulating the cellular activity of stapled peptides. Chemical Science, 2014, 5, 1804-1809.	7.4	165
2	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
3	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
4	Implications of 3D Domain Swapping for Protein Folding, Misfolding and Function. Advances in Experimental Medicine and Biology, 2012, 747, 137-152.	1.6	91
5	Sequential Unfolding of Ankyrin Repeats in Tumor Suppressor p16. Structure, 2003, 11, 67-73.	3.3	83
6	Three Different Binding Sites of Cks1 Are Required for p27-Ubiquitin Ligation. Journal of Biological Chemistry, 2002, 277, 42233-42240.	3.4	80
7	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
8	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
9	Mechanical Unfolding of an Ankyrin Repeat Protein. Biophysical Journal, 2010, 98, 1294-1301.	0.5	56
10	Macrocyclized Extended Peptides: Inhibiting the Substrate-Recognition Domain of Tankyrase. Journal of the American Chemical Society, 2017, 139, 2245-2256.	13.7	55
11	Tandem-repeat proteins: regularity plus modularity equals design-ability. Current Opinion in Structural Biology, 2013, 23, 622-631.	5.7	52
12	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
13	The howâ€™s and whyâ€™s of protein folding intermediates. Archives of Biochemistry and Biophysics, 2013, 531, 14-23.	3.0	47
14	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
15	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
16	Bioorthogonal protein-DNA conjugation methods for force spectroscopy. Scientific Reports, 2019, 9, 13820.	3.3	34
17	Biophysical Characterisation of the Small Ankyrin Repeat Protein Myotrophin. Journal of Molecular Biology, 2007, 365, 1245-1255.	4.2	33
18	Complex Energy Landscape of a Giant Repeat Protein. Structure, 2013, 21, 1954-1965.	3.3	33

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19	Binding of EMSY to HP1Î²: implications for recruitment of HP1Î² and BS69. EMBO Reports, 2005, 6, 675-680.	4.5	29
20	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
21	Toolbox of Diverse Linkers for Navigating the Cellular Efficacy Landscape of Stapled Peptides. ACS Chemical Biology, 2019, 14, 526-533.	3.4	28
22	Kinetic and thermodynamic effects of phosphorylation on p53 binding to MDM2. Scientific Reports, 2019, 9, 693.	3.3	25
23	Crystal Structure of the ENT Domain of Human EMSY. Journal of Molecular Biology, 2005, 350, 964-973.	4.2	24
24	Mapping the Topography of a Protein Energy Landscape. Journal of the American Chemical Society, 2015, 137, 14610-14625.	13.7	24
25	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
26	Activation of Ubiquitin Ligase SCFSkp2 by Cks1: Insights from Hydrogen Exchange Mass Spectrometry. Journal of Molecular Biology, 2006, 363, 673-686.	4.2	23
27	A New Methodology for Incorporating Chiral Linkers into Stapled Peptides. ChemBioChem, 2017, 18, 1066-1071.	2.6	23
28	Targeted covalent inhibitors of MDM2 using electrophile-bearing stapled peptides. Chemical Communications, 2019, 55, 7914-7917.	4.1	23
29	The AAA+ protease ClpXP can easily degrade a 31 and a 52-knotted protein. Scientific Reports, 2019, 9, 2421.	3.3	22
30	Folding and Association of the Human Cell Cycle Regulatory Proteins ckshs1 and ckshs2. Biochemistry, 2002, 41, 1202-1210.	2.5	21
31	Cooperative organization in a macromolecular complex. Nature Structural and Molecular Biology, 2003, 10, 718-724.	8.2	21
32	Effects of Ligand Binding on the Mechanical Properties of Ankyrin Repeat Protein Gankyrin. PLoS Computational Biology, 2013, 9, e1002864.	3.2	18
33	A method for rapid high-throughput biophysical analysis of proteins. Scientific Reports, 2017, 7, 9071.	3.3	18
34	Comparison of BRCT domains of BRCA1 and 53BP1: A biophysical analysis. Protein Science, 2004, 13, 617-625.	7.6	17
35	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
36	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

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37	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
38	Structure-Based Discovery of Lipoteichoic Acid Synthase Inhibitors. Journal of Chemical Information and Modeling, 2022, 62, 2586-2599.	5.4	13
39	Dissecting and reprogramming the folding and assembly of tandem-repeat proteins. Biochemical Society Transactions, 2015, 43, 881-888.	3.4	11
40	Nanoscale click-reactive scaffolds from peptide self-assembly. Journal of Nanobiotechnology, 2017, 15, 70.	9.1	11
41	Subdomain Architecture and Stability of a Giant Repeat Protein. Journal of Physical Chemistry B, 2013, 117, 13029-13037.	2.6	10
42	Context-Dependent Energetics of Loop Extensions in a Family of Tandem-Repeat Proteins. Biophysical Journal, 2018, 114, 2552-2562.	0.5	10
43	Scalable Geometrically Designed Protein Cages Assembled via Genetically Encoded Split Inteins. Structure, 2019, 27, 776-784.e4.	3.3	9
44	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
45	Micromechanics of soft materials using microfluidics. MRS Bulletin, 2022, 47, 119-126.	3.5	8
46	Programmed Protein Self-Assembly Driven by Genetically Encoded Intein-Mediated Native Chemical Ligation. ACS Synthetic Biology, 2018, 7, 1067-1074.	3.8	7
47	PyFolding: Open-Source Graphing, Simulation, and Analysis of the Biophysical Properties of Proteins. Biophysical Journal, 2018, 114, 516-521.	0.5	7
48	Functionalized Double Strain-Promoted Stapled Peptides for Inhibiting the p53-MDM2 Interaction. ACS Omega, 2020, 5, 1157-1169.	3.5	7
49	Engineering mono- and multi-valent inhibitors on a modular scaffold. Chemical Science, 2021, 12, 880-895.	7.4	7
50	From Artificial Antibodies to Nanosprings. Advances in Experimental Medicine and Biology, 2012, 747, 153-166.	1.6	6
51	Using FlAsH To Probe Conformational Changes in a Large HEAT Repeat Protein. ChemBioChem, 2012, 13, 1199-1205.	2.6	6
52	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
53	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
54	The Pathological G51D Mutation in Alpha-Synuclein Oligomers Confers Distinct Structural Attributes and Cellular Toxicity. Molecules, 2022, 27, 1293.	3.8	6

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55	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
56	Single-Molecule FRET Reveals Hidden Complexity in a Protein Energy Landscape. Structure, 2015, 23, 190-198.	3.3	5
57	Testing the length limit of loop grafting in a helical repeat protein. Current Research in Structural Biology, 2021, 3, 30-40.	2.2	5
58	When ribosomes pick the structure. Nature Chemistry, 2014, 6, 378-379.	13.6	4
59	Decoupling a tandem-repeat protein: Impact of multiple loop insertions on a modular scaffold. Scientific Reports, 2019, 9, 15439.	3.3	3
60	Probing the unfolded protein response in long-lived naked mole-rats. Biochemical and Biophysical Research Communications, 2020, 529, 1151-1157.	2.1	3
61	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
62	Multivalent Interaction of Beta-Catenin With its Intrinsically Disordered Binding Partner Adenomatous Polyposis Coli. Frontiers in Molecular Biosciences, 0, 9, .	3.5	3
63	Exploring the binding of rationally engineered tandem-repeat proteins to E3 ubiquitin ligase Keap1. Protein Engineering, Design and Selection, 2021, 34, .	2.1	1
64	A Virus that Can Take the Heat. Structure, 2014, 22, 1549-1550.	3.3	0
65	Editorial Overview: Biophysical and computational methods. Current Opinion in Structural Biology, 2019, 58, vii-ix.	5.7	0