

Stewart N Loh

List of Publications by Year in descending order

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56
papers

2,059
citations

218381

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253896

43
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63
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63
docs citations

63
times ranked

2176
citing authors

#	ARTICLE	IF	CITATIONS
1	Engineering a Fluorescent Protein Color Switch Using Entropy-Driven \hat{I}^2 -Strand Exchange. ACS Sensors, 2022, 7, 263-271.	4.0	10
2	Discovery of a novel SHIP1 agonist that promotes degradation of lipid-laden phagocytic cargo by microglia. IScience, 2022, 25, 104170.	1.9	17
3	Intrinsically Disordered N-terminal Domain (NTD) of p53 Interacts with Mitochondrial PTP Regulator Cyclophilin D. Journal of Molecular Biology, 2022, 434, 167552.	2.0	11
4	p53 and Zinc: A Malleable Relationship. Frontiers in Molecular Biosciences, 2022, 9, 895887.	1.6	12
5	Engineering protein activity into off-the-shelf DNA devices. Cell Reports Methods, 2022, 2, 100202.	1.4	6
6	Benzothiazolyl and Benzoxazolyl Hydrazones Function as Zinc Metallochaperones to Reactivate Mutant p53. Journal of Medicinal Chemistry, 2021, 64, 2024-2045.	2.9	19
7	EGCG binds intrinsically disordered N-terminal domain of p53 and disrupts p53-MDM2 interaction. Nature Communications, 2021, 12, 986.	5.8	77
8	Arsenic and an Old Place: Rescuing p53 Mutants in Cancer. Cancer Cell, 2021, 39, 140-142.	7.7	6
9	Engineering A Modular Protein Color Switch using An Entropy-driven Beta Strand Exchange. FASEB Journal, 2021, 35, .	0.2	1
10	The Next Frontier for Designing Switchable Proteins: Rational Enhancement of Kinetics. Journal of Physical Chemistry B, 2021, 125, 9069-9077.	1.2	3
11	The tumor suppressor folliculin inhibits lactate dehydrogenase A and regulates the Warburg effect. Nature Structural and Molecular Biology, 2021, 28, 662-670.	3.6	19
12	Loss of bound zinc facilitates amyloid fibril formation of leukocyte-cell-derived chemotaxin 2 (LECT2). Journal of Biological Chemistry, 2021, 296, 100446.	1.6	15
13	Urea Denaturation, Zinc Binding, and DNA Binding Assays of Mutant p53 DNA-binding Domains and Full-length Proteins. Bio-protocol, 2021, 11, e4188.	0.2	1
14	Follow the Mutations: Toward Class-Specific, Small-Molecule Reactivation of p53. Biomolecules, 2020, 10, 303.	1.8	25
15	Zinc shapes the folding landscape of p53 and establishes a pathway for reactivating structurally diverse cancer mutants. ELife, 2020, 9, .	2.8	42
16	A Single Protein Disruption Site Results in Efficient Reassembly by Multiple Engineering Methods. Biophysical Journal, 2019, 117, 56-65.	0.2	7
17	Combinatorial Therapy of Zinc Metallochaperones with Mutant p53 Reactivation and Diminished Copper Binding. Molecular Cancer Therapeutics, 2019, 18, 1355-1365.	1.9	19
18	Large enhancement of response times of a protein conformational switch by computational design. Nature Communications, 2018, 9, 1013.	5.8	31

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19	Zinc Metallochaperones Reactivate Mutant p53 Using an ON/OFF Switch Mechanism: A New Paradigm in Cancer Therapeutics. <i>Clinical Cancer Research</i> , 2018, 24, 4505-4517.	3.2	31
20	Construction of Allosteric Protein Switches by Alternate Frame Folding and Intermolecular Fragment Exchange. <i>Methods in Molecular Biology</i> , 2017, 1596, 27-41.	0.4	8
21	Small Molecule-Induced Domain Swapping as a Mechanism for Controlling Protein Function and Assembly. <i>Scientific Reports</i> , 2017, 7, 44388.	1.6	24
22	Quantification of Membrane Protein-Detergent Complex Interactions. <i>Journal of Physical Chemistry B</i> , 2017, 121, 10228-10241.	1.2	20
23	Tumor suppressor Tsc1 is a new Hsp90 co-chaperone that facilitates folding of kinase and non-kinase clients. <i>EMBO Journal</i> , 2017, 36, 3650-3665.	3.5	64
24	Interrogating Detergent Desolvation of Nanopore-Forming Proteins by Fluorescence Polarization Spectroscopy. <i>Analytical Chemistry</i> , 2017, 89, 8013-8020.	3.2	13
25	The FNIP co-chaperones decelerate the Hsp90 chaperone cycle and enhance drug binding. <i>Nature Communications</i> , 2016, 7, 12037.	5.8	56
26	Synthetic Metallochaperone ZMC1 Rescues Mutant p53 Conformation by Transporting Zinc into Cells as an Ionophore. <i>Molecular Pharmacology</i> , 2015, 87, 825-831.	1.0	66
27	Engineered Domain Swapping as an On/Off Switch for Protein Function. <i>Chemistry and Biology</i> , 2015, 22, 1384-1393.	6.2	28
28	Reactivating mutant p53 using small molecules as zinc metallochaperones: awakening a sleeping giant in cancer. <i>Drug Discovery Today</i> , 2015, 20, 1391-1397.	3.2	74
29	Small molecule restoration of wildtype structure and function of mutant p53 using a novel zinc-metallochaperone based mechanism. <i>Oncotarget</i> , 2014, 5, 8879-8892.	0.8	90
30	Converting a Binding Protein into a Biosensing Conformational Switch Using Protein Fragment Exchange. <i>Biochemistry</i> , 2014, 53, 5505-5514.	1.2	21
31	Stepwise Conversion of a Binding Protein to a Fluorescent Switch: Application to <i>Thermoanaerobacter tengcongensis</i> Ribose Binding Protein. <i>Biochemistry</i> , 2013, 52, 600-612.	1.2	19
32	Engineering Domain-Swapped Binding Interfaces by Mutually Exclusive Folding. <i>Journal of Molecular Biology</i> , 2012, 416, 495-502.	2.0	22
33	Protein Conformational Switches: From Nature to Design. <i>Chemistry - A European Journal</i> , 2012, 18, 7984-7999.	1.7	120
34	Structural Characterization of Two Alternate Conformations in a Calbindin D _{9k} -Based Molecular Switch. <i>Biochemistry</i> , 2011, 50, 5583-5589.	1.2	9
35	Converting a protein into a switch for biosensing and functional regulation. <i>Protein Science</i> , 2011, 20, 19-29.	3.1	44
36	Probing local structural fluctuations in myoglobin by size-dependent thiol-disulfide exchange. <i>Protein Science</i> , 2010, 19, 1587-1594.	3.1	5

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37	On the mechanism of protein foldâ€switching by a molecular sensor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3260-3269.	1.5	20
38	Engineering an artificial zymogen by alternate frame protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2824-2829.	3.3	34
39	The missing Zinc: p53 misfolding and cancer. <i>Metallomics</i> , 2010, 2, 442.	1.0	111
40	Folding of Tetrameric p53: Oligomerization and Tumorigenic Mutations Induce Misfolding and Loss of Function. <i>Journal of Molecular Biology</i> , 2010, 395, 705-716.	2.0	37
41	Structural and Thermodynamic Analysis of a Conformationally Strained Circular Permutant of Barnase. <i>Biochemistry</i> , 2009, 48, 3497-3507.	1.2	32
42	Effect of Interdomain Linker Length on an Antagonistic Foldingâ€Unfolding Equilibrium between Two Protein Domains. <i>Journal of Molecular Biology</i> , 2009, 386, 854-868.	2.0	42
43	A Ca ²⁺ -Sensing Molecular Switch Based on Alternate Frame Protein Folding. <i>ACS Chemical Biology</i> , 2008, 3, 723-732.	1.6	51
44	Disrupting Proteins To Treat Cancer. <i>ACS Chemical Biology</i> , 2008, 3, 140-141.	1.6	2
45	Dynamics of equilibrium structural fluctuations of apomyoglobin measured by fluorescence correlation spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10459-10464.	3.3	73
46	Thermodynamic Analysis of an Antagonistic Foldingâ€Unfolding Equilibrium Between Two Protein Domains. <i>Journal of Molecular Biology</i> , 2007, 371, 308-316.	2.0	28
47	Zn ²⁺ -Dependent Misfolding of the p53 DNA Binding Domain. <i>Biochemistry</i> , 2007, 46, 2630-2639.	1.2	48
48	Modular Enzyme Design: Regulation by Mutually Exclusive Protein Folding. <i>Journal of Molecular Biology</i> , 2006, 357, 1058-1062.	2.0	35
49	Folding and misfolding mechanisms of the p53 DNA binding domain at physiological temperature. <i>Protein Science</i> , 2006, 15, 2457-2465.	3.1	31
50	Kinetic Partitioning During Folding of the p53 DNA Binding Domain. <i>Journal of Molecular Biology</i> , 2005, 350, 906-918.	2.0	41
51	Structure, Function, and Aggregation of the Zinc-Free Form of the p53 DNA Binding Domain. <i>Biochemistry</i> , 2003, 42, 2396-2403.	1.2	159
52	Allosteric Switching by Mutually Exclusive Folding of Protein Domains. <i>Journal of Molecular Biology</i> , 2003, 332, 529-536.	2.0	80
53	On the nature of conformational openings: native and unfolded-state hydrogen and thiol-disulfide exchange studies of ferric aquomyoglobin. <i>Journal of Molecular Biology</i> , 2001, 314, 153-166.	2.0	22
54	Identifying the Site of Initial Tertiary Structure Disruption during Apomyoglobin Unfolding. <i>Biochemistry</i> , 1999, 38, 14433-14439.	1.2	21

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55	Changes in side chain packing during apomyoglobin folding characterized by pulsed thiol-disulfide exchange. <i>Nature Structural and Molecular Biology</i> , 1998, 5, 730-737.	3.6	43
56	Solvent effects on the energetics of prolyl peptide bond isomerization. <i>Journal of the American Chemical Society</i> , 1992, 114, 5437-5439.	6.6	109