

Madeleine Strickland

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

368
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758635

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all docs

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docs citations

25
times ranked

535
citing authors

#	ARTICLE	IF	CITATIONS
1	Tsg101/ESCRT-I recruitment regulated by the dual binding modes of K63-linked diubiquitin. <i>Structure</i> , 2022, 30, 289-299.e6.	1.6	5
2	Novel Tsg101 Binding Partners Regulate Viral L Domain Trafficking. <i>Viruses</i> , 2021, 13, 1147.	1.5	7
3	Structural basis for polyglutamate chain initiation and elongation by TTL family enzymes. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 802-813.	3.6	35
4	Selective Targeting of Virus Replication by Proton Pump Inhibitors. <i>Scientific Reports</i> , 2020, 10, 4003.	1.6	31
5	RNA Binding Suppresses Tsg101 Recognition of Ub-Modified Gag and Facilitates Recruitment to the Plasma Membrane. <i>Viruses</i> , 2020, 12, 447.	1.5	6
6	Comparison of Solution Properties of Polymethylated DOTA-like Lanthanide Complexes with Opposite Chirality of the Pendant Arms. <i>Inorganic Chemistry</i> , 2019, 58, 15788-15800.	1.9	7
7	Potential Regulatory Role of Competitive Encounter Complexes in Paralogous Phosphotransferase Systems. <i>Journal of Molecular Biology</i> , 2019, 431, 2331-2342.	2.0	8
8	Model of a Kinetically Driven Crosstalk between Paralogous Protein Encounter Complexes. <i>Biophysical Journal</i> , 2019, 117, 1655-1665.	0.2	6
9	Long-Range RNA Structural Information via a Paramagnetically Tagged Reporter Protein. <i>Journal of the American Chemical Society</i> , 2019, 141, 1430-1434.	6.6	16
10	Solvent saturation transfer to proteins (SSTP) for structural and functional characterization of proteins. <i>Journal of Biomolecular NMR</i> , 2018, 70, 11-20.	1.6	3
11	Residual Dipolar Coupling for Conformational and Dynamic Studies. , 2018, , 419-434.		0
12	Tsg101 chaperone function revealed by HIV-1 assembly inhibitors. <i>Nature Communications</i> , 2017, 8, 1391.	5.8	37
13	Residual Dipolar Coupling for Conformational and Dynamic Studies. , 2017, , 1-16.		0
14	Functional evolution of IGF2:IGF2R domain 11 binding generates novel structural interactions and a specific IGF2 antagonist. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2766-75.	3.3	21
15	Structure of the NPR:EINNtr Complex: Mechanism for Specificity in Paralogous Phosphotransferase Systems. <i>Structure</i> , 2016, 24, 2127-2137.	1.6	16
16	Characterizing the magnetic susceptibility tensor of lanthanide-containing polymethylated-DOTA complexes. <i>Journal of Biomolecular NMR</i> , 2016, 66, 125-139.	1.6	23
17	Increasing the Chemical Shift Dispersion of Unstructured Proteins with a Covalent Lanthanide Shift Reagent. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 14847-14851.	7.2	29
18	Verbesserung der Dispersion der chemischen Verschiebungen von unstrukturierten Proteinen durch einen kovalent gebundenen Lanthanoidkomplex. <i>Angewandte Chemie</i> , 2016, 128, 15069-15073.	1.6	1

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19	Analysis of the isomer ratios of polymethylated-DOTA complexes and the implications on protein structural studies. Dalton Transactions, 2016, 45, 4673-4687.	1.6	38
20	Exploiting image registration for automated resonance assignment in NMR. Journal of Biomolecular NMR, 2015, 62, 143-156.	1.6	1
21	The Conformational Changes Induced by Ubiquinone Binding in the Na ⁺ -pumping NADH:Ubiquinone Oxidoreductase (Na ⁺ -NQR) Are Kinetically Controlled by Conserved Glycines 140 and 141 of the NqrB Subunit. Journal of Biological Chemistry, 2014, 289, 23723-23733.	1.6	21
22	An Exon Splice Enhancer Primes IGF2:IGF2R Binding Site Structure and Function Evolution. Science, 2012, 338, 1209-1213.	6.0	40
23	Protein flexibility directs DNA recognition by the papillomavirus E2 proteins. Nucleic Acids Research, 2011, 39, 2969-2980.	6.5	14