Unarta, Ilona Christy

List of Publications by Year
in descending order

12 papers	244 citations	1163117 8 h-index	1199594 12 g-index
12 all docs	12 docs citations	12 times ranked	245 citing authors

#	Article	IF	Citations
1	Markov State Models to Study the Functional Dynamics of Proteins in the Wake of Machine Learning. Jacs Au, 2021, 1, 1330-1341.	7.9	56
2	Elucidation of the Dynamics of Transcription Elongation by RNA Polymerase II using Kinetic Network Models. Accounts of Chemical Research, 2016, 49, 687-694.	15.6	49
3	Mechanism of DNA alkylation-induced transcriptional stalling, lesion bypass, and mutagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7082-E7091.	7.1	31
4	Elucidating molecular mechanisms of functional conformational changes of proteins via Markov state models. Current Opinion in Structural Biology, 2021, 67, 69-77.	5.7	27
5	Molecular mechanisms of RNA polymerase II transcription elongation elucidated by kinetic network models. Current Opinion in Structural Biology, 2018, 49, 54-62.	5.7	23
6	Transcriptional processing of an unnatural base pair by eukaryotic RNA polymerase II. Nature Chemical Biology, 2021, 17, 906-914.	8.0	16
7	Structural dissection of an interaction between transcription initiation and termination factors implicated in promoter-terminator cross-talk. Journal of Biological Chemistry, 2018, 293, 1651-1665.	3.4	15
8	Incorporation efficiency and inhibition mechanism of 2â€²-substituted nucleotide analogs against SARS-CoV-2 RNA-dependent RNA polymerase. Physical Chemistry Chemical Physics, 2021, 23, 20117-20128.	2.8	9
9	Entropy of stapled peptide inhibitors in free state is the major contributor to the improvement of binding affinity with the GK domain. RSC Chemical Biology, 2021, 2, 1274-1284.	4.1	8
10	Recent Developments in Integral Equation Theory for Solvation to Treat Density Inhomogeneity at Soluteâ€"Solvent Interface. Advanced Theory and Simulations, 2019, 2, 1900049.	2.8	7
11	Identifying Transcription Error-Enriched Genomic Loci Using Nuclear Run-on Circular-Sequencing Coupled with Background Error Modeling. Journal of Molecular Biology, 2020, 432, 3933-3949.	4.2	2
12	EmPC-seq: Accurate RNA-sequencing and Bioinformatics Platform to Map RNA Polymerases and Remove Background Error. Bio-protocol, 2021, 11, e3921.	0.4	1