

Wilma K Olson

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

419
citations

1040056

9
h-index

888059

17
g-index

18
all docs

18
docs citations

18
times ranked

478
citing authors

#	ARTICLE	IF	CITATIONS
1	Revisiting DNA Sequence-Dependent Deformability in High-Resolution Structures: Effects of Flanking Base Pairs on Dinucleotide Morphology and Global Chain Configuration. <i>Life</i> , 2022, 12, 759.	2.4	6
2	Synergy between Protein Positioning and DNA Elasticity: Energy Minimization of Protein-Decorated DNA Minicircles. <i>Journal of Physical Chemistry B</i> , 2021, 125, 2277-2287.	2.6	7
3	Surprising Twists in Nucleosomal DNA with Implication for Higher-order Folding. <i>Journal of Molecular Biology</i> , 2021, 433, 167121.	4.2	7
4	Biophysical Reviews™ “Meet the Editors Series” a profile of Wilma K. Olson. <i>Biophysical Reviews</i> , 2020, 12, 9-12.	3.2	8
5	An analytical method to connect open curves for modeling protein-bound DNA minicircles. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2020, 53, 435601.	2.1	0
6	Effects of Noncanonical Base Pairing on RNA Folding: Structural Context and Spatial Arrangements of G•A Pairs. <i>Biochemistry</i> , 2019, 58, 2474-2487.	2.5	18
7	Contributions of Sequence to the Higher-Order Structures of DNA. <i>Biophysical Journal</i> , 2017, 112, 416-426.	0.5	21
8	Insights into genome architecture deduced from the properties of short Lac repressor-mediated DNA loops. <i>Biophysical Reviews</i> , 2016, 8, 135-144.	3.2	6
9	DNA topology confers sequence specificity to nonspecific architectural proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16742-16747.	7.1	41
10	What Controls DNA Looping?. <i>International Journal of Molecular Sciences</i> , 2014, 15, 15090-15108.	4.1	8
11	Weak operator binding enhances simulated lac repressor-mediated DNA looping. <i>Biopolymers</i> , 2013, 99, n/a-n/a.	2.4	11
12	Structural insights into the role of architectural proteins in DNA looping deduced from computer simulations. <i>Biochemical Society Transactions</i> , 2013, 41, 559-564.	3.4	9
13	Interplay of Protein and DNA Structure Revealed in Simulations of the lac Operon. <i>PLoS ONE</i> , 2013, 8, e56548.	2.5	28
14	Computational opportunities for remote collaboration and capacity building afforded by Web 2.0 and cloud computing. <i>Biophysical Reviews</i> , 2012, 4, 153-160.	3.2	4
15	Insights into gene expression and packaging from computer simulations. <i>Biophysical Reviews</i> , 2012, 4, 171-178.	3.2	11
16	Nucleic acid structural deformability deduced from anisotropic displacement parameters. <i>Biopolymers</i> , 2011, 95, 254-269.	2.4	2
17	Properties of the nucleic-acid bases in free and Watson-Crick hydrogen-bonded states: computational insights into the sequence-dependent features of double-helical DNA. <i>Biophysical Reviews</i> , 2009, 1, 13-20.	3.2	35
18	A Novel Roll-and-Slide Mechanism of DNA Folding in Chromatin: Implications for Nucleosome Positioning. <i>Journal of Molecular Biology</i> , 2007, 371, 725-738.	4.2	197