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List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

330
citations

1039880

9
h-index

940416

16
g-index

18
all docs

18
docs citations

18
times ranked

455
citing authors

#	ARTICLE	IF	CITATIONS
1	<sc>SDA</sc> 7: A modular and parallel implementation of the simulation of diffusional association software. <i>Journal of Computational Chemistry</i> , 2015, 36, 1631-1645.	1.5	64
2	Conformational selection and dynamic adaptation upon linker histone binding to the nucleosome. <i>Nucleic Acids Research</i> , 2016, 44, 6599-6613.	6.5	40
3	Engineering AraC to make it responsive to light instead of arabinose. <i>Nature Chemical Biology</i> , 2021, 17, 817-827.	3.9	40
4	Dependence of Chromatosome Structure on Linker Histone Sequence and Posttranslational Modification. <i>Biophysical Journal</i> , 2018, 114, 2363-2375.	0.2	31
5	Toward an Ensemble View of Chromatosome Structure: A Paradigm Shift from One to Many. <i>Structure</i> , 2018, 26, 1050-1057.	1.6	31
6	Early career researchers want Open Science. <i>Genome Biology</i> , 2017, 18, 221.	3.8	26
7	The active repertoire of <i>Escherichia coli</i> peptidoglycan amidases varies with physiochemical environment. <i>Molecular Microbiology</i> , 2021, 116, 311-328.	1.2	24
8	Chromatosome Structure and Dynamics from Molecular Simulations. <i>Annual Review of Physical Chemistry</i> , 2020, 71, 101-119.	4.8	23
9	Split intein-mediated selection of cells containing two plasmids using a single antibiotic. <i>Nature Communications</i> , 2019, 10, 4967.	5.8	20
10	Computation of FRAP recovery times for linker histone chromatin binding on the basis of Brownian dynamics simulations. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129653.	1.1	8
11	C-terminal eYFP fusion impairs <i>Escherichia coli</i> MinE function. <i>Open Biology</i> , 2020, 10, 200010.	1.5	7
12	finDr: A web server for in silico D-peptide ligand identification. <i>Synthetic and Systems Biotechnology</i> , 2021, 6, 402-413.	1.8	5
13	DNA sequence-dependent positioning of the linker histone in a nucleosome: A single-pair FRET study. <i>Biophysical Journal</i> , 2021, 120, 3747-3763.	0.2	4
14	patchwork: a user-friendly pH sensitivity analysis web server for protein sequences and structures. <i>Nucleic Acids Research</i> , 2022, 50, W560-W567.	6.5	3
15	Experimental Characterization of In Silico Red-Shift-Predicted iLOV ^{L470T/Q489K} and iLOV ^{V392K/F410V/A426S} Mutants. <i>ACS Omega</i> , 2022, 7, 19555-19560.	1.6	2
16	Computational design of a pentapeptide inhibitor for fibroblast growth factor receptor 3b (FGFR3b). <i>Turkish Journal of Biology</i> , 2013, 37, 675-682.	2.1	1