Ognjen Perisic

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5676610/publications.pdf

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17	561	840776 11	888059 17
papers	citations	h-index	g-index

17	17	17	820
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mechanism for the Unfolding of the TOP7 Protein in Steered Molecular Dynamics Simulations as Revealed by Mutual Information Analysis. Frontiers in Molecular Biosciences, 2021, 8, 696609.	3.5	1
2	Recognition of Potential COVID-19 Drug Treatments through the Study of Existing Proteinâ€“Drug and Proteinâ€“Protein Structures: An Analysis of Kinetically Active Residues. Biomolecules, 2020, 10, 1346.	4.0	13
3	Sensitive effect of linker histone binding mode and subtype on chromatin condensation. Nucleic Acids Research, 2019, 47, 4948-4957.	14.5	43
4	Heterodimer Binding Scaffolds Recognition via the Analysis of Kinetically Hot Residues. Pharmaceuticals, 2018, 11, 29.	3.8	5
5	Dependence of the Linker Histone and Chromatin Condensation on the Nucleosome Environment. Journal of Physical Chemistry B, 2017, 121, 7823-7832.	2.6	25
6	Gene Mutation Profiles in Primary Diffuse Large B Cell Lymphoma of Central Nervous System: Next Generation Sequencing Analyses. International Journal of Molecular Sciences, 2016, 17, 683.	4.1	29
7	Computational strategies to address chromatin structure problems. Physical Biology, 2016, 13, 035006.	1.8	14
8	Parallel targeted next generation sequencing of childhood and adult acute myeloid leukemia patients reveals uniform genomic profile of the disease. Tumor Biology, 2016, 37, 13391-13401.	1.8	13
9	On the Improvement of Free-Energy Calculation from Steered Molecular Dynamics Simulations Using Adaptive Stochastic Perturbation Protocols. PLoS ONE, 2014, 9, e101810.	2.5	13
10	Pulling-spring modulation as a method for improving the potential-of-mean-force reconstruction in single-molecule manipulation experiments. Physical Review E, 2013, 87, 013303.	2.1	4
11	Efficient free-energy-profile reconstruction using adaptive stochastic perturbation protocols. Physical Review E, 2011, 84, 056705.	2.1	4
12	Ligand efficiency indices for an effective mapping of chemico-biological space: the concept of an atlas-like representation. Drug Discovery Today, 2010, 15, 804-811.	6.4	102
13	Modeling Studies of Chromatin Fiber Structure as a Function of DNA Linker Length. Journal of Molecular Biology, 2010, 403, 777-802.	4.2	98
14	Mechanical Signaling on the Single Protein Level Studied Using Steered Molecular Dynamics. Cell Biochemistry and Biophysics, 2009, 55, 141-152.	1.8	27
15	Mesoscale simulations of two nucleosome-repeat length oligonucleosomes. Physical Chemistry Chemical Physics, 2009, 11, 10729.	2.8	45
16	Single-molecule force spectroscopy reveals a mechanically stable protein fold and the rational tuning of its mechanical stability. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9278-9283.	7.1	117
17	Improved protein fold assignment using support vector machines. International Journal of Bioinformatics Research and Applications, 2005, 1, 319.	0.2	8