# 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 | 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 |
| 2 | 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 |
| 3 | Modeling Studies of Chromatin Fiber Structure as a Function of DNA Linker Length. Journal of Molecular Biology, 2010, 403, 777-802. | 4.2 | 98 |
| 4 | Mesoscale simulations of two nucleosome-repeat length oligonucleosomes. Physical Chemistry Chemical Physics, 2009, 11, 10729. | 2.8 | 45 |
| 5 | Sensitive effect of linker histone binding mode and subtype on chromatin condensation. Nucleic Acids Research, 2019, 47, 4948-4957. | 14.5 | 43 |
| 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 | Mechanical Signaling on the Single Protein Level Studied Using Steered Molecular Dynamics. Cell Biochemistry and Biophysics, 2009, 55, 141-152. | 1.8 | 27 |
| 8 | Dependence of the Linker Histone and Chromatin Condensation on the Nucleosome Environment. Journal of Physical Chemistry B, 2017, 121, 7823-7832. | 2.6 | 25 |
| 9 | Computational strategies to address chromatin structure problems. Physical Biology, 2016, 13, 035006. | 1.8 | 14 |
| 10 | 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 |
| 11 | 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 |
| 12 | 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 |
| 13 | Improved protein fold assignment using support vector machines. International Journal of Bioinformatics Research and Applications, 2005, 1, 319. | 0.2 | 8 |
| 14 | Heterodimer Binding Scaffolds Recognition via the Analysis of Kinetically Hot Residues. Pharmaceuticals, 2018, 11, 29. | 3.8 | 5 |
| 15 | Efficient free-energy-profile reconstruction using adaptive stochastic perturbation protocols. Physical Review E, 2011, 84, 056705. | 2.1 | 4 |
| 16 | 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 |
| 17 | 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 |