Mayya Sedova

List of Publications by Year
in descending order

16 papers	473 citations	1040056 9 h-index	1058476 14 g-index
19 all docs	19 docs citations	19 times ranked	854 citing authors

#	Article	IF	Citations
1	FATCAT 2.0: towards a better understanding of the structural diversity of proteins. Nucleic Acids Research, 2020, 48, W60-W64.	14.5	134
2	BiologicalNetworks: visualization and analysis tool for systems biology. Nucleic Acids Research, 2006, 34, W466-W471.	14.5	83
3	PDBFlex: exploring flexibility in protein structures. Nucleic Acids Research, 2016, 44, D423-D428.	14.5	70
4	Coronavirus3D: 3D structural visualization of COVID-19 genomic divergence. Bioinformatics, 2020, 36, 4360-4362.	4.1	39
5	The interplay of SARS-CoV-2 evolution and constraints imposed by the structure and functionality of its proteins. PLoS Computational Biology, 2021, 17, e1009147.	3.2	35
6	BiologicalNetworks 2.0 - an integrative view of genome biology data. BMC Bioinformatics, 2010, 11, 610.	2.6	21
7	BiologicalNetworks - tools enabling the integration of multi-scale data for the host-pathogen studies. BMC Systems Biology, 2011, 5, 7.	3.0	18
8	PubServer: literature searches by homology. Nucleic Acids Research, 2014, 42, W430-W435.	14.5	13
9	Cancer3D 2.0: interactive analysis of 3D patterns of cancer mutations in cancer subsets. Nucleic Acids Research, 2019, 47, D895-D899.	14.5	12
10	Difference contact maps: From what to why in the analysis of the conformational flexibility of proteins. PLoS ONE, 2020, 15, e0226702.	2.5	11
11	CAMERA 2.0: A Data-centric Metagenomics Community Infrastructure Driven by Scientific Workflows. , 2010, , .		9
12	Protael: protein data visualization library for the web. Bioinformatics, 2016, 32, 602-604.	4.1	9
13	LUD, a new protein domain associated with lactate utilization. BMC Bioinformatics, 2013, 14, 341.	2.6	8
14	ModFlex: Towards Function Focused Protein Modeling. Journal of Molecular Biology, 2021, 433, 166828.	4.2	2
15	What the protein data bank tells us about the evolutionary conservation of protein conformational diversity. Protein Science, 2022, 31, .	7.6	2
16	Extending the Data Model for Data-Centric Metagenomics Analysis Using Scientific Workflows in CAMERA. , 2010, , .		0