

Mayya Sedova

List of Publications by Year in descending order

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Version: 2024-02-01

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