Justas Dapkunas

List of Publications by Year
in descending order

16 papers	572 citations	932766 10 h-index	996533 15 g-index
18 all docs	18 docs citations	18 times ranked	765 citing authors

#	Article	IF	Citations
1	SKEMPI 2.0: an updated benchmark of changes in protein–protein binding energy, kinetics and thermodynamics upon mutation. Bioinformatics, 2019, 35, 462-469.	1.8	191
2	Blind prediction of homo–and hetero–protein complexes: The CASP13–CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	1.5	99
3	Prediction of protein assemblies, the next frontier: The <scp>CASP14–CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	1.5	73
4	QSAR Analysis of Blood–Brain Distribution: The Influence of Plasma and Brain Tissue Binding. Journal of Pharmaceutical Sciences, 2011, 100, 2147-2160.	1.6	56
5	The PPI3D web server for searching, analyzing and modeling protein–protein interactions in the context of 3D structures. Bioinformatics, 2017, 33, 935-937.	1.8	39
6	Trainable structure–activity relationship model for virtual screening of CYP3A4 inhibition. Journal of Computer-Aided Molecular Design, 2010, 24, 891-906.	1.3	30
7	Modeling of protein complexes in <scp>CASP14</scp> with emphasis on the interaction interface prediction. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1834-1843.	1.5	14
8	Inferring the microscopic surface energy of protein–protein interfaces from mutation data. Proteins: Structure, Function and Bioinformatics, 2015, 83, 640-650.	1.5	13
9	Probabilistic Prediction of the Human CYP3A4 and CYP2D6 Metabolism Sites. Chemistry and Biodiversity, 2009, 6, 2101-2106.	1.0	12
10	Structural modeling of protein complexes: Current capabilities and challenges. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1222-1232.	1.5	12
11	Modeling of protein complexes in CAPRI Round 37 using template–based approach combined with model selection. Proteins: Structure, Function and Bioinformatics, 2018, 86, 292-301.	1.5	9
12	Mapping of Recognition Sites of Monoclonal Antibodies Responsible for the Inhibition of Pneumolysin Functional Activity. Biomolecules, 2020, 10, 1009.	1.8	7
13	Template-Based Modeling of Protein Complexes Using the PPI3D Web Server. Methods in Molecular Biology, 2020, 2165, 139-155.	0.4	6
14	Exogenous interleukin-1α signaling negatively impacts acquired chemoresistance and alters cell adhesion molecule expression pattern in colorectal carcinoma cells HCT116. Cytokine, 2019, 114, 38-46.	1.4	4
15	Template–based modeling of diverse protein interactions in CAPRI rounds 38–45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 939-947.	1.5	3
16	Donor Splice Site Variant in SLC9A6 Causes Christianson Syndrome in a Lithuanian Family: A Case Report. Medicina (Lithuania), 2022, 58, 351.	0.8	0