

# Justas Dapkunas

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

17 papers	303 citations	8 h-index	17 g-index
18 ext. papers	428 ext. citations	4.1 avg, IF	3.51 L-index

#	Paper	IF	Citations
17	Donor Splice Site Variant in Causes Christianson Syndrome in a Lithuanian Family: A Case Report.. <i>Medicina (Lithuania)</i> , <b>2022</b> , 58,	3.1	
16	Modeling of protein complexes in CASP14 with emphasis on the interaction interface prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2021</b> , 89, 1834-1843	4.2	2
15	Prediction of protein assemblies, the next frontier: The CASP14-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2021</b> , 89, 1800-1823	4.2	17
14	Template-based modeling of diverse protein interactions in CAPRI rounds 38-45. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2020</b> , 88, 939-947	4.2	3
13	Mapping of Recognition Sites of Monoclonal Antibodies Responsible for the Inhibition of Pneumolysin Functional Activity. <i>Biomolecules</i> , <b>2020</b> , 10,	5.9	6
12	Template-Based Modeling of Protein Complexes Using the PPI3D Web Server. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2165, 139-155	1.4	2
11	SKEMPI 2.0: an updated benchmark of changes in protein-protein binding energy, kinetics and thermodynamics upon mutation. <i>Bioinformatics</i> , <b>2019</b> , 35, 462-469	7.2	92
10	Structural modeling of protein complexes: Current capabilities and challenges. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2019</b> , 87, 1222-1232	4.2	8
9	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2019</b> , 87, 1200-1221	4.2	58
8	Exogenous interleukin-1 $\beta$ signaling negatively impacts acquired chemoresistance and alters cell adhesion molecule expression pattern in colorectal carcinoma cells HCT116. <i>Cytokine</i> , <b>2019</b> , 114, 38-46	4	4
7	Modeling of protein complexes in CAPRI Round 37 using template-based approach combined with model selection. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2018</b> , 86 Suppl 1, 292-301	4.2	8
6	The PPI3D web server for searching, analyzing and modeling protein-protein interactions in the context of 3D structures. <i>Bioinformatics</i> , <b>2017</b> , 33, 935-937	7.2	13
5	Inferring the microscopic surface energy of protein-protein interfaces from mutation data. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 640-50	4.2	10
4	QSAR analysis of blood-brain distribution: the influence of plasma and brain tissue binding. <i>Journal of Pharmaceutical Sciences</i> , <b>2011</b> , 100, 2147-60	3.9	41
3	Trainable structure-activity relationship model for virtual screening of CYP3A4 inhibition. <i>Journal of Computer-Aided Molecular Design</i> , <b>2010</b> , 24, 891-906	4.2	27
2	Probabilistic prediction of the human CYP3A4 and CYP2D6 metabolism sites. <i>Chemistry and Biodiversity</i> , <b>2009</b> , 6, 2101-6	2.5	10
1	SKEMPI 2.0: An updated benchmark of changes in protein-protein binding energy, kinetics and thermodynamics upon mutation		1

