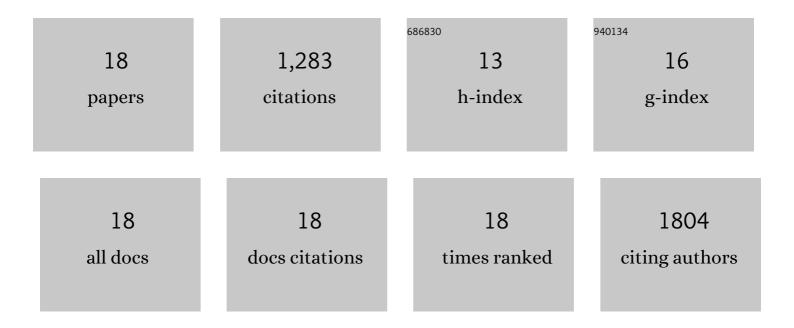
Michal Jamroz

List of Publications by Year in descending order

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MICHAL JAMPOZ

#	Article	lF	CITATIONS
1	Combining Structural Aggregation Propensity and Stability Predictions To Redesign Protein Solubility. Molecular Pharmaceutics, 2018, 15, 3846-3859.	2.3	45
2	Predicting Real-Valued Protein Residue Fluctuation Using FlexPred. Methods in Molecular Biology, 2017, 1484, 175-186.	0.4	4
3	Coarse-Grained Simulations of Membrane Insertion and Folding of Small Helical Proteins Using the CABS Model. Journal of Chemical Information and Modeling, 2016, 56, 2207-2215.	2.5	17
4	Ensemble-based evaluation for protein structure models. Bioinformatics, 2016, 32, i314-i321.	1.8	7
5	CABS-dock web server for the flexible docking of peptides to proteins without prior knowledge of the binding site. Nucleic Acids Research, 2015, 43, W419-W424.	6.5	331
6	AGGRESCAN3D (A3D): server for prediction of aggregation properties of protein structures. Nucleic Acids Research, 2015, 43, W306-W313.	6.5	201
7	KnotProt: a database of proteins with knots and slipknots. Nucleic Acids Research, 2015, 43, D306-D314.	6.5	159
8	CABS-flex predictions of protein flexibility compared with NMR ensembles. Bioinformatics, 2014, 30, 2150-2154.	1.8	75
9	Structure Prediction of the Second Extracellular Loop in G-Protein-Coupled Receptors. Biophysical Journal, 2014, 106, 2408-2416.	0.2	30
10	Protocols for Efficient Simulations of Long-Time Protein Dynamics Using Coarse-Grained CABS Model. Methods in Molecular Biology, 2014, 1137, 235-250.	0.4	13
11	Consistent View of Protein Fluctuations from All-Atom Molecular Dynamics and Coarse-Grained Dynamics with Knowledge-Based Force-Field. Journal of Chemical Theory and Computation, 2013, 9, 119-125.	2.3	85
12	ClusCo: clustering and comparison of protein models. BMC Bioinformatics, 2013, 14, 62.	1.2	32
13	CABS-flex: server for fast simulation of protein structure fluctuations. Nucleic Acids Research, 2013, 41, W427-W431.	6.5	132
14	CABS-fold: server for the de novo and consensus-based prediction of protein structure. Nucleic Acids Research, 2013, 41, W406-W411.	6.5	86
15	Structural features that predict realâ€value fluctuations of globular proteins. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1425-1435.	1.5	20
16	Multiscale Approach to Protein Folding Dynamics. , 2011, , 281-293.		11
17	Multiscale Protein and Peptide Docking. , 2011, , 21-33.		0
18	Modeling of loops in proteins: a multi-method approach. BMC Structural Biology, 2010, 10, 5.	2.3	35