

# Michal Jamroz

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5867820/publications.pdf>

Version: 2024-02-01

18  
papers

1,283  
citations

686830

13  
h-index

940134

16  
g-index

18  
all docs

18  
docs citations

18  
times ranked

1804  
citing authors

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