# Michal Jamroz

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | 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 |