Mateusz Kurcinski

List of Publications by Year
in descending order

30	1,589	516215 16	476904 29
papers	citations	h-index	g-index

32	32	32	1808
all docs	docs citations	times ranked	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. Nucleic Acids Research, 2015, 43, W419-W424.	6.5	331
2	CABS-flex 2.0: a web server for fast simulations of flexibility of protein structures. Nucleic Acids Research, 2018, 46, W338-W343.	6.5	249
3	Proteinâ€“peptide docking: opportunities and challenges. Drug Discovery Today, 2018, 23, 1530-1537.	3.2	212
4	Modeling of proteinâ€“peptide interactions using the CABS-dock web server for binding site search and flexible docking. Methods, 2016, 93, 72-83.	1.9	137
5	Aggrescan3D (A3D) 2.0: prediction and engineering of protein solubility. Nucleic Acids Research, 2019, 47, W300-W307.	6.5	91
6	CABS-flex standalone: a simulation environment for fast modeling of protein flexibility. Bioinformatics, 2019, 35, 694-695.	1.8	79
7	CABS-dock standalone: a toolbox for flexible proteinâ€“peptide docking. Bioinformatics, 2019, 35, 4170-4172.	1.8	55
8	Flexible docking of peptides to proteins using CABSâ€dock. Protein Science, 2020, 29, 211-222.	3.1	48
9	Human telomerase model shows the role of the TEN domain in advancing the double helix for the next polymerization step. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9443-9448.	3.3	47
10	Protein-peptide molecular docking with large-scale conformational changes: the p53-MDM2 interaction. Scientific Reports, 2016, 6, 37532.	1.6	44
11	Mechanism of Folding and Binding of an Intrinsically Disordered Protein As Revealed by ab Initio Simulations. Journal of Chemical Theory and Computation, 2014, 10, 2224-2231.	2.3	41
12	Proteinâ€“peptide docking using CABS-dock and contact information. Briefings in Bioinformatics, 2019, 20, 2299-2305.	3.2	35
13	Highly Flexible Protein-Peptide Docking Using CABS-Dock. Methods in Molecular Biology, 2017, 1561, 69-94.	0.4	33
14	Denatured proteins and early folding intermediates simulated in a reduced conformational space.. Acta Biochimica Polonica, 2019, 53, 131-143.	0.3	25
15	Aggrescan3D standalone package for structure-based prediction of protein aggregation properties. Bioinformatics, 2019, 35, 3834-3835.	1.8	22
16	Steps towards flexible docking: Modeling of three-dimensional structures of the nuclear receptors bound with peptide ligands mimicking co-activatorsâ€™ sequences. Journal of Steroid Biochemistry and Molecular Biology, 2007, 103, 357-360.	1.2	21
17	Hierarchical modeling of protein interactions. Journal of Molecular Modeling, 2007, 13, 691-698.	0.8	19
18	Modeling EphB4-EphrinB2 proteinâ€“protein interaction using flexible docking of a short linear motif. BioMedical Engineering OnLine, 2017, 16, 71.	1.3	17

#	Article	IF	Citations
19	MAPIYA contact map server for identification and visualization of molecular interactions in proteins and biological complexes. Nucleic Acids Research, 2022, 50, W474-W482.	6.5	14
20	Analysis and optimization of interactions between peptides mimicking the GD2 ganglioside and the monoclonal antibody 14G2a. International Journal of Molecular Medicine, 2011, 28, 47-57.	1.8	12
21	Coarse-Grained Modeling of Peptide Docking Associated with Large Conformation Transitions of the Binding Protein: Troponin I Fragmentâ€“Troponin C System. Molecules, 2015, 20, 10763-10780.	1.7	11
22	Theoretical study of molecular mechanism of binding TRAP220 coactivator to Retinoid X Receptor alpha, activated by 9-cis retinoic acid. Journal of Steroid Biochemistry and Molecular Biology, 2010, 121, 124-129.	1.2	10
23	Denatured proteins and early folding intermediates simulated in a reduced conformational space. Acta Biochimica Polonica, 2006, 53, 131-44.	0.3	10
24	A protocol for CABS-dock proteinâ€“peptide docking driven by side-chain contact information. BioMedical Engineering OnLine, 2017, 16, 73.	1.3	9
25	Proteinâ€“Protein Docking with Large-Scale Backbone Flexibility Using Coarse-Grained Monte-Carlo Simulations. International Journal of Molecular Sciences, 2021, 22, 7341.	1.8	5
26	MSITE: A new computational tool for comparison of homological proteins in holo form. Journal of Steroid Biochemistry and Molecular Biology, 2010, 121, 34-42.	1.2	3
27	Structural Insights into Ïƒ1 Receptor Interactions with Opioid Ligands by Molecular Dynamics Simulations. Molecules, 2018, 23, 456.	1.7	3
28	Protein Structure Prediction Using Coarse-Grained Models. Springer Series on Bio- and Neurosystems, 2019, , 27-59.	0.2	3
29	Protein-Peptide Docking with High Conformational Flexibility using CABS-dock Web Tool. Biophysical Journal, 2016, 110, 543a.	0.2	1
30	Multiscale Protein and Peptide Docking. , 2011, , 21-33.		0