

Mateusz Kurcinski

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,589
citations

516215

16
h-index

476904

29
g-index

32
all docs

32
docs citations

32
times ranked

1808
citing authors

#	ARTICLE	IF	CITATIONS
1	MAPIYA contact map server for identification and visualization of molecular interactions in proteins and biological complexes. <i>Nucleic Acids Research</i> , 2022, 50, W474-W482.	6.5	14
2	Proteinâ€“Protein Docking with Large-Scale Backbone Flexibility Using Coarse-Grained Monte-Carlo Simulations. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7341.	1.8	5
3	Flexible docking of peptides to proteins using CABSâ€“dock. <i>Protein Science</i> , 2020, 29, 211-222.	3.1	48
4	CABS-flex standalone: a simulation environment for fast modeling of protein flexibility. <i>Bioinformatics</i> , 2019, 35, 694-695.	1.8	79
5	Aggrescan3D (A3D) 2.0: prediction and engineering of protein solubility. <i>Nucleic Acids Research</i> , 2019, 47, W300-W307.	6.5	91
6	Aggrescan3D standalone package for structure-based prediction of protein aggregation properties. <i>Bioinformatics</i> , 2019, 35, 3834-3835.	1.8	22
7	CABS-dock standalone: a toolbox for flexible proteinâ€“peptide docking. <i>Bioinformatics</i> , 2019, 35, 4170-4172.	1.8	55
8	Proteinâ€“peptide docking using CABS-dock and contact information. <i>Briefings in Bioinformatics</i> , 2019, 20, 2299-2305.	3.2	35
9	Protein Structure Prediction Using Coarse-Grained Models. <i>Springer Series on Bio- and Neurosystems</i> , 2019, , 27-59.	0.2	3
10	Denatured proteins and early folding intermediates simulated in a reduced conformational space.. <i>Acta Biochimica Polonica</i> , 2019, 53, 131-143.	0.3	25
11	Proteinâ€“peptide docking: opportunities and challenges. <i>Drug Discovery Today</i> , 2018, 23, 1530-1537.	3.2	212
12	CABS-flex 2.0: a web server for fast simulations of flexibility of protein structures. <i>Nucleic Acids Research</i> , 2018, 46, W338-W343.	6.5	249
13	Structural Insights into Î²1 Receptor Interactions with Opioid Ligands by Molecular Dynamics Simulations. <i>Molecules</i> , 2018, 23, 456.	1.7	3
14	Highly Flexible Protein-Peptide Docking Using CABS-Dock. <i>Methods in Molecular Biology</i> , 2017, 1561, 69-94.	0.4	33
15	Modeling EphB4-EphrinB2 proteinâ€“protein interaction using flexible docking of a short linear motif. <i>BioMedical Engineering OnLine</i> , 2017, 16, 71.	1.3	17
16	A protocol for CABS-dock proteinâ€“peptide docking driven by side-chain contact information. <i>BioMedical Engineering OnLine</i> , 2017, 16, 73.	1.3	9
17	Protein-peptide molecular docking with large-scale conformational changes: the p53-MDM2 interaction. <i>Scientific Reports</i> , 2016, 6, 37532.	1.6	44
18	Protein-Peptide Docking with High Conformational Flexibility using CABS-dock Web Tool. <i>Biophysical Journal</i> , 2016, 110, 543a.	0.2	1

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19	Modeling of protein-peptide interactions using the CABS-dock web server for binding site search and flexible docking. <i>Methods</i> , 2016, 93, 72-83.	1.9	137
20	Coarse-Grained Modeling of Peptide Docking Associated with Large Conformation Transitions of the Binding Protein: Troponin I Fragment-Troponin C System. <i>Molecules</i> , 2015, 20, 10763-10780.	1.7	11
21	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
22	Mechanism of Folding and Binding of an Intrinsically Disordered Protein As Revealed by ab Initio Simulations. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 2224-2231.	2.3	41
23	Analysis and optimization of interactions between peptides mimicking the GD2 ganglioside and the monoclonal antibody 14G2a. <i>International Journal of Molecular Medicine</i> , 2011, 28, 47-57.	1.8	12
24	Human telomerase model shows the role of the TEN domain in advancing the double helix for the next polymerization step. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9443-9448.	3.3	47
25	Multiscale Protein and Peptide Docking. , 2011, , 21-33.		0
26	Theoretical study of molecular mechanism of binding TRAP220 coactivator to Retinoid X Receptor alpha, activated by 9-cis retinoic acid. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2010, 121, 124-129.	1.2	10
27	MSITE: A new computational tool for comparison of homological proteins in holo form. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2010, 121, 34-42.	1.2	3
28	Steps towards flexible docking: Modeling of three-dimensional structures of the nuclear receptors bound with peptide ligands mimicking co-activators' sequences. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2007, 103, 357-360.	1.2	21
29	Hierarchical modeling of protein interactions. <i>Journal of Molecular Modeling</i> , 2007, 13, 691-698.	0.8	19
30	Denatured proteins and early folding intermediates simulated in a reduced conformational space. <i>Acta Biochimica Polonica</i> , 2006, 53, 131-44.	0.3	10