

Zeynep Kurkcuoglu

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

347
citations

1040056

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1125743

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docs citations

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565
citing authors

#	ARTICLE	IF	CITATIONS
1	Pre- and post-docking sampling of conformational changes using ClustENM and HADDOCK for protein-protein and protein-DNA systems. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 292-306.	2.6	32
2	An overview of data-driven HADDOCK strategies in CAPRI rounds 38-45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1029-1036.	2.6	11
3	Understanding the Binding Specificity of G-Protein Coupled Receptors toward G-Proteins and Arrestins: Application to the Dopamine Receptor Family. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 3969-3984.	5.4	8
4	Performance of HADDOCK and a simple contact-based protein-ligand binding affinity predictor in the D3R Grand Challenge 2. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 175-185.	2.9	97
5	Conformational dynamics of bacterial trigger factor in apo and ribosome-bound states. <i>PLoS ONE</i> , 2017, 12, e0176262.	2.5	9
6	Ligand Docking to Intermediate and Close-To-Bound Conformers Generated by an Elastic Network Model Based Algorithm for Highly Flexible Proteins. <i>PLoS ONE</i> , 2016, 11, e0158063.	2.5	18
7	ClustENM: ENM-Based Sampling of Essential Conformational Space at Full Atomic Resolution. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 4549-4562.	5.3	43
8	How an Inhibitor Bound to Subunit Interface Alters Triosephosphate Isomerase Dynamics. <i>Biophysical Journal</i> , 2015, 109, 1169-1178.	0.5	28
9	Substrate Effect on Catalytic Loop and Global Dynamics of Triosephosphate Isomerase. <i>Entropy</i> , 2013, 15, 1085-1099.	2.2	4
10	Coupling between Catalytic Loop Motions and Enzyme Global Dynamics. <i>PLoS Computational Biology</i> , 2012, 8, e1002705.	3.2	42
11	Functional Dynamics of Proteins Elucidated by Statistical Analysis of Simulation Data. <i>Current Physical Chemistry</i> , 2012, 2, 443-451.	0.2	1
12	Blind Dockings of Benzothiazoles to Multiple Receptor Conformations of Triosephosphate Isomerase from <i>Trypanosoma cruzi</i> and Human. <i>Molecular Informatics</i> , 2011, 30, 986-995.	2.5	12
13	Collective dynamics of the ribosomal tunnel revealed by elastic network modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 837-845.	2.6	42