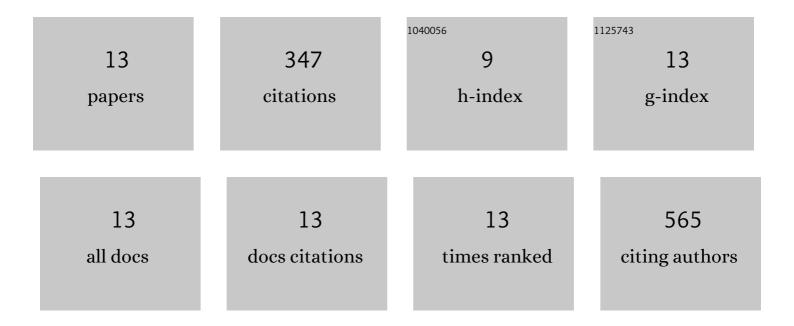
## Zeynep Kurkcuoglu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1229726/publications.pdf Version: 2024-02-01



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