

# Sudipto Mukherjee

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11428741/publications.pdf>

Version: 2024-02-01

12  
papers

1,737  
citations

759233

12  
h-index

1199594

12  
g-index

13  
all docs

13  
docs citations

13  
times ranked

2784  
citing authors

#	ARTICLE	IF	CITATIONS
1	DOCK 6: Combining techniques to model RNA–small molecule complexes. <i>Rna</i> , 2009, 15, 1219-1230.	3.5	616
2	DOCK 6: Impact of new features and current docking performance. <i>Journal of Computational Chemistry</i> , 2015, 36, 1132-1156.	3.3	552
3	Docking Validation Resources: Protein Family and Ligand Flexibility Experiments. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 1986-2000.	5.4	153
4	Evaluation of DOCK 6 as a pose generation and database enrichment tool. <i>Journal of Computer-Aided Molecular Design</i> , 2012, 26, 749-773.	2.9	128
5	Bridging Microscopic and Macroscopic Mechanisms of p53-MDM2 Binding with Kinetic Network Models. <i>Biophysical Journal</i> , 2017, 113, 785-793.	0.5	77
6	Implementation and evaluation of a docking–rescoring method using molecular footprint comparisons. <i>Journal of Computational Chemistry</i> , 2011, 32, 2273-2289.	3.3	52
7	Insights into Peptoid Helix Folding Cooperativity from an Improved Backbone Potential. <i>Journal of Physical Chemistry B</i> , 2015, 119, 15407-15417.	2.6	39
8	Origins of Resistance to the HIVgp41 Viral Entry Inhibitor T20. <i>Biochemistry</i> , 2010, 49, 3575-3592.	2.5	33
9	Grid-based molecular footprint comparison method for docking and <i>de novo</i> design: Application to HIVgp41. <i>Journal of Computational Chemistry</i> , 2013, 34, 1226-1240.	3.3	24
10	Microsecond simulations of mdm2 and its complex with p53 yield insight into force field accuracy and conformational dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1665-1676.	2.6	24
11	Precisely tuneable energy transfer system using peptoid helix-based molecular scaffold. <i>Scientific Reports</i> , 2017, 7, 4786.	3.3	22
12	Markov models of the apo-MDM2 lid region reveal diffuse yet two-state binding dynamics and receptor poses for computational docking. <i>Scientific Reports</i> , 2016, 6, 31631.	3.3	17