

Krishna Praneeth Kilambi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11882410/publications.pdf>

Version: 2024-02-01

10
papers

679
citations

933447

10
h-index

1372567

10
g-index

10
all docs

10
docs citations

10
times ranked

1403
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and kinetic basis for the selectivity of aducanumab for aggregated forms of amyloid- β . Scientific Reports, 2018, 8, 6412.	3.3	182
2	Functional Loss of Semaphorin 3C and/or Semaphorin 3D and Their Epistatic Interaction with Ret Are Critical to Hirschsprung Disease Liability. American Journal of Human Genetics, 2015, 96, 581-596.	6.2	118
3	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	2.6	87
4	Rapid Calculation of Protein pKa Values Using Rosetta. Biophysical Journal, 2012, 103, 587-595.	0.5	61
5	Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design. PLoS ONE, 2013, 8, e67051.	2.5	59
6	Blind prediction of interfacial water positions in CAPRI. Proteins: Structure, Function and Bioinformatics, 2014, 82, 620-632.	2.6	50
7	A generalized approach to sampling backbone conformations with RosettaDock for CAPRI rounds 13-19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3115-3123.	2.6	46
8	Structure-based cross-docking analysis of antibody-antigen interactions. Scientific Reports, 2017, 7, 8145.	3.3	37
9	Extending RosettaDock with water, sugar, and pH for prediction of complex structures and affinities for CAPRI rounds 20-27. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2201-2209.	2.6	22
10	Protein-Protein Docking with Dynamic Residue Protonation States. PLoS Computational Biology, 2014, 10, e1004018.	3.2	17