Daniel Kuhn

List of Publications by Year
in descending order

13 papers	2,058 citations	759055 12 h-index	1125617 13 g-index
17 all docs	17 docs citations	17 times ranked	2742 citing authors

#	Article	IF	Citations
1	Unexpected Nanomolar Inhibition of Carbonic Anhydrase by COX-2-Selective Celecoxib:Â New Pharmacological Opportunities Due to Related Binding Site Recognition. Journal of Medicinal Chemistry, 2004, 47, 550-557.	2.9	426
2	A New Method to Detect Related Function Among Proteins Independent of Sequence and Fold Homology. Journal of Molecular Biology, 2002, 323, 387-406.	2.0	406
3	DoGSiteScorer: a web server for automatic binding site prediction, analysis and druggability assessment. Bioinformatics, 2012, 28, 2074-2075.	1.8	381
4	Combining Global and Local Measures for Structure-Based Druggability Predictions. Journal of Chemical Information and Modeling, 2012, 52, 360-372.	2.5	346
5	Large-Scale Assessment of Binding Free Energy Calculations in Active Drug Discovery Projects. Journal of Chemical Information and Modeling, 2020, 60, 5457-5474.	2.5	147
6	From the Similarity Analysis of Protein Cavities to the Functional Classification of Protein Families Using Cavbase. Journal of Molecular Biology, 2006, 359, 1023-1044.	2.0	89
7	Functional Classification of Protein Kinase Binding Sites Using Cavbase. ChemMedChem, 2007, 2, 1432-1447.	1.6	70
8	An Efficient Method for the Synthesis of Peptide Aldehyde Libraries Employed in the Discovery of Reversible SARS Coronavirus Main Protease (SARSâ€CoV M pro) Inhibitors. ChemBioChem, 2006, 7, 1048-1055.	1.3	50
9	Efficient similarity search in protein structure databases by k-clique hashing. Bioinformatics, 2004, 20, 1522-1526.	1.8	46
10	Discovery and Optimization of 2-Arylquinazolin-4-ones into a Potent and Selective Tankyrase Inhibitor Modulating Wnt Pathway Activity. Journal of Medicinal Chemistry, 2019, 62, 7897-7909.	2.9	26
11	CACHE (Critical Assessment of Computational Hit-finding Experiments): A publicâ€“private partnership benchmarking initiative to enable the development of computational methods for hit-finding. Nature Reviews Chemistry, 2022, 6, 287-295.	13.8	22
12	Predicting enzymatic function from global binding site descriptors. Proteins: Structure, Function and Bioinformatics, 2013, 81, 479-489.	1.5	13
13	Graph Alignment: Fuzzy Pattern Mining for the Structural Analysis of Protein Active Sites. IEEE International Conference on Fuzzy Systems, 2007, , .	0.0	1