

Daniel Kuhn

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2658081/publications.pdf>

Version: 2024-02-01

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