Sebastian Salentin

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7497761/publications.pdf

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		686830	996533
15	2,557	13	15
papers	citations	h-index	g-index

17	17	17	3475
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	PLIP: fully automated proteinâ€“ligand interaction profiler. Nucleic Acids Research, 2015, 43, W443-W447.	6.5	1,381
2	PLIP 2021: expanding the scope of the proteinâ€“ligand interaction profiler to DNA and RNA. Nucleic Acids Research, 2021, 49, W530-W534.	6.5	691
3	Current and Future Roles of Artificial Intelligence in Medicinal Chemistry Synthesis. Journal of Medicinal Chemistry, 2020, 63, 8667-8682.	2.9	118
4	Polypharmacology rescored: Proteinâ€“ligand interaction profiles for remote binding site similarity assessment. Progress in Biophysics and Molecular Biology, 2014, 116, 174-186.	1.4	92
5	UniLectin3D, a database of carbohydrate binding proteins with curated information on 3D structures and interacting ligands. Nucleic Acids Research, 2019, 47, D1236-D1244.	6.5	82
6	From malaria to cancer: Computational drug repositioning of amodiaquine using PLIP interaction patterns. Scientific Reports, 2017, 7, 11401.	1.6	41
7	Discovery of Mycobacterium tuberculosis InhA Inhibitors by Binding Sites Comparison and Ligands Prediction. Journal of Medicinal Chemistry, 2016, 59, 11069-11078.	2.9	26
8	The structural basis of the genetic code: amino acid recognition by aminoacyl-tRNA synthetases. Scientific Reports, 2020, 10, 12647.	1.6	23
9	Repositioned Drugs for Chagas Disease Unveiled via Structure-Based Drug Repositioning. International Journal of Molecular Sciences, 2020, 21, 8809.	1.8	19
10	Structure-based drug repositioning explains ibrutinib as VEGFR2 inhibitor. PLoS ONE, 2020, 15, e0233089.	1.1	19
11	Backbone Brackets and Arginine Tweezers delineate Class I and Class II aminoacyl tRNA synthetases. PLoS Computational Biology, 2018, 14, e1006101.	1.5	17
12	Computational Drug Repositioning for Chagas Disease Using Protein-Ligand Interaction Profiling. International Journal of Molecular Sciences, 2020, 21, 4270.	1.8	16
13	Computational Drug Repositioning by Target Hopping: A Use Case in Chagas Disease. Current Pharmaceutical Design, 2016, 22, 3124-3134.	0.9	16
14	Structural binding site comparisons reveal Crizotinib as a novel LRRK2 inhibitor. Computational and Structural Biotechnology Journal, 2021, 19, 3674-3681.	1.9	9
15	MAGPIE: Simplifying access and execution of computational models in the life sciences. PLoS Computational Biology, 2017, 13, e1005898.	1.5	6