

# Tailong Lei

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8170692/publications.pdf>

Version: 2024-02-01

12  
papers

635  
citations

840776

11  
h-index

1199594

12  
g-index

12  
all docs

12  
docs citations

12  
times ranked

744  
citing authors

#	ARTICLE	IF	CITATIONS
1	ADMET evaluation in drug discovery: 15. Accurate prediction of rat oral acute toxicity using relevance vector machine and consensus modeling. <i>Journal of Cheminformatics</i> , 2016, 8, 6.	6.1	102
2	ADMET Evaluation in Drug Discovery. 19. Reliable Prediction of Human Cytochrome P450 Inhibition Using Artificial Intelligence Approaches. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4587-4601.	5.4	85
3	Assessing the performance of MM/PBSA and MM/GBSA methods. 8. Predicting binding free energies and poses of protein-RNA complexes. <i>Rna</i> , 2018, 24, 1183-1194.	3.5	84
4	Do we need different machine learning algorithms for QSAR modeling? A comprehensive assessment of 16 machine learning algorithms on 14 QSAR data sets. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	70
5	ADMET Evaluation in Drug Discovery. 18. Reliable Prediction of Chemical-Induced Urinary Tract Toxicity by Boosting Machine Learning Approaches. <i>Molecular Pharmaceutics</i> , 2017, 14, 3935-3953.	4.6	66
6	ADMET Evaluation in Drug Discovery. Part 17: Development of Quantitative and Qualitative Prediction Models for Chemical-Induced Respiratory Toxicity. <i>Molecular Pharmaceutics</i> , 2017, 14, 2407-2421.	4.6	59
7	farPPI: a webserver for accurate prediction of protein-ligand binding structures for small-molecule PPI inhibitors by MM/PB(GB)SA methods. <i>Bioinformatics</i> , 2019, 35, 1777-1779.	4.1	59
8	ADMET evaluation in drug discovery. 20. Prediction of breast cancer resistance protein inhibition through machine learning. <i>Journal of Cheminformatics</i> , 2020, 12, 16.	6.1	45
9	Reliability of Docking-Based Virtual Screening for GPCR Ligands with Homology Modeled Structures: A Case Study of the Angiotensin II Type I Receptor. <i>ACS Chemical Neuroscience</i> , 2019, 10, 677-689.	3.5	23
10	Comprehensive assessment of nine docking programs on type II kinase inhibitors: prediction accuracy of sampling power, scoring power and screening power. <i>Briefings in Bioinformatics</i> , 2018, , .	6.5	16
11	Importance of protein flexibility on molecular recognition: modeling binding mechanisms of aminopyrazine inhibitors to Nek2. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 5591-5605.	2.8	15
12	Importance of Incorporating Protein Flexibility in Molecule Modeling: A Theoretical Study on Type I1/2 NIK Inhibitors. <i>Frontiers in Pharmacology</i> , 2019, 10, 345.	3.5	11