

# CITATION REPORT

List of articles citing

Adverse drug reaction prediction using scores produced by large-scale drug-protein target docking on high-performance computing machines

DOI: 10.1371/journal.pone.0106298  
PLoS ONE, 2014, 9, e106298.

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**Version:** 2024-04-23

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#	Paper	IF	Citations
49	Supercomputers predict important ADRs for drug candidates. <i>Reactions Weekly</i> , <b>2014</b> , 1526, 13-13	0	
48	Opportunities for drug repositioning from phenome-wide association studies. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 342-5	44.5	91
47	Caffeoylquinic acids competitively inhibit pancreatic lipase through binding to the catalytic triad. <i>International Journal of Biological Macromolecules</i> , <b>2015</b> , 80, 529-35	7.9	38
46	Systems biology approaches for identifying adverse drug reactions and elucidating their underlying biological mechanisms. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , <b>2016</b> , 8, 104-22	6.6	30
45	Detection of new drug indications from electronic medical records. <b>2016</b> ,		
44	System pharmacology: Application of network theory in predicting potential adverse drug reaction based on gene expression data. <b>2016</b> ,		2
43	Impact of Binding Site Comparisons on Medicinal Chemistry and Rational Molecular Design. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 4121-51	8.3	74
42	Ensemble-based docking: From hit discovery to metabolism and toxicity predictions. <i>Bioorganic and Medicinal Chemistry</i> , <b>2016</b> , 24, 4928-4935	3.4	30
41	Improving drug safety: From adverse drug reaction knowledge discovery to clinical implementation. <i>Methods</i> , <b>2016</b> , 110, 14-25	4.6	20
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39	Non-Specificity of Drug-Target Interactions [Consequences for Drug Discovery. <i>ACS Symposium Series</i> , <b>2016</b> , 91-142	0.4	0
38	An improved approach for predicting drug-target interaction: proteochemometrics to molecular docking. <i>Molecular BioSystems</i> , <b>2016</b> , 12, 1006-14		18
37	In silico assessment of adverse drug reactions and associated mechanisms. <i>Drug Discovery Today</i> , <b>2016</b> , 21, 58-71	8.8	34
36	CADD medicine: design is the potion that can cure my disease. <i>Journal of Computer-Aided Molecular Design</i> , <b>2017</b> , 31, 249-253	4.2	6
35	Discover Toxicology: An Early Safety Assessment Approach. <i>AAPS Advances in the Pharmaceutical Sciences Series</i> , <b>2017</b> , 119-162	0.5	2
34	Identifying the common genetic networks of ADR (adverse drug reaction) clusters and developing an ADR classification model. <i>Molecular BioSystems</i> , <b>2017</b> , 13, 1788-1796		8
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32	Predicting adverse drug reactions through interpretable deep learning framework. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 476	3.6	52
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27	Single-Domain Antibodies and the Promise of Modular Targeting in Cancer Imaging and Treatment. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 273	8.4	46
26	Inferring new relations between medical entities using literature curated term co-occurrences. <i>JAMIA Open</i> , <b>2019</b> , 2, 378-385	2.9	
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13	Virtual screening in drug discovery: a precious tool for a still-demanding challenge. <b>2020</b> , 309-327	0
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4	Machine Learning Prediction of Drug Side Effects in Clinical Trials. <i>SSRN Electronic Journal</i> ,	1
3	A Knowledge Graph Embedding Based Approach to Predict the Adverse Drug Reactions Using a Deep Neural Network. <i>Journal of Biomedical Informatics</i> , <b>2022</b> , 104122	10.2 1
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1	An extensive survey on the use of supervised machine learning techniques in the past two decades for prediction of drug side effects.	0