Heng Luo

List of Publications by Year
in descending order

34 papers	2,906 citations	279487 23 h-index	395343 33 g-index
34 all docs	34 docs citations	34 times ranked	5807 citing authors

#	Article	IF	Citations
1	Study on the Characteristics of Small-Molecule Kinase Inhibitors-Related Drug-Induced Liver Injury. Frontiers in Pharmacology, 2022, 13, 838397.	1.6	0
2	Transparent Super-Repellent Surfaces with Low Haze and High Jet Impact Resistance. ACS Applied Materials & Interfaces, 2021, 13, 13813-13821.	4.0	26
3	Bioinspired â€œSkinâ€•with Cooperative Thermo-Optical Effect for Daytime Radiative Cooling. ACS Applied Materials & Interfaces, 2020, 12, 25286-25293.	4.0	84
4	Machine-Learning Prediction of Oral Drug-Induced Liver Injury (DILI) via Multiple Features and Endpoints. BioMed Research International, 2020, 2020, 1-10.	0.9	9
5	Carbon Vesicles: A Symmetryâ€Breaking Strategy for Wideâ€Band and Solventâ€Processable Ultrablack Coating Materials. Advanced Functional Materials, 2020, 30, 1909877.	7.8	18
6	Combining Docking Pose Rank and Structure with Deep Learning Improves Proteinâ€“Ligand Binding Mode Prediction over a Baseline Docking Approach. Journal of Chemical Information and Modeling, 2020, 60, 4170-4179.	2.5	64
7	Superhydrophobic/Superhydrophilic Janus Fabrics Reducing Blood Loss. Advanced Healthcare Materials, 2018, 7, e1701086.	3.9	94
8	Molecular Docking for Prediction and Interpretation of Adverse Drug Reactions. Combinatorial Chemistry and High Throughput Screening, 2018, 21, 314-322.	0.6	14
9	sNebula, a network-based algorithm to predict binding between human leukocyte antigens and peptides. Scientific Reports, 2016, 6, 32115.	1.6	34
10	DPDR-CPI, a server that predicts Drug Positioning and Drug Repositioning via Chemical-Protein Interactome. Scientific Reports, 2016, 6, 35996.	1.6	27
11	Applying network analysis and Nebula (neighbor-edges based and unbiased leverage algorithm) to ToxCast data. Environment International, 2016, 89-90, 81-92.	4.8	6
12	HLA-B*59:01: a marker for Stevensâ€“Johnson syndrome/toxic epidermal necrolysis caused by methazolamide in Han Chinese. Pharmacogenomics Journal, 2016, 16, 83-87.	0.9	50
13	Molecular Docking for Identification of Potential Targets for Drug Repurposing. Current Topics in Medicinal Chemistry, 2016, 16, 3636-3645.	1.0	31
14	Homology Model and Ligand Binding Interactions of the Extracellular Domain of the Human <i>Î±</i>4<i>Î²</i>2 Nicotinic Acetylcholine Receptor. Journal of Biomedical Science and Engineering, 2016, 09, 41-100.	0.2	5
15	Machine Learning Methods for Predicting HLA-Peptide Binding Activity. Bioinformatics and Biology Insights, 2015, 9s3, BBI.S29466.	1.0	68
16	Understanding and predicting binding between human leukocyte antigens (HLAs) and peptides by network analysis. BMC Bioinformatics, 2015, 16, S9.	1.2	19
17	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	3.8	325
18	Development and Validation of Decision Forest Model for Estrogen Receptor Binding Prediction of Chemicals Using Large Data Sets. Chemical Research in Toxicology, 2015, 28, 2343-2351.	1.7	47

#	Article	IF	Citations
19	Comparing genetic variants detected in the 1000 genomes project with SNPs determined by the International HapMap Consortium. Journal of Genetics, 2015, 94, 731-740.	0.4	20
20	Drug Repositioning for Diabetes Based on 'Omics' Data Mining. PLoS ONE, 2015, 10, e0126082.	1.1	74
21	Estrogenic Activity Data Extraction and in Silico Prediction Show the Endocrine Disruption Potential of Bisphenol A Replacement Compounds. Chemical Research in Toxicology, 2015, 28, 1784-1795.	1.7	68
22	HLADR: a database system for enhancing the discovery of biomarkers for predicting human leukocyte antigen-mediated idiosyncratic adverse drug reactions. Biomarkers in Medicine, 2015, 9, 1079-1093.	0.6	7
23	Molecular Docking to Identify Associations Between Drugs and Class I Human Leukocyte Antigens for Predicting Idiosyncratic Drug Reactions. Combinatorial Chemistry and High Throughput Screening, 2015, 18, 296-304.	0.6	69
24	HLA-B*13:01 is associated with salazosulfapyridine-induced drug rash with eosinophilia and systemic symptoms in Chinese Han population. Pharmacogenomics, 2014, 15, 1461-1469.	0.6	40
25	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. Nature Communications, 2014, 5, 3230.	5.8	316
26	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	9.4	883
27	DDI-CPI, a server that predicts drugâ€“drug interactions through implementing the chemicalâ€“protein interactome. Nucleic Acids Research, 2014, 42, W46-W52.	6.5	63
28	Haystack, a web-based tool for metabolomics research. BMC Bioinformatics, 2014, 15, S12.	1.2	11
29	Competitive molecular docking approach for predicting estrogen receptor subtype Î± agonists and antagonists. BMC Bioinformatics, 2014, 15, S4.	1.2	58
30	Whole genome sequencing of 35 individuals provides insights into the genetic architecture of Korean population. BMC Bioinformatics, 2014, 15, S6.	1.2	34
31	FOLDNA, a Web Server for Self-Assembled DNA Nanostructure Autoscaffolds and Autostaples. Journal of Nanotechnology, 2012, 2012, 1-5.	1.5	3
32	DRAR-CPI: a server for identifying drug repositioning potential and adverse drug reactions via the chemicalâ€“protein interactome. Nucleic Acids Research, 2011, 39, W492-W498.	6.5	189
33	Exploring Off-Targets and Off-Systems for Adverse Drug Reactions via Chemical-Protein Interactome â€” Clozapine-Induced Agranulocytosis as a Case Study. PLoS Computational Biology, 2011, 7, e1002016.	1.5	93
34	SePreSA: a server for the prediction of populations susceptible to serious adverse drug reactions implementing the methodology of a chemicalâ€“protein interactome. Nucleic Acids Research, 2009, 37, W406-W412.	6.5	57