Leihong Wu

List of Publications by Year
in descending order

114 papers	10,081 citations	61984 43 h-index	36028 97 g-index
123 all docs	123 docs citations	123 times ranked	12476 citing authors

#	Article	IF	Citations
1	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. Nature Biotechnology, 2006, 24, 1151-1161.	17.5	1,927
2	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
3	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. Nature Biotechnology, 2014, 32, 926-932.	17.5	420
4	Rat toxicogenomic study reveals analytical consistency across microarray platforms. Nature Biotechnology, 2006, 24, 1162-1169.	17.5	389
5	FDA-approved drug labeling for the study of drug-induced liver injury. Drug Discovery Today, 2011, 16, 697-703.	6.4	337
6	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
7	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. Nature Communications, 2014, 5, 3230.	12.8	316
8	High lipophilicity and high daily dose of oral medications are associated with significant risk for drug-induced liver injury. Hepatology, 2013, 58, 388-396.	7.3	288
9	DILIrank: the largest reference drug list ranked by the risk for developing drug-induced liver injury in humans. Drug Discovery Today, 2016, 21, 648-653.	6.4	248
10	Mold^2, Molecular Descriptors from 2D Structures for Chemoinformatics and Toxicoinformatics. Journal of Chemical Information and Modeling, 2008, 48, 1337-1344.	5.4	241
11	Decision Forest:‰ Combining the Predictions of Multiple Independent Decision Tree Models. Journal of Chemical Information and Computer Sciences, 2003, 43, 525-531.	2.8	199
12	ArrayTrack--supporting toxicogenomic research at the U.S. Food and Drug Administration National Center for Toxicological Research.. Environmental Health Perspectives, 2003, 111, 1819-1826.	6.0	197
13	A Decade of Toxicogenomic Research and Its Contribution to Toxicological Science. Toxicological Sciences, 2012, 130, 217-228.	3.1	153
14	An investigation of biomarkers derived from legacy microarray data for their utility in the RNA-seq era. Genome Biology, 2014, 15, 523.	8.8	147
15	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	17.5	126
16	Toward predictive models for drug-induced liver injury in humans: are we there yet?. Biomarkers in Medicine, 2014, 8, 201-213.	1.4	124
17	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
18	Toxicogenomics: A 2020 Vision. Trends in Pharmacological Sciences, 2019, 40, 92-103.	8.7	116

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19	A Network Pharmacology Study of Chinese Medicine QiShenYiQi to Reveal Its Underlying Multi-Compound, Multi-Target, Multi-Pathway Mode of Action. PLoS ONE, 2014, 9, e95004.	2.5	104
20	Development of public toxicogenomics software for microarray data management and analysis. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2004, 549, 241-253.	1.0	98
21	Quantitative Structure-Activity Relationship Models for Predicting Drug-Induced Liver Injury Based on FDA-Approved Drug Labeling Annotation and Using a Large Collection of Drugs. Toxicological Sciences, 2013, 136, 242-249.	3.1	96
22	Assessment of Prediction Confidence and Domain Extrapolation of Two Structure-Activity Relationship Models for Predicting Estrogen Receptor Binding Activity. Environmental Health Perspectives, 2004, 112, 1249-1254.	6.0	87
23	Erratum to â€œA Network Pharmacology Approach to Evaluating the Efficacy of Chinese Medicine Using Genome-Wide Transcriptional Expression Dataâ€. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-1.	1.2	84
24	Development of Decision Forest Models for Prediction of Drug-Induced Liver Injury in Humans Using A Large Set of FDA-approved Drugs. Scientific Reports, 2017, 7, 17311.	3.3	84
25	Translating Clinical Findings into Knowledge in Drug Safety Evaluation - Drug Induced Liver Injury Prediction System (DILIps). PLoS Computational Biology, 2011, 7, e1002310.	3.2	80
26	Assessment of Prediction Confidence and Domain Extrapolation of Two Structureâ€"Activity Relationship Models for Predicting Estrogen Receptor Binding Activity. Environmental Health Perspectives, 2004, 112, 1249-1254.	6.0	78
27	Biomarkers for drug-induced liver injury. Expert Review of Gastroenterology and Hepatology, 2010, 4, 225-234.	3.0	78
28	Drug-induced liver injury severity and toxicity (DILIst): binary classification of 1279 drugs by human hepatotoxicity. Drug Discovery Today, 2020, 25, 201-208.	6.4	77
29	A Model to predict severity of drugâ€induced liver injury in humans. Hepatology, 2016, 64, 931-940.	7.3	74
30	Lessons Learned from Two Decades of Anticancer Drugs. Trends in Pharmacological Sciences, 2017, 38, 852-872.	8.7	74
31	Comparing SVM and ANN based Machine Learning Methods for Species Identification of Food Contaminating Beetles. Scientific Reports, 2018, 8, 6532.	3.3	72
32	ArrayTrack: An FDA and Public Genomic Tool. Methods in Molecular Biology, 2009, 563, 379-398.	0.9	67
33	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	17.5	66
34	Is Toxicogenomics a More Reliable and Sensitive Biomarker than Conventional Indicators from Rats To Predict Drug-Induced Liver Injury in Humans?. Chemical Research in Toxicology, 2012, 25, 122-129.	3.3	57
35	MicroRNA hsa-miR-370-3p suppresses the expression and induction of CYP2D6 by facilitating mRNA degradation. Biochemical Pharmacology, 2017, 140, 139-149.	4.4	57
36	A testing strategy to predict risk for drug-induced liver injury in humans using high-content screen assays and the â€˜rule-of-twoâ€™ model. Archives of Toxicology, 2014, 88, 1439-1449.	4.2	54

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37	The Liver Toxicity Knowledge Base (LKTB) and drug-induced liver injury (DILI) classification for assessment of human liver injury. Expert Review of Gastroenterology and Hepatology, 2018, 12, 31-38.	3.0	54
38	The Liver Toxicity Biomarker Study: Phase I Design and Preliminary Results. Toxicologic Pathology, 2009, 37, 52-64.	1.8	53
39	Comprehensive Assessments of RNA-seq by the SEQC Consortium: FDA-Led Efforts Advance Precision Medicine. Pharmaceutics, 2016, 8, 8.	4.5	53
40	Associations of Drug Lipophilicity and Extent of Metabolism with Drug-Induced Liver Injury. International Journal of Molecular Sciences, 2017, 18, 1335.	4.1	53
41	DNA Microarrays Are Predictive of Cancer Prognosis: A Re-evaluation. Clinical Cancer Research, 2010, 16, 629-636.	7.0	52
42	Identifying roles of â€œJun-Chen-Zuo-Shiâ€•component herbs of QiShenYiQi formula in treating acute myocardial ischemia by network pharmacology. Chinese Medicine, 2014, 9, 24.	4.0	51
43	Regulation of cytochrome P450 expression by microRNAs and long noncoding RNAs: Epigenetic mechanisms in environmental toxicology and carcinogenesis. Journal of Environmental Science and Health, Part C: Environmental Carcinogenesis and Ecotoxicology Reviews, 2019, 37, 180-214.	2.9	50
44	Identification of the effective constituents for anti-inflammatory activity of Ju-Zhi-Jiang-Tang, an ancient traditional Chinese medicine formula. Journal of Chromatography A, 2014, 1348, 105-124.	3.7	45
45	A Network Pharmacology Approach to Evaluating the Efficacy of Chinese Medicine Using Genome-Wide Transcriptional Expression Data. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-8.	1.2	42
46	Multiple microRNAs function as self-protective modules in acetaminophen-induced hepatotoxicity in humans. Archives of Toxicology, 2018, 92, 845-858.	4.2	42
47	DeepDILI: Deep Learning-Powered Drug-Induced Liver Injury Prediction Using Model-Level Representation. Chemical Research in Toxicology, 2021, 34, 550-565.	3.3	41
48	Relating Anatomical Therapeutic Indications by the Ensemble Similarity of Drug Sets. Journal of Chemical Information and Modeling, 2013, 53, 2154-2160.	5.4	37
49	Evaluation of multiple mechanism-based toxicity endpoints in primary cultured human hepatocytes for the identification of drugs with clinical hepatotoxicity: Results from 152 marketed drugs with known liver injury profiles. Chemico-Biological Interactions, 2016, 255, 3-11.	4.0	37
50	A systematic evaluation of microRNAs in regulating human hepatic CYP2E1. Biochemical Pharmacology, 2017, 138, 174-184.	4.4	36
51	In vitro to in vivo extrapolation for drug-induced liver injury using a pair ranking method. ALTEX: Alternatives To Animal Experimentation, 2017, 34, 399-407.	1.5	35
52	Trade-off Predictivity and Explainability for Machine-Learning Powered Predictive Toxicology: An in-Depth Investigation with Tox21 Data Sets. Chemical Research in Toxicology, 2021, 34, 541-549.	3.3	31
53	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. Scientific Data, 2014, 1, 140021.	5.3	30
54	Mechanistically linked serum miRNAs distinguish between drug induced and fatty liver disease of different grades. Scientific Reports, 2016, 6, 23709.	3.3	29

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55	Study of serious adverse drug reactions using FDA-approved drug labeling and MedDRA. BMC Bioinformatics, 2019, 20, 97.	2.6	29
56	A deep learning model to recognize food contaminating beetle species based on elytra fragments. Computers and Electronics in Agriculture, 2019, 166, 105002.	7.7	28
57	Toxicogenomic analysis of the particle dose- and size-response relationship of silica particles-induced toxicity in mice. Nanotechnology, 2013, 24, 015106.	2.6	27
58	Transcriptional Responses Reveal Similarities Between Preclinical Rat Liver Testing Systems. Frontiers in Genetics, 2018, 9, 74.	2.3	27
59	Constructing a robust protein-protein interaction network by integrating multiple public databases. BMC Bioinformatics, 2011, 12, S7.	2.6	24
60	T2D@ZJU: a knowledgebase integrating heterogeneous connections associated with type 2 diabetes mellitus. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat052.	3.0	24
61	Deep Learning on High-Throughput Transcriptomics to Predict Drug-Induced Liver Injury. Frontiers in Bioengineering and Biotechnology, 2020, 8, 562677.	4.1	24
62	A Unifying Ontology to Integrate Histological and Clinical Observations for Drug-Induced Liver Injury. American Journal of Pathology, 2013, 182, 1180-1187.	3.8	23
63	Integrating Drug's Mode of Action into Quantitative Structure–Activity Relationships for Improved Prediction of Drug-Induced Liver Injury. Journal of Chemical Information and Modeling, 2017, 57, 1000-1006.	5.4	23
64	Tox-GAN: An Artificial Intelligence Approach Alternative to Animal Studies—A Case Study With Toxicogenomics. Toxicological Sciences, 2022, 186, 242-259.	3.1	23
65	Comprehensive RNA-Seq transcriptomic profiling across 11 organs, 4 ages, and 2 sexes of Fischer 344 rats. Scientific Data, 2014, 1, 140013.	5.3	22
66	Direct comparison of performance of single nucleotide variant calling in human genome with alignment-based and assembly-based approaches. Scientific Reports, 2017, 7, 10963.	3.3	22
67	Fabry's disease and stroke: Effectiveness of enzyme replacement therapy (ERT) in stroke prevention, a review with meta-analysis. Journal of Clinical Neuroscience, 2019, 65, 83-86.	1.5	22
68	DeepCarc: Deep Learning-Powered Carcinogenicity Prediction Using Model-Level Representation. Frontiers in Artificial Intelligence, 2021, 4, 757780.	3.4	22
69	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. Scientific Data, 2014, 1, 140020.	5.3	21
70	The Development of a Database for Herbal and Dietary Supplement Induced Liver Toxicity. International Journal of Molecular Sciences, 2018, 19, 2955.	4.1	21
71	ArrayTrack: a free FDA bioinformatics tool to support emerging biomedical research -- an update. Human Genomics, 2010, 4, 428-34.	2.9	19
72	Can Transcriptomic Profiles from Cancer Cell Lines Be Used for Toxicity Assessment?. Chemical Research in Toxicology, 2020, 33, 271-280.	3.3	18

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73	Consensus Ranking Approach to Understanding the Underlying Mechanism With QSAR. Journal of Chemical Information and Modeling, 2010, 50, 1941-1948.	5.4	17
74	LTMap: a web server for assessing the potential liver toxicity by genome–wide transcriptional expression data. Journal of Applied Toxicology, 2014, 34, 805-809.	2.8	16
75	Novel reference genes in colorectal cancer identify a distinct subset of high stage tumors and their associated histologically normal colonic tissues. BMC Medical Genetics, 2019, 20, 138.	2.1	16
76	Long noncoding RNA LINC00844-mediated molecular network regulates expression of drug metabolizing enzymes and nuclear receptors in human liver cells. Archives of Toxicology, 2020, 94, 1637-1653.	4.2	16
77	Systematic Identification of Molecular Targets and Pathways Related to Human Organ Level Toxicity. Chemical Research in Toxicology, 2021, 34, 412-421.	3.3	16
78	R-ODAF: Omics data analysis framework for regulatory application. Regulatory Toxicology and Pharmacology, 2022, 131, 105143.	2.7	16
79	Towards the development of an omics data analysis framework. Regulatory Toxicology and Pharmacology, 2020, 112, 104621.	2.7	15
80	Cross-Platform Comparison of Microarray-Based Multiple-Class Prediction. PLoS ONE, 2011, 6, e16067.	2.5	14
81	MicroRNAs hsa-miR-495-3p and hsa-miR-486-5p suppress basal and rifampicin-induced expression of human sulfotransferase 2A1 (SULT2A1) by facilitating mRNA degradation. Biochemical Pharmacology, 2019, 169, 113617.	4.4	14
82	Selecting a single model or combining multiple models for microarray-based classifier development? â€" A comparative analysis based on large and diverse datasets generated from the MAQC-II project. BMC Bioinformatics, 2011, 12, S3.	2.6	13
83	Challenges, Solutions, and Quality Metrics of Personal Genome Assembly in Advancing Precision Medicine. Pharmaceutics, 2016, 8, 15.	4.5	13
84	The landscape of hepatobiliary adverse reactions across 53 herbal and dietary supplements reveals immune-mediated injury as a common cause of hepatitis. Archives of Toxicology, 2020, 94, 273-293.	4.2	13
85	CHD@ZJU: a knowledgebase providing network-based research platform on coronary heart disease. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat047.	3.0	12
86	Technical advance in targeted NGS analysis enables identification of lung cancer risk-associated low frequency TP53, PIK3CA, and BRAF mutations in airway epithelial cells. BMC Cancer, 2019, 19, 1081.	2.6	12
87	Computational Toxicology. Chemical Research in Toxicology, 2020, 33, 687-688.	3.3	12
88	Integrating adverse outcome pathways (AOPs) and high throughput in vitro assays for better risk evaluations, a study with drug-induced liver injury (DILI). ALTEX: Alternatives To Animal Experimentation, 2020, 37, 187-196.	1.5	12
89	Species Identification of Food Contaminating Beetles by Recognizing Patterns in Microscopic Images of Elytra Fragments. PLoS ONE, 2016, 11, e0157940.	2.5	11
90	Identification of Translational microRNA Biomarker Candidates for Ketoconazole-Induced Liver Injury Using Next-Generation Sequencing. Toxicological Sciences, 2020, 179, 31-43.	3.1	10

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91	DLI-IT: a deep learning approach to drug label identification through image and text embedding. BMC Medical Informatics and Decision Making, 2020, 20, 68.	3.0	10
92	Introduction to Special Issue: Computational Toxicology. Chemical Research in Toxicology, 2021, 34, 171-175.	3.3	10
93	Enhanced QSAR Model Performance by Integrating Structural and Gene Expression Information. Molecules, 2013, 18, 10789-10801.	3.8	9
94	NETBAGs: a network-based clustering approach with gene signatures for cancer subtyping analysis. Biomarkers in Medicine, 2015, 9, 1053-1065.	1.4	9
95	Development of a Battery of *In Silico* Prediction Tools for Drug-Induced Liver Injury from the Vantage Point of Translational Safety Assessment. Chemical Research in Toxicology, 2021, 34, 601-615.	3.3	9
96	Advancing NGS quality control to enable measurement of actionable mutations in circulating tumor DNA. Cell Reports Methods, 2021, 1, 100106.	2.9	9
97	Impact of Sequencing Depth and Library Preparation on Toxicological Interpretation of RNA-Seq Data in a â€œThree-Sampleâ€•Scenario. Chemical Research in Toxicology, 2021, 34, 529-540.	3.3	8
98	Determination of Minimum Training Sample Size for Microarray-Based Cancer Outcome Predictionâ€"An Empirical Assessment. PLoS ONE, 2013, 8, e68579.	2.5	8
99	Network-based Assessment on Chemical-induced Cholestatic Liver Injury. Current Topics in Medicinal Chemistry, 2016, 16, 3668-3677.	2.1	8
100	Bioactivity Signatures of Drugs vs. Environmental Chemicals Revealed by Tox21 High-Throughput Screening Assays. Frontiers in Big Data, 2019, 2, 50.	2.9	7
101	Competitive docking model for prediction of the human nicotinic acetylcholine receptor Î±7 binding of tobacco constituents. Oncotarget, 2018, 9, 16899-16916.	1.8	7
102	Shifting from Population-wide to Personalized Cancer Prognosis with Microarrays. PLoS ONE, 2012, 7, e29534.	2.5	6
103	Coordinated Regulation of UGT2B15 Expression by Long Noncoding RNA LINC00574 and hsa-miR-129-5p in HepaRG Cells. Drug Metabolism and Disposition, 2020, 48, 297-306.	3.3	6
104	Landscape of circRNAs Across 11 Organs and 4 Ages in Fischer 344 Rats. Chemical Research in Toxicology, 2021, 34, 240-246.	3.3	6
105	Does Applicability Domain Exist in Microarray-Based Genomic Research?. PLoS ONE, 2010, 5, e11055.	2.5	5
106	HetEnc: a deep learning predictive model for multi-type biological dataset. BMC Genomics, 2019, 20, 638.	2.8	4
107	Editorial: Integrative Toxicogenomics: Analytical Strategies to Amalgamate Exposure Effects With Genomic Sciences. Frontiers in Genetics, 2018, 9, 563.	2.3	2
108	MicroRNA-Dependent Gene Regulation of the Human Cytochrome P450. , 2019, , 129-138.		2

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109	Integrative approaches for studying the role of noncoding RNAs in influencing drug efficacy and toxicity. Expert Opinion on Drug Metabolism and Toxicology, 2022, 18, 151-163.	3.3	2
110	Optimized imaging methods for species-level identification of food-contaminating beetles. Scientific Reports, 2021, 11, 7957.	3.3	1
111	Predicting the Risks of Drug-Induced Liver Injury in Humans Utilizing Computational Modeling. Challenges and Advances in Computational Chemistry and Physics, 2019, , 259-278.	0.6	0
112	Abstract 1556: Algorithms for discovery of somatic single nucleotide mutation display specific artifacts and different detection capabilities under the effect of read coverage and sample heterogeneity. , 2017, , .		0
113	Abstract 1623: Inter-laboratory harmonization of next generation sequencing somatic mutation assays for cancer response prediction. , 2018, , .		0
114	Abstract 432: Novel method for NGS analysis of actionable mutations in circulating tumor DNA specimens: improved quality control and 20-fold lower sequencing required. , 2019, , .		0