

Zhichao Liu

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

4,035
citations

172207

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128067

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g-index

95
all docs

95
docs citations

95
times ranked

5164
citing authors

#	ARTICLE	IF	CITATIONS
1	AI-powered drug repurposing for developing COVID-19 treatments. , 2024, , 144-154.		4
2	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. <i>Genome Biology</i> , 2022, 23, 2.	3.8	18
3	Towards accurate and reliable resolution of structural variants for clinical diagnosis. <i>Genome Biology</i> , 2022, 23, 68.	3.8	34
4	Tox-GAN: An Artificial Intelligence Approach Alternative to Animal Studiesâ€™A Case Study With Toxicogenomics. <i>Toxicological Sciences</i> , 2022, 186, 242-259.	1.4	23
5	Editorial: Emerging Technologies Powering Rare and Neglected Disease Diagnosis and Therapy Development. <i>Frontiers in Pharmacology</i> , 2022, 13, 877401.	1.6	1
6	Best practice and reproducible science are required to advance artificial intelligence in real-world applications. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	1
7	Improving cardiotoxicity prediction in cancer treatment: integration of conventional circulating biomarkers and novel exploratory tools. <i>Archives of Toxicology</i> , 2021, 95, 791-805.	1.9	4
8	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	9.4	126
9	Unraveling Gene Fusions for Drug Repositioning in High-Risk Neuroblastoma. <i>Frontiers in Pharmacology</i> , 2021, 12, 608778.	1.6	4
10	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	3.8	20
11	Optimized imaging methods for species-level identification of food-contaminating beetles. <i>Scientific Reports</i> , 2021, 11, 7957.	1.6	1
12	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , 2021, 22, 111.	3.8	29
13	InferBERT: A Transformer-Based Causal Inference Framework for Enhancing Pharmacovigilance. <i>Frontiers in Artificial Intelligence</i> , 2021, 4, 659622.	2.0	19
14	AI-based language models powering drug discovery and development. <i>Drug Discovery Today</i> , 2021, 26, 2593-2607.	3.2	48
15	Towards population-specific pharmacogenomics in the era of next-generation sequencing. <i>Drug Discovery Today</i> , 2021, 26, 1776-1783.	3.2	2
16	X-CNV: genome-wide prediction of the pathogenicity of copy number variations. <i>Genome Medicine</i> , 2021, 13, 132.	3.6	24
17	DICE: A Drug Indication Classification and Encyclopedia for AI-Based Indication Extraction. <i>Frontiers in Artificial Intelligence</i> , 2021, 4, 711467.	2.0	2
18	DeepDILI: Deep Learning-Powered Drug-Induced Liver Injury Prediction Using Model-Level Representation. <i>Chemical Research in Toxicology</i> , 2021, 34, 550-565.	1.7	41

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19	Effect of process parameters on tensile properties of SS 316 prepared by directional energy deposition. <i>Procedia CIRP</i> , 2021, 103, 115-121.	1.0	7
20	DeepCarc: Deep Learning-Powered Carcinogenicity Prediction Using Model-Level Representation. <i>Frontiers in Artificial Intelligence</i> , 2021, 4, 757780.	2.0	22
21	BERT-Based Natural Language Processing of Drug Labeling Documents: A Case Study for Classifying Drug-Induced Liver Injury Risk. <i>Frontiers in Artificial Intelligence</i> , 2021, 4, 729834.	2.0	10
22	Drug-induced liver injury severity and toxicity (DIList): binary classification of 1279 drugs by human hepatotoxicity. <i>Drug Discovery Today</i> , 2020, 25, 201-208.	3.2	77
23	Can Transcriptomic Profiles from Cancer Cell Lines Be Used for Toxicity Assessment?. <i>Chemical Research in Toxicology</i> , 2020, 33, 271-280.	1.7	18
24	Drug Repositioning for Noonan and LEOPARD Syndromes by Integrating Transcriptomics With a Structure-Based Approach. <i>Frontiers in Pharmacology</i> , 2020, 11, 927.	1.6	9
25	FDALabel for drug repurposing studies and beyond. <i>Nature Biotechnology</i> , 2020, 38, 1378-1379.	9.4	8
26	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. <i>Nucleic Acids Research</i> , 2020, 48, 8320-8331.	6.5	19
27	Deep Learning on High-Throughput Transcriptomics to Predict Drug-Induced Liver Injury. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 562677.	2.0	24
28	Linking Pharmacogenomic Information on Drug Safety and Efficacy with Ethnic Minority Populations. <i>Pharmaceutics</i> , 2020, 12, 1021.	2.0	3
29	Identification of Translational microRNA Biomarker Candidates for Ketoconazole-Induced Liver Injury Using Next-Generation Sequencing. <i>Toxicological Sciences</i> , 2020, 179, 31-43.	1.4	10
30	Study of pharmacogenomic information in FDA-approved drug labeling to facilitate application of precision medicine. <i>Drug Discovery Today</i> , 2020, 25, 813-820.	3.2	29
31	Integrating adverse outcome pathways (AOPs) and high throughput in vitro assays for better risk evaluations, a study with drug-induced liver injury (DILI). <i>ALTEX: Alternatives To Animal Experimentation</i> , 2020, 37, 187-196.	0.9	12
32	Editorial: Advancing Genomics for Rare Disease Diagnosis and Therapy Development. <i>Frontiers in Pharmacology</i> , 2020, 11, 598889.	1.6	0
33	Drug-Induced Rhabdomyolysis Atlas (DIRA) for idiosyncratic adverse drug reaction management. <i>Drug Discovery Today</i> , 2019, 24, 9-15.	3.2	22
34	Five-Feature Model for Developing the Classifier for Synergistic vs. Antagonistic Drug Combinations Built by XGBoost. <i>Frontiers in Genetics</i> , 2019, 10, 600.	1.1	41
35	Toward Clinical Implementation of Next-Generation Sequencing-Based Genetic Testing in Rare Diseases: Where Are We?. <i>Trends in Genetics</i> , 2019, 35, 852-867.	2.9	65
36	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. <i>Biochemical Pharmacology</i> , 2019, 169, 113617.	2.0	14

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37	A deep learning model to recognize food contaminating beetle species based on elytra fragments. Computers and Electronics in Agriculture, 2019, 166, 105002.	3.7	28
38	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
39	A Pair Ranking (PRank) Method for Assessing Assay Transferability Among the Toxicogenomics Testing Systems. Challenges and Advances in Computational Chemistry and Physics, 2019, , 159-180.	0.6	0
40	Study of serious adverse drug reactions using FDA-approved drug labeling and MedDRA. BMC Bioinformatics, 2019, 20, 97.	1.2	29
41	Similarities and differences between variants called with human reference genome HG19 or HG38. BMC Bioinformatics, 2019, 20, 101.	1.2	33
42	Toxicogenomics: A 2020 Vision. Trends in Pharmacological Sciences, 2019, 40, 92-103.	4.0	116
43	Drug-Induced Liver Injury (DILI) Classification and Its Application on Human DILI Risk Prediction. Methods in Pharmacology and Toxicology, 2018, , 45-59.	0.1	5
44	Computational drug repositioning for rare diseases in the era of precision medicine. Drug Discovery Today, 2018, 23, 382-394.	3.2	76
45	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.	1.4	54
46	Advancing Genomics for Drug Development and Safety Evaluation. International Journal of Genomics, 2018, 2018, 1-2.	0.8	0
47	Transcriptional Responses Reveal Similarities Between Preclinical Rat Liver Testing Systems. Frontiers in Genetics, 2018, 9, 74.	1.1	27
48	Comparing SVM and ANN based Machine Learning Methods for Species Identification of Food Contaminating Beetles. Scientific Reports, 2018, 8, 6532.	1.6	72
49	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.	2.5	23
50	Lessons Learned from Two Decades of Anticancer Drugs. Trends in Pharmacological Sciences, 2017, 38, 852-872.	4.0	74
51	Mechanistic roles of microRNAs in hepatocarcinogenesis: A study of thioacetamide with multiple doses and time-points of rats. Scientific Reports, 2017, 7, 3054.	1.6	14
52	Scaling bioinformatics applications on HPC. BMC Bioinformatics, 2017, 18, 501.	1.2	9
53	Mutation status coupled with RNA-sequencing data can efficiently identify important non-significantly mutated genes serving as diagnostic biomarkers of endometrial cancer. BMC Bioinformatics, 2017, 18, 472.	1.2	5
54	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.	0.9	35

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55	A novel procedure on next generation sequencing data analysis using text mining algorithm. BMC Bioinformatics, 2016, 17, 213.	1.2	16
56	Potential Reuse of Oncology Drugs in the Treatment of Rare Diseases. Trends in Pharmacological Sciences, 2016, 37, 843-857.	4.0	18
57	Mechanistically linked serum miRNAs distinguish between drug induced and fatty liver disease of different grades. Scientific Reports, 2016, 6, 23709.	1.6	29
58	Application of dynamic topic models to toxicogenomics data. BMC Bioinformatics, 2016, 17, 368.	1.2	22
59	FDA drug labeling: rich resources to facilitate precision medicine, drug safety, and regulatory science. Drug Discovery Today, 2016, 21, 1566-1570.	3.2	38
60	Supporting read-across using biological data. ALTEX: Alternatives To Animal Experimentation, 2016, 33, 167-182.	0.9	78
61	A heuristic approach to determine an appropriate number of topics in topic modeling. BMC Bioinformatics, 2015, 16, S8.	1.2	202
62	Molecular regulation of miRNAs and potential biomarkers in the progression of hepatic steatosis to NASH. Biomarkers in Medicine, 2015, 9, 1189-1200.	0.6	12
63	NETBAGs: a network-based clustering approach with gene signatures for cancer subtyping analysis. Biomarkers in Medicine, 2015, 9, 1053-1065.	0.6	9
64	Deciphering miRNA transcription factor feed-forward loops to identify drug repurposing candidates for cystic fibrosis. Genome Medicine, 2014, 6, 94.	3.6	27
65	Discovering Functional Modules by Topic Modeling RNA-Seq Based Toxicogenomic Data. Chemical Research in Toxicology, 2014, 27, 1528-1536.	1.7	13
66	A phenome-guided drug repositioning through a latent variable model. BMC Bioinformatics, 2014, 15, 267.	1.2	35
67	Of text and gene “ using text mining methods to uncover hidden knowledge in toxicogenomics. BMC Systems Biology, 2014, 8, 93.	3.0	19
68	Drug-Induced Rhabdomyolysis: From Systems Pharmacology Analysis to Biochemical Flux. Chemical Research in Toxicology, 2014, 27, 421-432.	1.7	27
69	Exploring the FDA Adverse Event Reporting System to Generate Hypotheses for Monitoring of Disease Characteristics. Clinical Pharmacology and Therapeutics, 2014, 95, 496-498.	2.3	33
70	A Unifying Ontology to Integrate Histological and Clinical Observations for Drug-Induced Liver Injury. American Journal of Pathology, 2013, 182, 1180-1187.	1.9	23
71	In silico drug repositioning “ what we need to know. Drug Discovery Today, 2013, 18, 110-115.	3.2	153
72	Omics Biomarkers in Risk Assessment. , 2013, , 195-213.		2

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73	The Liver Toxicity Knowledge Base: A Systems Approach to a Complex End Point. <i>Clinical Pharmacology and Therapeutics</i> , 2013, 93, 409-412.	2.3	76
74	atBioNetâ€“ an integrated network analysis tool for genomics and biomarker discovery. <i>BMC Genomics</i> , 2012, 13, 325.	1.2	33
75	Investigating drug repositioning opportunities in FDA drug labels through topic modeling. <i>BMC Bioinformatics</i> , 2012, 13, S6.	1.2	54
76	Comparative Analysis of Predictive Models for Nongenotoxic Hepatocarcinogenicity Using Both Toxicogenomics and Quantitative Structureâ€“Activity Relationships. <i>Chemical Research in Toxicology</i> , 2011, 24, 1062-1070.	1.7	35
77	FDA-approved drug labeling for the study of drug-induced liver injury. <i>Drug Discovery Today</i> , 2011, 16, 697-703.	3.2	337
78	Mining FDA drug labels using an unsupervised learning technique - topic modeling. <i>BMC Bioinformatics</i> , 2011, 12, S11.	1.2	93
79	Constructing a robust protein-protein interaction network by integrating multiple public databases. <i>BMC Bioinformatics</i> , 2011, 12, S7.	1.2	24
80	Simultaneous Identification and Quantitative Determination of Amino Acids in Mixture by NMR Spectroscopy Using Chemometric Resolution. <i>Spectroscopy Letters</i> , 2011, 44, 244-250.	0.5	6
81	Translating Clinical Findings into Knowledge in Drug Safety Evaluation - Drug Induced Liver Injury Prediction System (DILips). <i>PLoS Computational Biology</i> , 2011, 7, e1002310.	1.5	80
82	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	9.4	795
83	Improving the Robustness and Stability of Partial Least Squares Regression for Nearâ€“infrared Spectral Analysis. <i>Chinese Journal of Chemistry</i> , 2009, 27, 1328-1332.	2.6	1
84	A practical approach for near infrared spectral quantitative analysis of complex samples using partial least squares modeling. <i>Science in China Series B: Chemistry</i> , 2009, 52, 1021-1027.	0.8	7
85	Resolving multi-component overlapping GC-MS signals by immune algorithms. <i>TrAC - Trends in Analytical Chemistry</i> , 2009, 28, 1312-1321.	5.8	29
86	A wavelength selection method based on randomization test for near-infrared spectral analysis. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2009, 97, 189-193.	1.8	128
87	High-throughput approach for analysis of multicomponent gas chromatographicâ€“mass spectrometric signals. <i>Journal of Chromatography A</i> , 2009, 1216, 1469-1475.	1.8	23
88	A weighted multiscale regression for multivariate calibration of near infrared spectra. <i>Analyst, The</i> , 2009, 134, 261-266.	1.7	29
89	Extraction of chemical information from complex analytical signals by a non-negative independent component analysis. <i>Analyst, The</i> , 2009, 134, 2095.	1.7	23
90	Outlier detection in near-infrared spectroscopic analysis by using Monte Carlo cross-validation. <i>Science in China Series B: Chemistry</i> , 2008, 51, 751-759.	0.8	44

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91	Sequential extraction of mass spectra and chromatographic profiles from overlapping gas chromatography-mass spectroscopy signals. <i>Journal of Chromatography A</i> , 2008, 1190, 358-364.	1.8	33
92	Fluorescence resonance energy transfer between acridine orange and rhodamine 6G and analytical application in micelles of dodecyl benzene sodium sulfonate. <i>Journal of Luminescence</i> , 2006, 118, 99-105.	1.5	11
93	Fluorescence Resonance Energy Transfer Between Acridine Orange and Rhodamine B and Analytical Application on Determination of Vitamin B12. <i>Analytical Letters</i> , 2005, 38, 1367-1377.	1.0	21