

R Stephanie Huang

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

4,502
citations

257357

24
h-index

161767

54
g-index

60
all docs

60
docs citations

60
times ranked

4752
citing authors

#	ARTICLE	IF	CITATIONS
1	pRRophetic: An R Package for Prediction of Clinical Chemotherapeutic Response from Tumor Gene Expression Levels. <i>PLoS ONE</i> , 2014, 9, e107468.	1.1	1,363
2	Clinical drug response can be predicted using baseline gene expression levels and in vitro drug sensitivity in cell lines. <i>Genome Biology</i> , 2014, 15, R47.	13.9	645
3	oncoPredict: an R package for predicting <i>in vivo</i> or cancer patient drug response and biomarkers from cell line screening data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	492
4	A genome-wide approach to identify genetic variants that contribute to etoposide-induced cytotoxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9758-9763.	3.3	195
5	Identification of Genetic Variants Contributing to Cisplatin-Induced Cytotoxicity by Use of a Genomewide Approach. <i>American Journal of Human Genetics</i> , 2007, 81, 427-437.	2.6	173
6	Population differences in microRNA expression and biological implications. <i>RNA Biology</i> , 2011, 8, 692-701.	1.5	138
7	Pharmacogenetics and pharmacogenomics of anticancer agents. <i>Ca-A Cancer Journal for Clinicians</i> , 2009, 59, 42-55.	157.7	122
8	Discovering novel pharmacogenomic biomarkers by imputing drug response in cancer patients from large genomics studies. <i>Genome Research</i> , 2017, 27, 1743-1751.	2.4	101
9	The impact of the Cancer Genome Atlas on lung cancer. <i>Translational Research</i> , 2015, 166, 568-585.	2.2	83
10	Effect of population and gender on chemotherapeutic agent-induced cytotoxicity. <i>Molecular Cancer Therapeutics</i> , 2007, 6, 31-36.	1.9	82
11	Identification of MicroRNAs as Breast Cancer Prognosis Markers through the Cancer Genome Atlas. <i>PLoS ONE</i> , 2016, 11, e0168284.	1.1	81
12	Circulating MicroRNAs as Biomarkers for Inflammatory Diseases. <i>MicroRNA (Sharjah, United Arab)</i> Tj ETQqO 0 0 rgBT /Overlock 10 Tf 50	0.6	77
13	Genetic Variants Contributing to Daunorubicin-Induced Cytotoxicity. <i>Cancer Research</i> , 2008, 68, 3161-3168.	0.4	74
14	Genetic variants associated with carboplatin-induced cytotoxicity in cell lines derived from Africans. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 3038-3046.	1.9	66
15	Platinum Sensitivity-Related Germline Polymorphism Discovered via a Cell-Based Approach and Analysis of Its Association with Outcome in Ovarian Cancer Patients. <i>Clinical Cancer Research</i> , 2011, 17, 5490-5500.	3.2	57
16	Pharmacogenomics of Cisplatin Sensitivity in Non-small Cell Lung Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 198-209.	3.0	54
17	Consistency in large pharmacogenomic studies. <i>Nature</i> , 2016, 540, E1-E2.	13.7	52
18	High Expression of miR-532-5p, a Tumor Suppressor, Leads to Better Prognosis in Ovarian Cancer Both <i>In Vivo</i> and <i>In Vitro</i> . <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1123-1131.	1.9	49

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19	The Promise of Pharmacogenomics in Reducing Toxicity During Acute Lymphoblastic Leukemia Maintenance Treatment. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 82-93.	3.0	45
20	The impact of microRNA expression on cellular proliferation. <i>Human Genetics</i> , 2014, 133, 931-938.	1.8	40
21	Computationally predicting clinical drug combination efficacy with cancer cell line screens and independent drug action. <i>Nature Communications</i> , 2020, 11, 5848.	5.8	39
22	Discovering long noncoding RNA predictors of anticancer drug sensitivity beyond protein-coding genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22020-22029.	3.3	37
23	Cancer biomarker discovery is improved by accounting for variability in general levels of drug sensitivity in pre-clinical models. <i>Genome Biology</i> , 2016, 17, 190.	3.8	35
24	Population-specific GSTM1 copy number variation. <i>Human Molecular Genetics</i> , 2009, 18, 366-372.	1.4	34
25	Cancer expression quantitative trait loci (eQTLs) can be determined from heterogeneous tumor gene expression data by modeling variation in tumor purity. <i>Genome Biology</i> , 2018, 19, 130.	3.8	27
26	More than fishing for a cure: The promises and pitfalls of high throughput cancer cell line screens. , 2018, 191, 178-189.		26
27	Pharmacogenomics discovery and implementation in genome-wide association studies era. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 1-9.	6.6	25
28	Integrative analyses of genetic variation, epigenetic regulation, and the transcriptome to elucidate the biology of platinum sensitivity. <i>BMC Genomics</i> , 2014, 15, 292.	1.2	23
29	Identification of genetic variants and gene expression relationships associated with pharmacogenes in humans. <i>Pharmacogenetics and Genomics</i> , 2008, 18, 545-549.	0.7	22
30	Gene Set Enrichment Analyses Revealed Differences in Gene Expression Patterns between Males and Females. <i>In Silico Biology</i> , 2009, 9, 55-63.	0.4	22
31	Pharmacogenomics of EGFR-targeted therapies in non-small cell lung cancer: EGFR and beyond. <i>Chinese Journal of Cancer</i> , 2015, 34, 149-60.	4.9	20
32	MicroRNA biogenesis and cellular proliferation. <i>Translational Research</i> , 2015, 166, 145-151.	2.2	18
33	Predicting Response to Histone Deacetylase Inhibitors Using High-Throughput Genomics. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv247.	3.0	18
34	Opposing transcriptional programs of KLF5 and AR emerge during therapy for advanced prostate cancer. <i>Nature Communications</i> , 2021, 12, 6377.	5.8	16
35	Pharmacogenetics and Pharmacogenomics of Targeted Therapeutics in Chronic Myeloid Leukemia. <i>Molecular Diagnosis and Therapy</i> , 2017, 21, 621-631.	1.6	14
36	Long Non-Coding RNA ANRIL as a Potential Biomarker of Chemosensitivity and Clinical Outcomes in Osteosarcoma. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11168.	1.8	14

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37	Approaches to the discovery of pharmacogenomic markers in oncology: 2000â€“2010â€“2020. <i>Pharmacogenomics</i> , 2010, 11, 471-474.	0.6	13
38	Pharmacogenomics of Medications Commonly Used in the Intensive Care Unit. <i>Frontiers in Pharmacology</i> , 2018, 9, 1436.	1.6	12
39	Oncogene or tumor suppressor? Long noncoding RNAs role in patient's prognosis varies depending on disease type. <i>Translational Research</i> , 2021, 230, 98-110.	2.2	11
40	Identifying and Validating a Combined mRNA and MicroRNA Signature in Response to Imatinib Treatment in a Chronic Myeloid Leukemia Cell Line. <i>PLoS ONE</i> , 2014, 9, e115003.	1.1	10
41	Exploring the Link between the Germline and Somatic Genome in Cancer. <i>Cancer Discovery</i> , 2017, 7, 354-355.	7.7	10
42	Lymphoblastoid Cell Lines as a Tool to Study Inter-Individual Differences in the Response to Glucose. <i>PLoS ONE</i> , 2016, 11, e0160504.	1.1	9
43	A 10-miRNA risk score-based prediction model for pathological complete response to neoadjuvant chemotherapy in hormone receptor-positive breast cancer. <i>Science China Life Sciences</i> , 2022, 65, 2205-2217.	2.3	7
44	Translating pharmacogenomics discoveries into the clinic: an implementation framework. <i>Genome Medicine</i> , 2013, 5, 94.	3.6	6
45	Integrative â€œOmicâ€•Analysis for Tamoxifen Sensitivity through Cell Based Models. <i>PLoS ONE</i> , 2014, 9, e93420.	1.1	6
46	Long non-coding RNA transcriptome of uncharacterized samples can be accurately imputed using protein-coding genes. <i>Briefings in Bioinformatics</i> , 2020, 21, 637-648.	3.2	6
47	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2021, , .	3.2	6
48	Facilitating Drug Discovery in Breast Cancer by Virtually Screening Patients Using In Vitro Drug Response Modeling. <i>Cancers</i> , 2021, 13, 885.	1.7	6
49	A Long Noncoding RNA, GAS5 Can Be a Biomarker for Docetaxel Response in Castration Resistant Prostate Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 675215.	1.3	6
50	Genetic Variation Is the Major Determinant of Individual Differences in Leukocyte Endothelial Adhesion. <i>PLoS ONE</i> , 2014, 9, e87883.	1.1	5
51	Utility of patient-derived lymphoblastoid cell lines as an <i>ex vivo</i> capecitabine sensitivity prediction model for breast cancer patients. <i>Oncotarget</i> , 2016, 7, 38359-38366.	0.8	4
52	Emerging role of long non-coding RNAs in cancer precision medicine. <i>Molecular and Cellular Oncology</i> , 2020, 7, 1684130.	0.3	3
53	MicroRNA targeting energy metabolism in ovarian cancer: a potent contender for future therapeutics. <i>Annals of Translational Medicine</i> , 2019, 7, S299-S299.	0.7	1
54	iMIRAGE: an R package to impute microRNA expression using protein-coding genes. <i>Bioinformatics</i> , 2020, 36, 2608-2610.	1.8	1

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55	Discovering drugs to overcome chemoresistance in ovarian cancers based on the cancer genome atlas tumor transcriptome profile. <i>Oncotarget</i> , 2017, 8, 115102-115113.	0.8	1
56	Institutional Profile: Pharmacogenomic research in R Stephanie Huang Laboratory. <i>Pharmacogenomics</i> , 2017, 18, 519-522.	0.6	0
57	HGG-12. HUMAN IPSC-DERIVED H3.3K27M NEUROSPHERES: A NOVEL MODEL FOR INVESTIGATING DIPG PATHOGENESIS AND DRUG RESPONSE. <i>Neuro-Oncology</i> , 2021, 23, i19-i20.	0.6	0
58	TMOD-07. HUMAN DIFFUSE MIDLINE GLIOMA AVATARS AS A PLATFORM TO SEARCH FOR NOVEL THERAPEUTIC TARGETS. <i>Neuro-Oncology</i> , 2020, 22, ii229-ii229.	0.6	0