

# R Stephanie Huang

## List of Publications by Citations

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**Version:** 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

55  
papers

2,223  
citations

22  
h-index

47  
g-index

60  
ext. papers

3,458  
ext. citations

11.9  
avg, IF

5.34  
L-index

#	Paper	IF	Citations
55	Clinical drug response can be predicted using baseline gene expression levels and in vitro drug sensitivity in cell lines. <i>Genome Biology</i> , <b>2014</b> , 15, R47	18.3	297
54	pRRophetic: an R package for prediction of clinical chemotherapeutic response from tumor gene expression levels. <i>PLoS ONE</i> , <b>2014</b> , 9, e107468	3.7	297
53	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> , <b>2007</b> , 104, 9758-63	11.5	179
52	Identification of genetic variants contributing to cisplatin-induced cytotoxicity by use of a genomewide approach. <i>American Journal of Human Genetics</i> , <b>2007</b> , 81, 427-37	11	159
51	Population differences in microRNA expression and biological implications. <i>RNA Biology</i> , <b>2011</b> , 8, 692-704	1.8	115
50	Pharmacogenetics and pharmacogenomics of anticancer agents. <i>Ca-A Cancer Journal for Clinicians</i> , <b>2009</b> , 59, 42-55	220.7	95
49	HGG-12. HUMAN IPSC-DERIVED H3.3K27M NEUROSPHERES: A NOVEL MODEL FOR INVESTIGATING DIPG PATHOGENESIS AND DRUG RESPONSE. <i>Neuro-Oncology</i> , <b>2021</b> , 23, i19-i20	1	78
48	Effect of population and gender on chemotherapeutic agent-induced cytotoxicity. <i>Molecular Cancer Therapeutics</i> , <b>2007</b> , 6, 31-6	6.1	74
47	Discovering novel pharmacogenomic biomarkers by imputing drug response in cancer patients from large genomics studies. <i>Genome Research</i> , <b>2017</b> , 27, 1743-1751	9.7	65
46	Identification of MicroRNAs as Breast Cancer Prognosis Markers through the Cancer Genome Atlas. <i>PLoS ONE</i> , <b>2016</b> , 11, e0168284	3.7	63
45	Circulating microRNAs as biomarkers for inflammatory diseases. <i>MicroRNA (Shariqah, United Arab Emirates)</i> , <b>2013</b> , 2, 63-71	2.9	62
44	Genetic variants contributing to daunorubicin-induced cytotoxicity. <i>Cancer Research</i> , <b>2008</b> , 68, 3161-8	10.1	62
43	Genetic variants associated with carboplatin-induced cytotoxicity in cell lines derived from Africans. <i>Molecular Cancer Therapeutics</i> , <b>2008</b> , 7, 3038-46	6.1	57
42	The impact of the Cancer Genome Atlas on lung cancer. <i>Translational Research</i> , <b>2015</b> , 166, 568-85	11	56
41	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> , <b>2011</b> , 17, 5490-500	12.9	55
40	Pharmacogenomics of cisplatin sensitivity in non-small cell lung cancer. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2014</b> , 12, 198-209	6.5	42
39	High Expression of miR-532-5p, a Tumor Suppressor, Leads to Better Prognosis in Ovarian Cancer Both In Vivo and In Vitro. <i>Molecular Cancer Therapeutics</i> , <b>2016</b> , 15, 1123-31	6.1	38

38	Consistency in large pharmacogenomic studies. <i>Nature</i> , <b>2016</b> , 540, E1-E2	50.4	35
37	Population-specific GSTM1 copy number variation. <i>Human Molecular Genetics</i> , <b>2009</b> , 18, 366-72	5.6	33
36	The Promise of Pharmacogenomics in Reducing Toxicity During Acute Lymphoblastic Leukemia Maintenance Treatment. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2017</b> , 15, 82-93	6.5	32
35	The impact of microRNA expression on cellular proliferation. <i>Human Genetics</i> , <b>2014</b> , 133, 931-8	6.3	29
34	Cancer biomarker discovery is improved by accounting for variability in general levels of drug sensitivity in pre-clinical models. <i>Genome Biology</i> , <b>2016</b> , 17, 190	18.3	27
33	Pharmacogenomics discovery and implementation in genome-wide association studies era. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , <b>2013</b> , 5, 1-9	6.6	22
32	Gene Set Enrichment Analyses Revealed Differences in Gene Expression Patterns between Males and Females. <i>In Silico Biology</i> , <b>2009</b> , 9, 55-63	2	20
31	Integrative analyses of genetic variation, epigenetic regulation, and the transcriptome to elucidate the biology of platinum sensitivity. <i>BMC Genomics</i> , <b>2014</b> , 15, 292	4.5	19
30	Identification of genetic variants and gene expression relationships associated with pharmacogenes in humans. <i>Pharmacogenetics and Genomics</i> , <b>2008</b> , 18, 545-9	1.9	19
29	Pharmacogenomics of EGFR-targeted therapies in non-small cell lung cancer: EGFR and beyond. <i>Chinese Journal of Cancer</i> , <b>2015</b> , 34, 149-60		18
28	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> , <b>2019</b> , 116, 22020-22029 <sup>16</sup>	11.5	16
27	MicroRNA biogenesis and cellular proliferation. <i>Translational Research</i> , <b>2015</b> , 166, 145-51	11	16
26	oncoPredict: an R package for predicting in vivo or cancer patient drug response and biomarkers from cell line screening data. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	16
25	Computationally predicting clinical drug combination efficacy with cancer cell line screens and independent drug action. <i>Nature Communications</i> , <b>2020</b> , 11, 5848	17.4	14
24	Predicting Response to Histone Deacetylase Inhibitors Using High-Throughput Genomics. <i>Journal of the National Cancer Institute</i> , <b>2015</b> , 107,	9.7	13
23	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> , <b>2018</b> , 19, 130	18.3	12
22	More than fishing for a cure: The promises and pitfalls of high throughput cancer cell line screens. <i>Pharmacology &amp; Therapeutics</i> , <b>2018</b> , 191, 178-189	13.9	12
21	Approaches to the discovery of pharmacogenomic markers in oncology: 2000-2010-2020. <i>Pharmacogenomics</i> , <b>2010</b> , 11, 471-4	2.6	11

20	Pharmacogenetics and Pharmacogenomics of Targeted Therapeutics in Chronic Myeloid Leukemia. <i>Molecular Diagnosis and Therapy</i> , <b>2017</b> , 21, 621-631	4.5	8
19	Exploring the Link between the Germline and Somatic Genome in Cancer. <i>Cancer Discovery</i> , <b>2017</b> , 7, 354-355	3.4	7
18	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> , <b>2014</b> , 9, e115003	3.7	7
17	Translating pharmacogenomics discoveries into the clinic: an implementation framework. <i>Genome Medicine</i> , <b>2013</b> , 5, 94	14.4	6
16	Pharmacogenomics of Medications Commonly Used in the Intensive Care Unit. <i>Frontiers in Pharmacology</i> , <b>2018</b> , 9, 1436	5.6	6
15	Lymphoblastoid Cell Lines as a Tool to Study Inter-Individual Differences in the Response to Glucose. <i>PLoS ONE</i> , <b>2016</b> , 11, e0160504	3.7	5
14	Genetic variation is the major determinant of individual differences in leukocyte endothelial adhesion. <i>PLoS ONE</i> , <b>2014</b> , 9, e87883	3.7	4
13	Oncogene or tumor suppressor? Long noncoding RNAs role in patient's prognosis varies depending on disease type. <i>Translational Research</i> , <b>2021</b> , 230, 98-110	11	4
12	Integrative "omic" analysis for tamoxifen sensitivity through cell based models. <i>PLoS ONE</i> , <b>2014</b> , 9, e93439	3.9	3
11	Utility of patient-derived lymphoblastoid cell lines as an ex vivo capecitabine sensitivity prediction model for breast cancer patients. <i>Oncotarget</i> , <b>2016</b> , 7, 38359-38366	3.3	3
10	Long non-coding RNA transcriptome of uncharacterized samples can be accurately imputed using protein-coding genes. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 637-648	13.4	3
9	Emerging role of long non-coding RNAs in cancer precision medicine. <i>Molecular and Cellular Oncology</i> , <b>2020</b> , 7, 1684130	1.2	2
8	Discovering drugs to overcome chemoresistance in ovarian cancers based on the cancer genome atlas tumor transcriptome profile. <i>Oncotarget</i> , <b>2017</b> , 8, 115102-115113	3.3	1
7	iMIRAGE: an R package to impute microRNA expression using protein-coding genes. <i>Bioinformatics</i> , <b>2020</b> , 36, 2608-2610	7.2	1
6	Facilitating Drug Discovery in Breast Cancer by Virtually Screening Patients Using In Vitro Drug Response Modeling. <i>Cancers</i> , <b>2021</b> , 13,	6.6	1
5	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> , <b>2022</b> , 1	8.5	1
4	Opposing transcriptional programs of KLF5 and AR emerge during therapy for advanced prostate cancer. <i>Nature Communications</i> , <b>2021</b> , 12, 6377	17.4	0
3	A Long Noncoding RNA, GAS5 Can Be a Biomarker for Docetaxel Response in Castration Resistant Prostate Cancer. <i>Frontiers in Oncology</i> , <b>2021</b> , 11, 675215	5.3	0

- 2 Institutional Profile: Pharmacogenomic research in R Stephanie Huang Laboratory. *Pharmacogenomics*, **2017**, 18, 519-522 2.6
- 1 TMOD-07. HUMAN DIFFUSE MIDLINE GLIOMA AVATARS AS A PLATFORM TO SEARCH FOR NOVEL THERAPEUTIC TARGETS. *Neuro-Oncology*, **2020**, 22, ii229-ii229 1