R Stephanie Huang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	pRRophetic: An R Package for Prediction of Clinical Chemotherapeutic Response from Tumor Gene Expression Levels. PLoS ONE, 2014, 9, e107468.	2.5	1,363
2	Clinical drug response can be predicted using baseline gene expression levels and in vitro drug sensitivity in cell lines. Genome Biology, 2014, 15, R47.	9.6	645
3	oncoPredict: an R package for predicting <i>in vivo</i> or cancer patient drug response and biomarkers from cell line screening data. Briefings in Bioinformatics, 2021, 22, .	6.5	492
4	A genome-wide approach to identify genetic variants that contribute to etoposide-induced cytotoxicity. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9758-9763.	7.1	195
5	Identification of Genetic Variants Contributing to Cisplatin-Induced Cytotoxicity by Use of a Genomewide Approach. American Journal of Human Genetics, 2007, 81, 427-437.	6.2	173
6	Population differences in microRNA expression and biological implications. RNA Biology, 2011, 8, 692-701.	3.1	138
7	Pharmacogenetics and pharmacogenomics of anticancer agents. Ca-A Cancer Journal for Clinicians, 2009, 59, 42-55.	329.8	122
8	Discovering novel pharmacogenomic biomarkers by imputing drug response in cancer patients from large genomics studies. Genome Research, 2017, 27, 1743-1751.	5.5	101
9	The impact of the Cancer Genome Atlas on lung cancer. Translational Research, 2015, 166, 568-585.	5.0	83
10	Effect of population and gender on chemotherapeutic agent–induced cytotoxicity. Molecular Cancer Therapeutics, 2007, 6, 31-36.	4.1	82
11	Identification of MicroRNAs as Breast Cancer Prognosis Markers through the Cancer Genome Atlas. PLoS ONE, 2016, 11, e0168284.	2.5	81
12	Circulating MicroRNAs as Biomarkers for Inflammatory Diseases. MicroRNA (Shariqah, United Arab) Tj ETQq0 0 0	rgBT /Ove 1.2	rlock 10 Tf 5
13	Genetic Variants Contributing to Daunorubicin-Induced Cytotoxicity. Cancer Research, 2008, 68, 3161-3168.	0.9	74
14	Genetic variants associated with carboplatin-induced cytotoxicity in cell lines derived from Africans. Molecular Cancer Therapeutics, 2008, 7, 3038-3046.	4.1	66
15	Platinum Sensitivity–Related Germline Polymorphism Discovered via a Cell-Based Approach and Analysis of Its Association with Outcome in Ovarian Cancer Patients. Clinical Cancer Research, 2011, 17, 5490-5500.	7.0	57
16	Pharmacogenomics of Cisplatin Sensitivity in Non-small Cell Lung Cancer. Genomics, Proteomics and Bioinformatics, 2014, 12, 198-209.	6.9	54

17	Consistency in large pharmacogenomic studies. Nature, 2016, 540, E1-E2.	27.8	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> . Molecular Cancer Therapeutics, 2016, 15, 1123-1131.	4.1	49

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19	The Promise of Pharmacogenomics in Reducing Toxicity During Acute Lymphoblastic Leukemia Maintenance Treatment. Genomics, Proteomics and Bioinformatics, 2017, 15, 82-93.	6.9	45
20	The impact of microRNA expression on cellular proliferation. Human Genetics, 2014, 133, 931-938.	3.8	40
21	Computationally predicting clinical drug combination efficacy with cancer cell line screens and independent drug action. Nature Communications, 2020, 11, 5848.	12.8	39
22	Discovering long noncoding RNA predictors of anticancer drug sensitivity beyond protein-coding genes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22020-22029.	7.1	37
23	Cancer biomarker discovery is improved by accounting for variability in general levels of drug sensitivity in pre-clinical models. Genome Biology, 2016, 17, 190.	8.8	35
24	Population-specific GSTM1 copy number variation. Human Molecular Genetics, 2009, 18, 366-372.	2.9	34
25	Cancer expression quantitative trait loci (eQTLs) can be determined from heterogeneous tumor gene expression data by modeling variation in tumor purity. Genome Biology, 2018, 19, 130.	8.8	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 genomeâ€wide association studies era. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 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. BMC Genomics, 2014, 15, 292.	2.8	23
29	Identification of genetic variants and gene expression relationships associated with pharmacogenes in humans. Pharmacogenetics and Genomics, 2008, 18, 545-549.	1.5	22
30	Gene Set Enrichment Analyses Revealed Differences in Gene Expression Patterns between Males and Females. In Silico Biology, 2009, 9, 55-63.	0.9	22
31	Pharmacogenomics of EGFR-targeted therapies in non–small cell lung cancer: EGFR and beyond. Chinese Journal of Cancer, 2015, 34, 149-60.	4.9	20
32	MicroRNA biogenesis and cellular proliferation. Translational Research, 2015, 166, 145-151.	5.0	18
33	Predicting Response to Histone Deacetylase Inhibitors Using High-Throughput Genomics. Journal of the National Cancer Institute, 2015, 107, djv247.	6.3	18
34	Opposing transcriptional programs of KLF5 and AR emerge during therapy for advanced prostate cancer. Nature Communications, 2021, 12, 6377.	12.8	16
35	Pharmacogenetics and Pharmacogenomics of Targeted Therapeutics in Chronic Myeloid Leukemia. Molecular Diagnosis and Therapy, 2017, 21, 621-631.	3.8	14
36	Long Non-Coding RNA ANRIL as a Potential Biomarker of Chemosensitivity and Clinical Outcomes in Osteosarcoma. International Journal of Molecular Sciences, 2021, 22, 11168.	4.1	14

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37	Approaches to the discovery of pharmacogenomic markers in oncology: 2000–2010–2020. Pharmacogenomics, 2010, 11, 471-474.	1.3	13
38	Pharmacogenomics of Medications Commonly Used in the Intensive Care Unit. Frontiers in Pharmacology, 2018, 9, 1436.	3.5	12
39	Oncogene or tumor suppressor? Long noncoding RNAs role in patient's prognosis varies depending on disease type. Translational Research, 2021, 230, 98-110.	5.0	11
40	Identifying and Validating a Combined mRNA and MicroRNA Signature in Response to Imatinib Treatment in a Chronic Myeloid Leukemia Cell Line. PLoS ONE, 2014, 9, e115003.	2.5	10
41	Exploring the Link between the Germline and Somatic Genome in Cancer. Cancer Discovery, 2017, 7, 354-355.	9.4	10
42	Lymphoblastoid Cell Lines as a Tool to Study Inter-Individual Differences in the Response to Glucose. PLoS ONE, 2016, 11, e0160504.	2.5	9
43	A 10-miRNA risk score-based prediction model for pathological complete response to neoadjuvant chemotherapy in hormone receptor-positive breast cancer. Science China Life Sciences, 2022, 65, 2205-2217.	4.9	7
44	Translating pharmacogenomics discoveries into the clinic: an implementation framework. Genome Medicine, 2013, 5, 94.	8.2	6
45	Integrative "Omic―Analysis for Tamoxifen Sensitivity through Cell Based Models. PLoS ONE, 2014, 9, e93420.	2.5	6
46	Long non-coding RNA transcriptome of uncharacterized samples can be accurately imputed using protein-coding genes. Briefings in Bioinformatics, 2020, 21, 637-648.	6.5	6
47	OUP accepted manuscript. Briefings in Bioinformatics, 2021, , .	6.5	6
48	Facilitating Drug Discovery in Breast Cancer by Virtually Screening Patients Using In Vitro Drug Response Modeling. Cancers, 2021, 13, 885.	3.7	6
49	A Long Noncoding RNA, GAS5 Can Be a Biomarker for Docetaxel Response in Castration Resistant Prostate Cancer. Frontiers in Oncology, 2021, 11, 675215.	2.8	6
50	Genetic Variation Is the Major Determinant of Individual Differences in Leukocyte Endothelial Adhesion. PLoS ONE, 2014, 9, e87883.	2.5	5
51	Utility of patient-derived lymphoblastoid cell lines as an <i>ex vivo</i> capecitabine sensitivity prediction model for breast cancer patients. Oncotarget, 2016, 7, 38359-38366.	1.8	4
52	Emerging role of long non-coding RNAs in cancer precision medicine. Molecular and Cellular Oncology, 2020, 7, 1684130.	0.7	3
53	MicroRNA targeting energy metabolism in ovarian cancer: a potent contender for future therapeutics. Annals of Translational Medicine, 2019, 7, S299-S299.	1.7	1
54	iMIRAGE: an R package to impute microRNA expression using protein-coding genes. Bioinformatics, 2020, 36, 2608-2610.	4.1	1

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55	Discovering drugs to overcome chemoresistance in ovarian cancers based on the cancer genome atlas tumor transcriptome profile. Oncotarget, 2017, 8, 115102-115113.	1.8	1
56	Institutional Profile: Pharmacogenomic research in R Stephanie Huang Laboratory. Pharmacogenomics, 2017, 18, 519-522.	1.3	0
57	HGG-12. HUMAN IPSC-DERIVED H3.3K27M NEUROSPHERES: A NOVEL MODEL FOR INVESTIGATING DIPG PATHOGENESIS AND DRUG RESPONSE. Neuro-Oncology, 2021, 23, i19-i20.	1.2	0
58	TMOD-07. HUMAN DIFFUSE MIDLINE GLIOMA AVATARS AS A PLATFORM TO SEARCH FOR NOVEL THERAPEUTIC TARGETS. Neuro-Oncology, 2020, 22, ii229-ii229.	1.2	0