

Tammy Moser Havener

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

310
citations

933447

10
h-index

888059

17
g-index

21
all docs

21
docs citations

21
times ranked

669
citing authors

#	ARTICLE	IF	CITATIONS
1	High-throughput screening and genome-wide analyses of 44 anticancer drugs in the 1000 Genomes cell lines reveals an association of the NQO1 gene with the response of multiple anticancer drugs. PLoS Genetics, 2021, 17, e1009732.	3.5	6
2	Race and smoking status associated with paclitaxel drug response in patient-derived lymphoblastoid cell lines. Pharmacogenetics and Genomics, 2021, 31, 48-52.	1.5	0
3	Synergistic drug combinations and machine learning for drug repurposing in chordoma. Scientific Reports, 2020, 10, 12982.	3.3	27
4	Synergistic Chemotherapy Drug Response Is a Genetic Trait in Lymphoblastoid Cell Lines. Frontiers in Genetics, 2019, 10, 829.	2.3	5
5	Design of a Cyclin G Associated Kinase (GAK)/Epidermal Growth Factor Receptor (EGFR) Inhibitor Set to Interrogate the Relationship of EGFR and GAK in Chordoma. Journal of Medicinal Chemistry, 2019, 62, 4772-4778.	6.4	34
6	Genetic Variants in <i>CPA6</i> and <i>PRPF31</i> Are Associated With Variation in Response to Metformin in Individuals With Type 2 Diabetes. Diabetes, 2018, 67, 1428-1440.	0.6	32
7	Genetic Variants in <i>HSD17B3</i> , <i>SMAD3</i> , and <i>IPO11</i> Impact Circulating Lipids in Response to Fenofibrate in Individuals With Type 2 Diabetes. Clinical Pharmacology and Therapeutics, 2018, 103, 712-721.	4.7	30
8	The influence of Neanderthal alleles on cytotoxic response. PeerJ, 2018, 6, e5691.	2.0	1
9	Common and rare genetic markers of lipid variation in subjects with type 2 diabetes from the ACCORD clinical trial. PeerJ, 2017, 5, e3187.	2.0	11
10	Incorporating Concomitant Medications into Genome-Wide Analyses for the Study of Complex Disease and Drug Response. Frontiers in Genetics, 2016, 7, 138.	2.3	2
11	Evaluating the role of admixture in cancer therapy via <i>in vitro</i> drug response and multivariate genome-wide associations. Pharmacogenomics, 2015, 16, 1451-1463.	1.3	8
12	Abstract LB-246: Evaluating the role of admixture in cancer therapy via <i>in vitro</i> drug response and multivariate genome-wide associations. , 2015, , .		1
13	Genome-wide association and pharmacological profiling of 29 anticancer agents using lymphoblastoid cell lines. Pharmacogenomics, 2014, 15, 137-146.	1.3	27
14	A genome-wide association analysis of temozolomide response using lymphoblastoid cell lines shows a clinically relevant association with MGMT. Pharmacogenetics and Genomics, 2012, 22, 796-802.	1.5	32
15	Multivariate methods and software for association mapping in dose-response genome-wide association studies. BioData Mining, 2012, 5, 21.	4.0	17
16	A comparison of association methods for cytotoxicity mapping in pharmacogenomics. Frontiers in Genetics, 2011, 2, 86.	2.3	14
17	Identification and Replication of Loci Involved in Camptothecin-Induced Cytotoxicity Using CEPH Pedigrees. PLoS ONE, 2011, 6, e17561.	2.5	14
18	Pharmacogenomic characterization of US FDA-approved cytotoxic drugs. Pharmacogenomics, 2011, 12, 1407-1415.	1.3	44

#	ARTICLE	IF	CITATIONS
19	Institutional Profile: UNC Institute for Pharmacogenomics and Individualized Therapy: interdisciplinary research for individual care. <i>Pharmacogenomics</i> , 2010, 11, 13-21.	1.3	1