Aritro Nath

List of Publications by Year in descending order

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Δριτρο Νλτμ

#	Article	IF	CITATIONS
1	Elevated free fatty acid uptake via CD36 promotes epithelial-mesenchymal transition in hepatocellular carcinoma. Scientific Reports, 2015, 5, 14752.	3.3	241
2	Genetic alterations in fatty acid transport and metabolism genes are associated with metastatic progression and poor prognosis of human cancers. Scientific Reports, 2016, 6, 18669.	3.3	155
3	Discovering novel pharmacogenomic biomarkers by imputing drug response in cancer patients from large genomics studies. Genome Research, 2017, 27, 1743-1751.	5.5	101
4	Rapid Fine Conformational Epitope Mapping Using Comprehensive Mutagenesis and Deep Sequencing. Journal of Biological Chemistry, 2015, 290, 26457-26470.	3.4	67
5	The Double-stranded RNA–dependent Protein Kinase Differentially Regulates Insulin Receptor Substrates 1 and 2 in HepG2 Cells. Molecular Biology of the Cell, 2010, 21, 3449-3458.	2.1	51
6	Signaling dynamics of palmitate-induced ER stress responses mediated by ATF4 in HepG2 cells. BMC Systems Biology, 2013, 7, 9.	3.0	37
7	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
8	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
9	Evolution of core archetypal phenotypes in progressive high grade serous ovarian cancer. Nature Communications, 2021, 12, 3039.	12.8	24
10	Leveraging Single-Cell Approaches in Cancer Precision Medicine. Trends in Cancer, 2021, 7, 359-372.	7.4	18
11	Exploiting collateral sensitivity controls growth of mixed culture of sensitive and resistant cells and decreases selection for resistant cells in a cell line model. Cancer Cell International, 2020, 20, 253.	4.1	17
12	Pharmacogenetics and Pharmacogenomics of Targeted Therapeutics in Chronic Myeloid Leukemia. Molecular Diagnosis and Therapy, 2017, 21, 621-631.	3.8	14
13	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
14	Palmitate-Induced IRE1–XBP1–ZEB Signaling Represses Desmoplakin Expression and Promotes Cancer Cell Migration. Molecular Cancer Research, 2021, 19, 240-248.	3.4	11
15	Ensemble Classification of Cancer Types and Biomarker Identification. Drug Development Research, 2012, 73, 414-419.	2.9	9
16	A`one-two punch' therapy strategy to target chemoresistance in estrogen receptor positive breast cancer. Translational Oncology, 2021, 14, 100946.	3.7	8
17	Synergy Analysis Reveals Association between Insulin Signaling and Desmoplakin Expression in Palmitate Treated HepG2 Cells. PLoS ONE, 2011, 6, e28138.	2.5	6
18	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

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19	Clinical evaluation of germline polymorphisms associated with capecitabine toxicity in breast cancer: TBCRC-015. Breast Cancer Research and Treatment, 2020, 181, 623-633.	2.5	6
20	ENDORSE: a prognostic model for endocrine therapy in estrogenâ€receptorâ€positive breast cancers. Molecular Systems Biology, 2022, 18, .	7.2	5
21	The success story of drug repurposing in breast cancer. , 2020, , 173-190.		4
22	RAGE Inhibitors as Alternatives to Dexamethasone for Managing Cerebral Edema Following Brain Tumor Surgery. Neurotherapeutics, 2022, 19, 635-648.	4.4	4
23	Emerging role of long non-coding RNAs in cancer precision medicine. Molecular and Cellular Oncology, 2020, 7, 1684130.	0.7	3
24	Relevance of Network Hierarchy in Cancer Drug-Target Selection. , 2012, , 339-362.		3
25	Characterization of transcription factor response kinetics in parallel. BMC Biotechnology, 2016, 16, 62.	3.3	2
26	MicroRNA targeting energy metabolism in ovarian cancer: a potent contender for future therapeutics. Annals of Translational Medicine, 2019, 7, S299-S299.	1.7	1
27	iMIRACE: an R package to impute microRNA expression using protein-coding genes. Bioinformatics, 2020, 36, 2608-2610.	4.1	1
28	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
29	Institutional Profile: Pharmacogenomic research in R Stephanie Huang Laboratory. Pharmacogenomics, 2017, 18, 519-522.	1.3	0
30	Abstract 3141: Evolution of core archetypal phenotypes in progressive high grade serous ovarian cancer. , 2021, , .		0
31	Abstract 341: Predicting clinical endocrine response in advanced breast cancers using a reproducible low-dimensional biomarker. , 2021, , .		0
32	Abstract C29: Free fatty acid induced epithelial to mesenchymal transition (EMT) in hepatocellular carcinoma cells. , 2013, , .		0
33	Abstract 5157: Elevated uptake of free fatty acids via CD36 promotes epithelial-mesenchymal transition in hepatocellular carcinoma. , 2015, , .		0
34	Abstract A1-58: Revisiting cancer energetics: Establishing a link between altered fatty-acid metabolism and metastasis. , 2015, , .		0
35	Abstract 2039: Exploring the longitudinal transcriptomic landscape of tyrosine kinase inhibitor treatment response in chronic myeloid leukemia patients. , 2016, , .		0
36	Abstract 5035: IDWAS: Imputing drug response in large cohorts of cancer patients to discover novel predictive biomarkers. , 2017, , .		0

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#	Article	IF	CITATIONS
37	Abstract 3481: Leveraging protein coding gene expression profiles to accurately impute lncRNA transcriptome of cancer cells. , 2017, , .		0
38	Abstract 3897: Pharmacogenomic landscape of long non-coding RNAs in human cancers. , 2018, , .		0
39	Abstract 3578: Comprehensive pharmacogenomic analysis establishes lncRNAs as protein-coding independent biomarker of drug response in human cancers. , 2019, , .		0
40	The role of long non-coding RNA ANRIL in chemosensitivity in osteosarcoma and clinical outcomes Journal of Clinical Oncology, 2020, 38, e22515-e22515.	1.6	0
41	Abstract 3578: Comprehensive pharmacogenomic analysis establishes IncRNAs as protein-coding independent biomarker of drug response in human cancers. , 2019, , .		0