

Aritro Nath

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

875
citations

759233

12
h-index

552781

26
g-index

48
all docs

48
docs citations

48
times ranked

1850
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | RAGE Inhibitors as Alternatives to Dexamethasone for Managing Cerebral Edema Following Brain Tumor Surgery. <i>Neurotherapeutics</i> , 2022, 19, 635-648. | 4.4 | 4 |
| 2 | ENDORSE: a prognostic model for endocrine therapy in estrogen receptor-positive breast cancers. <i>Molecular Systems Biology</i> , 2022, 18, . | 7.2 | 5 |
| 3 | A 'one-two punch' therapy strategy to target chemoresistance in estrogen receptor positive breast cancer. <i>Translational Oncology</i> , 2021, 14, 100946. | 3.7 | 8 |
| 4 | Palmitate-Induced IRE1-XBP1-ZEB Signaling Represses Desmoplakin Expression and Promotes Cancer Cell Migration. <i>Molecular Cancer Research</i> , 2021, 19, 240-248. | 3.4 | 11 |
| 5 | Leveraging Single-Cell Approaches in Cancer Precision Medicine. <i>Trends in Cancer</i> , 2021, 7, 359-372. | 7.4 | 18 |
| 6 | Evolution of core archetypal phenotypes in progressive high grade serous ovarian cancer. <i>Nature Communications</i> , 2021, 12, 3039. | 12.8 | 24 |
| 7 | Abstract 3141: Evolution of core archetypal phenotypes in progressive high grade serous ovarian cancer. , 2021, , . | | 0 |
| 8 | Abstract 341: Predicting clinical endocrine response in advanced breast cancers using a reproducible low-dimensional biomarker. , 2021, , . | | 0 |
| 9 | 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. | 4.1 | 14 |
| 10 | 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. | 6.5 | 6 |
| 11 | Emerging role of long non-coding RNAs in cancer precision medicine. <i>Molecular and Cellular Oncology</i> , 2020, 7, 1684130. | 0.7 | 3 |
| 12 | iMIRAGE: an R package to impute microRNA expression using protein-coding genes. <i>Bioinformatics</i> , 2020, 36, 2608-2610. | 4.1 | 1 |
| 13 | Clinical evaluation of germline polymorphisms associated with capecitabine toxicity in breast cancer: TBCRC-015. <i>Breast Cancer Research and Treatment</i> , 2020, 181, 623-633. | 2.5 | 6 |
| 14 | Exploiting collateral sensitivity controls growth of mixed culture of sensitive and resistant cells and decreases selection for resistant cells in a cell line model. <i>Cancer Cell International</i> , 2020, 20, 253. | 4.1 | 17 |
| 15 | The success story of drug repurposing in breast cancer. , 2020, , 173-190. | | 4 |
| 16 | The role of long non-coding RNA ANRIL in chemosensitivity in osteosarcoma and clinical outcomes.. <i>Journal of Clinical Oncology</i> , 2020, 38, e22515-e22515. | 1.6 | 0 |
| 17 | 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. | 7.1 | 37 |
| 18 | MicroRNA targeting energy metabolism in ovarian cancer: a potent contender for future therapeutics. <i>Annals of Translational Medicine</i> , 2019, 7, S299-S299. | 1.7 | 1 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Abstract 3578: Comprehensive pharmacogenomic analysis establishes lncRNAs as protein-coding independent biomarker of drug response in human cancers. , 2019, , . | | 0 |
| 20 | Abstract 3578: Comprehensive pharmacogenomic analysis establishes lncRNAs as protein-coding independent biomarker of drug response in human cancers. , 2019, , . | | 0 |
| 21 | 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. | 8.8 | 27 |
| 22 | Abstract 3897: Pharmacogenomic landscape of long non-coding RNAs in human cancers. , 2018, , . | | 0 |
| 23 | Institutional Profile: Pharmacogenomic research in R Stephanie Huang Laboratory. <i>Pharmacogenomics</i> , 2017, 18, 519-522. | 1.3 | 0 |
| 24 | Pharmacogenetics and Pharmacogenomics of Targeted Therapeutics in Chronic Myeloid Leukemia. <i>Molecular Diagnosis and Therapy</i> , 2017, 21, 621-631. | 3.8 | 14 |
| 25 | Discovering novel pharmacogenomic biomarkers by imputing drug response in cancer patients from large genomics studies. <i>Genome Research</i> , 2017, 27, 1743-1751. | 5.5 | 101 |
| 26 | Discovering drugs to overcome chemoresistance in ovarian cancers based on the cancer genome atlas tumor transcriptome profile. <i>Oncotarget</i> , 2017, 8, 115102-115113. | 1.8 | 1 |
| 27 | Abstract 5035: IDWAS: Imputing drug response in large cohorts of cancer patients to discover novel predictive biomarkers. , 2017, , . | | 0 |
| 28 | Abstract 3481: Leveraging protein coding gene expression profiles to accurately impute lncRNA transcriptome of cancer cells. , 2017, , . | | 0 |
| 29 | Characterization of transcription factor response kinetics in parallel. <i>BMC Biotechnology</i> , 2016, 16, 62. | 3.3 | 2 |
| 30 | Genetic alterations in fatty acid transport and metabolism genes are associated with metastatic progression and poor prognosis of human cancers. <i>Scientific Reports</i> , 2016, 6, 18669. | 3.3 | 155 |
| 31 | Abstract 2039: Exploring the longitudinal transcriptomic landscape of tyrosine kinase inhibitor treatment response in chronic myeloid leukemia patients. , 2016, , . | | 0 |
| 32 | Elevated free fatty acid uptake via CD36 promotes epithelial-mesenchymal transition in hepatocellular carcinoma. <i>Scientific Reports</i> , 2015, 5, 14752. | 3.3 | 241 |
| 33 | Rapid Fine Conformational Epitope Mapping Using Comprehensive Mutagenesis and Deep Sequencing. <i>Journal of Biological Chemistry</i> , 2015, 290, 26457-26470. | 3.4 | 67 |
| 34 | Abstract 5157: Elevated uptake of free fatty acids via CD36 promotes epithelial-mesenchymal transition in hepatocellular carcinoma. , 2015, , . | | 0 |
| 35 | Abstract A1-58: Revisiting cancer energetics: Establishing a link between altered fatty-acid metabolism and metastasis. , 2015, , . | | 0 |
| 36 | Signaling dynamics of palmitate-induced ER stress responses mediated by ATF4 in HepG2 cells. <i>BMC Systems Biology</i> , 2013, 7, 9. | 3.0 | 37 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | Abstract C29: Free fatty acid induced epithelial to mesenchymal transition (EMT) in hepatocellular carcinoma cells. , 2013, , . | | 0 |
| 38 | Ensemble Classification of Cancer Types and Biomarker Identification. Drug Development Research, 2012, 73, 414-419. | 2.9 | 9 |
| 39 | Relevance of Network Hierarchy in Cancer Drug-Target Selection. , 2012, , 339-362. | | 3 |
| 40 | Synergy Analysis Reveals Association between Insulin Signaling and Desmoplakin Expression in Palmitate Treated HepG2 Cells. PLoS ONE, 2011, 6, e28138. | 2.5 | 6 |
| 41 | The Double-stranded RNAâ€“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 |