Resource Summary Report

Generated by dkNET on May 19, 2025

caArray

RRID:SCR_006053
Type: Tool

Proper Citation

caArray (RRID:SCR_006053)

Resource Information

URL: https://array.nci.nih.gov/caarray/

Proper Citation: caArray (RRID:SCR_006053)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on Sep 18, 2018. Open-source, web and programmatically accessible microarray data management system. caArray guides the annotation and exchange of array data using a federated model of local installations whose results are shareable across the cancer Biomedical Informatics Grid (caBIG). caArray furthers translational cancer research through acquisition, dissemination and aggregation of semantically interoperable array data to support subsequent analysis by tools and services on and off the Grid. As array technology advances and matures, caArray will extend its logical library of assay management.

Abbreviations: caArray

Synonyms: caArray - Array Data Management System, caArray Data Portal

Resource Type: service resource, database, data or information resource, storage service resource, data repository

Keywords: microarray, gene expression, data sharing, service resource, data management, annotation, interoperability, life sciences

Related Condition: Cancer

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: caArray

Resource ID: SCR_006053

Alternate IDs: nlx_151452, OMICS_00864

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250519T203431+0000

Ratings and Alerts

No rating or validation information has been found for caArray.

No alerts have been found for caArray.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 35 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Park WY, et al. (2023) Apoptosis-induced nuclear expulsion in tumor cells drives S100a4-mediated metastatic outgrowth through the RAGE pathway. Nature cancer, 4(3), 419.

Xu Y, et al. (2023) Loss of BLK expression as a potential predictor of poor prognosis and immune checkpoint blockade response in NSCLC and contribute to tumor progression. Translational oncology, 33, 101671.

Giannos P, et al. (2021) Identification of Prognostic Gene Biomarkers in Non-Small Cell Lung Cancer Progression by Integrated Bioinformatics Analysis. Biology, 10(11).

Yang Y, et al. (2021) Targeting lactate dehydrogenase a improves radiotherapy efficacy in non-small cell lung cancer: from bedside to bench. Journal of translational medicine, 19(1), 170.

Gao L, et al. (2021) Identification of the susceptibility genes for COVID-19 in lung adenocarcinoma with global data and biological computation methods. Computational and structural biotechnology journal, 19, 6229.

Jang HR, et al. (2021) PLK1/vimentin signaling facilitates immune escape by recruiting Smad2/3 to PD-L1 promoter in metastatic lung adenocarcinoma. Cell death and

differentiation, 28(9), 2745.

Ko PH, et al. (2020) Semaphorin 5A suppresses the proliferation and migration of lung adenocarcinoma cells. International journal of oncology, 56(1), 165.

Shin SB, et al. (2020) Active PLK1-driven metastasis is amplified by TGF-? signaling that forms a positive feedback loop in non-small cell lung cancer. Oncogene, 39(4), 767.

Huang WC, et al. (2019) Cisplatin resistant lung cancer cells promoted M2 polarization of tumor-associated macrophages via the Src/CD155/MIF functional pathway. Journal of experimental & clinical cancer research : CR, 38(1), 180.

Nishimura T, et al. (2019) Cancer stem-like properties and gefitinib resistance are dependent on purine synthetic metabolism mediated by the mitochondrial enzyme MTHFD2. Oncogene, 38(14), 2464.

Wang P, et al. (2018) Distinct Prognostic Values of Alcohol Dehydrogenase Family Members for Non-Small Cell Lung Cancer. Medical science monitor : international medical journal of experimental and clinical research, 24, 3578.

Thapa S, et al. (2018) Significance of aquaporins' expression in the prognosis of gastric cancer. Bioscience reports, 38(3).

Zhang X, et al. (2018) G-quadruplex structures at the promoter of HOXC10 regulate its expression. Biochimica et biophysica acta. Gene regulatory mechanisms, 1861(11), 1018.

Li Z, et al. (2017) EYA2 promotes lung cancer cell proliferation by downregulating the expression of PTEN. Oncotarget, 8(67), 110837.

Roelands J, et al. (2017) A collection of annotated and harmonized human breast cancer transcriptome datasets, including immunologic classification. F1000Research, 6, 296.

Wu J, et al. (2017) Nomogram integrating gene expression signatures with clinicopathological features to predict survival in operable NSCLC: a pooled analysis of 2164 patients. Journal of experimental & clinical cancer research : CR, 36(1), 4.

Hendrickx W, et al. (2017) Identification of genetic determinants of breast cancer immune phenotypes by integrative genome-scale analysis. Oncoimmunology, 6(2), e1253654.

Bauer AK, et al. (2017) Toll-like receptor expression in human non-small cell lung carcinoma: potential prognostic indicators of disease. Oncotarget, 8(54), 91860.

Jabs V, et al. (2017) Integrative analysis of genome-wide gene copy number changes and gene expression in non-small cell lung cancer. PloS one, 12(11), e0187246.

Qu J, et al. (2016) Molecular basis of antibody binding to mucin glycopeptides in lung cancer. International journal of oncology, 48(2), 587.