Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 17, 2025

NIA Array Analysis

RRID:SCR_010948
Type: Tool

Proper Citation

NIA Array Analysis (RRID:SCR_010948)

Resource Information

URL: http://lgsun.grc.nia.nih.gov/ANOVA/

Proper Citation: NIA Array Analysis (RRID:SCR_010948)

Description: Data analysis server / software designed to test statistical significance of gene microarray data, visualize the results, and provide links to clone information and gene index. Several public datasets are also available.

Abbreviations: NIA Array Analysis

Resource Type: data analysis service, data set, data or information resource, analysis service resource, production service resource, software resource, service resource

Defining Citation: PMID:15734774

Keywords: gene expression, microarray, principal component analysis, significance analysis, gene annotation, anova, hierarchical clustering, pattern matching

Funding:

Resource Name: NIA Array Analysis

Resource ID: SCR_010948

Alternate IDs: OMICS_00774

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250417T065403+0000

Ratings and Alerts

No rating or validation information has been found for NIA Array Analysis.

No alerts have been found for NIA Array Analysis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 48 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Jiang H, et al. (2022) Long Noncoding RNA AF131217.1 Regulated Coronary Slow Flow-Induced Inflammation Affecting Coronary Slow Flow via KLF4. Brazilian journal of cardiovascular surgery, 37(4), 525.

Lu J, et al. (2022) Cytomegalovirus infection reduced CD70 expression, signaling and expansion of viral specific memory CD8+ T cells in healthy human adults. Immunity & ageing : I & A, 19(1), 54.

Snider AP, et al. (2021) Transcriptomic data of bovine ovarian granulosa cells of control and High A4 cows. Data in brief, 37, 107217.

McFee RM, et al. (2021) A high-androgen microenvironment inhibits granulosa cell proliferation and alters cell identity. Molecular and cellular endocrinology, 531, 111288.

Sasaki N, et al. (2021) Cell Surface and Functional Features of Cortical Bone Stem Cells. International journal of molecular sciences, 22(21).

Dos Santos EC, et al. (2020) The pathogen Moniliophthora perniciosa promotes differential proteomic modulation of cacao genotypes with contrasting resistance to witches´ broom disease. BMC plant biology, 20(1), 1.

Liu Y, et al. (2020) Serum microRNA-365 suppresses non-small-cell lung cancer metastasis and invasion in patients with bone metastasis of lung cancer. The Journal of international medical research, 48(10), 300060520939718.

Stylianou N, et al. (2019) A molecular portrait of epithelial-mesenchymal plasticity in prostate cancer associated with clinical outcome. Oncogene, 38(7), 913.

Miura Y, et al. (2018) Characteristic glycopeptides associated with extreme human longevity identified through plasma glycoproteomics. Biochimica et biophysica acta. General subjects, 1862(6), 1462.

Itakura Y, et al. (2018) Qualitative and quantitative alterations in intracellular and membrane glycoproteins maintain the balance between cellular senescence and human aging. Aging, 10(8), 2190.

Hirayama M, et al. (2017) Identification of transcription factors that promote the differentiation of human pluripotent stem cells into lacrimal gland epithelium-like cells. NPJ aging and mechanisms of disease, 3, 1.

Arai Y, et al. (2017) Salt suppresses IFN? inducible chemokines through the IFN?-JAK1-STAT1 signaling pathway in proximal tubular cells. Scientific reports, 7, 46580.

Romereim SM, et al. (2017) Transcriptomes of bovine ovarian follicular and luteal cells. Data in brief, 10, 335.

Romereim SM, et al. (2017) Gene expression profiling of bovine ovarian follicular and luteal cells provides insight into cellular identities and functions. Molecular and cellular endocrinology, 439, 379.

Yamamizu K, et al. (2016) Generation and gene expression profiling of 48 transcription-factor-inducible mouse embryonic stem cell lines. Scientific reports, 6, 25667.

Tagliaferri D, et al. (2016) Retinoic Acid Specifically Enhances Embryonic Stem Cell Metastate Marked by Zscan4. PloS one, 11(2), e0147683.

Itakura Y, et al. (2016) N- and O-glycan cell surface protein modifications associated with cellular senescence and human aging. Cell & bioscience, 6, 14.

Martin Gonzalez J, et al. (2016) Embryonic Stem Cell Culture Conditions Support Distinct States Associated with Different Developmental Stages and Potency. Stem cell reports, 7(2), 177.

Fraige K, et al. (2015) Metabolite and proteome changes during the ripening of Syrah and Cabernet Sauvignon grape varieties cultured in a nontraditional wine region in Brazil. Journal of proteomics, 113, 206.

He W, et al. (2014) Defining differentially methylated regions specific for the acquisition of pluripotency and maintenance in human pluripotent stem cells via microarray. PloS one, 9(9), e108350.