

Resource Summary Report

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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/>

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

Defining Citation: [PMID:15734774](#)

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

Resource Name: NIA Array Analysis

Resource ID: SCR_010948

Alternate IDs: OMICS_00774

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260821T193907+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 50 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Itakura Y, et al. (2023) Spatiotemporal changes of tissue glycans depending on localization in cardiac aging. *Regenerative therapy*, 22, 68.

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.

Czernicka M, et al. (2022) Proteomic Studies of Roots in Hypoxia-Sensitive and -Tolerant Tomato Accessions Reveal Candidate Proteins Associated with Stress Priming. *Cells*, 11(3).

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.

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

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

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 γ inducible chemokines through the IFN γ -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.

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.

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