Resource Summary Report

Generated by dkNET on Aug 17, 2026

AmaZonia: Explore the Jungle of Microarrays Results

RRID:SCR_008405
Type: Tool

Proper Citation

AmaZonia: Explore the Jungle of Microarrays Results (RRID:SCR_008405)

Resource Information

URL: http://amazonia.montp.inserm.fr/

Proper Citation: AmaZonia: Explore the Jungle of Microarrays Results (RRID:SCR_008405)

Description: A web interface and associated tools for easy query of public human transcriptome data by keyword, through thematic pages with list annotations. Amazonia provides a thematic entry to public transcriptomes: users may for instance query a gene on a Stem Cells page, where they will see the expression of their favorite gene across selected microarray experiments related to stem cell biology. This selection of samples can be customized at will among the 6331 samples currently present in the database. Every transcriptome study results in the identification of lists of genes relevant to a given biological condition. In order to include this valuable information in any new query in the Amazonia database, they indicate for each gene in which lists it is included. This is a straightforward and efficient way to synthesize hundreds of microarray publications., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: AmaZonia

Resource Type: data or information resource, database

Keywords: molecular neuroanatomy, microarray, transcriptome, human, data, stem cell, gene expression

Funding: Association Franaise contre les Myopathies ;
Canceropole Grand Sud-Ouest

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: AmaZonia: Explore the Jungle of Microarrays Results

Resource ID: SCR_008405

Alternate IDs: nif-0000-30089

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260815T182912+0000

Ratings and Alerts

No rating or validation information has been found for AmaZonia: Explore the Jungle of Microarrays Results.

No alerts have been found for AmaZonia: Explore the Jungle of Microarrays Results.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

de Queiroz GN, et al. (2024) NT157 exhibits antineoplastic effects by targeting IRS and STAT3/5 signaling in multiple myeloma. Hematology, transfusion and cell therapy, 46 Suppl 6(Suppl 6), S112.

Carvalho MFL, et al. (2024) Comprehensive analysis of the HCK gene in myeloid neoplasms: Insights into biological functions, prognosis, and response to antineoplastic agents. Hematology, transfusion and cell therapy, 46(3), 273.

Kassambara A, et al. (2013) Inhibition of DEPDC1A, a bad prognostic marker in multiple myeloma, delays growth and induces mature plasma cell markers in malignant plasma cells. PloS one, 8(4), e62752.

Moreaux J, et al. (2012) STEAP1 is overexpressed in cancers: a promising therapeutic target. Biochemical and biophysical research communications, 429(3-4), 148.

Kassambara A, et al. (2012) Identification of pluripotent and adult stem cell genes unrelated to cell cycle and associated with poor prognosis in multiple myeloma. PloS one, 7(7), e42161.

Assou S, et al. (2012) Transcriptome analysis during human trophectoderm specification suggests new roles of metabolic and epigenetic genes. PloS one, 7(6), e39306.

Son MY, et al. (2011) Involvement of neuropeptide Y and its Y1 and Y5 receptors in maintaining self-renewal and proliferation of human embryonic stem cells. Journal of cellular and molecular medicine, 15(1), 152.

Bret C, et al. (2011) SULFs in human neoplasia: implication as progression and prognosis factors. Journal of translational medicine, 9, 72.

Schoenhals M, et al. (2009) Embryonic stem cell markers expression in cancers. Biochemical and biophysical research communications, 383(2), 157.