Resource Summary Report

Generated by NIF on Apr 26, 2025

RNA Abundance Database

RRID:SCR_002771
Type: Tool

Proper Citation

RNA Abundance Database (RRID:SCR_002771)

Resource Information

URL: http://www.cbil.upenn.edu/RAD

Proper Citation: RNA Abundance Database (RRID:SCR_002771)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, Documented on March 24, 2014. A resource for gene expression studies, storing highly curated MIAME-compliant studies (i.e. experiments) employing a variety of technologies such as filter arrays, 2-channel microarrays, Affymetrix chips, SAGE, MPSS and RT-PCR. Data were available for querying and downloading based on the MGED ontology, publications or genes. Both public and private studies (the latter viewable only by users having appropriate logins and permissions) were available from this website. Specific details on protocols, biomaterials, study designs, etc., are collected through a user-friendly suite of web annotation forms. Software has been developed to generate MAGE-ML documents to enable easy export of studies stored in RAD to any other database accepting data in this format. RAD is part of a more general Genomics Unified Schema (http://gusdb.org), which includes a richly annotated gene index (http://allgenes.org), thus providing a platform that integrates genomic and transcriptomic data from multiple organisms. NOTE: Due to changes in technology and funding, the RAD website is no longer available. RAD as a schema is still very much active and incorporated in the GUS (Genomics Unified Schema) database system used by CBIL (EuPathDB, Beta Cell Genomics) and others. The schema for RAD can be viewed along with the other GUS namespaces through our Schema Browser.

Abbreviations: RAD

Synonyms: RNA Abundance Database

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

Keywords: gene expression, gene, affymetrix, biomaterial, genomics, microarray, mpss, ontology, rna, rt-pcr, sage, functional genomics, transcript abundance

Funding: NIH ;
NHGRI RO1-HG-01539;
NIDDK U01DK56947;
NHGRI K25-HG-02296;
NHGRI K25-HG-00052

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: RNA Abundance Database

Resource ID: SCR_002771

Alternate IDs: nif-0000-00133, OMICS_00869

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250426T055559+0000

Ratings and Alerts

No rating or validation information has been found for RNA Abundance Database .

No alerts have been found for RNA Abundance Database .

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Bermúdez M, et al. (2015) CEMP1 Induces Transformation in Human Gingival Fibroblasts. PloS one, 10(5), e0127286.

Gao S, et al. (2011) Quantitative utilization of prior biological knowledge in the Bayesian network modeling of gene expression data. BMC bioinformatics, 12, 359.

Gao N, et al. (2007) Foxa2 controls vesicle docking and insulin secretion in mature Beta cells. Cell metabolism, 6(4), 267.

Passerini AG, et al. (2005) Regional determinants of arterial endothelial phenotype dominate

the impact of gender or short-term exposure to a high-fat diet. Biochemical and biophysical research communications, 332(1), 142.