

# Resource Summary Report

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## 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:** resource, storage service resource, data repository, service resource, database, data or information 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, r3d100000017

**Alternate URLs:** <https://doi.org/10.17616/R3QP4Q>

**Record Creation Time:** 20220129T080215+0000

**Record Last Update:** 20260805T044044+0000

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## Ratings and Alerts

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

No alerts have been found for RNA Abundance Database .

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Bermudez 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.