

Resource Summary Report

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dbRES: A web-oriented database for annotated RNA Editing Site

RRID:SCR_002322

Type: Tool

Proper Citation

dbRES: A web-oriented database for annotated RNA Editing Site (RRID:SCR_002322)

Resource Information

URL: <http://bioinfo.au.tsinghua.edu.cn/dbRES/>

Proper Citation: dbRES: A web-oriented database for annotated RNA Editing Site (RRID:SCR_002322)

Description: dbRES is a web-oriented comprehensive database for RNA Editing Site. dbRES contain only experimental validated RNA Editing Site. All the data in dbRES was manually collected from literatures reporting related experiment result or the GeneBank database. dbRES now contains all together 5437 RNA edit site data. dbRES covers altogether 95 organisms from 251 transcripts. RNA editing is a post-transcriptional modification of RNA and markedly increases the complexity of the transcriptome. RNA editing occurs in the nucleus, as well as in mitochondria and plastids. To date such changes have been observed in prokaryotes, plants, animals and virus. The diversity of this widespread phenomenon includes nucleoside modifications, nucleotide additions and insertions, either in coding or non-coding sequences of RNA, which can occur concomitantly with transcription and splicing processes.

Synonyms: dbRES

Resource Type: data or information resource, database

Defining Citation: [PMID:17088288](#)

Keywords: rna, rna editing, rna editing site

Resource Name: dbRES: A web-oriented database for annotated RNA Editing Site

Resource ID: SCR_002322

Alternate IDs: nif-0000-02732

Record Creation Time: 20220129T080212+0000

Ratings and Alerts

No rating or validation information has been found for dbRES: A web-oriented database for annotated RNA Editing Site.

No alerts have been found for dbRES: A web-oriented database for annotated RNA Editing Site.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Sahadevan S, et al. (2015) Identification of gene co-expression clusters in liver tissues from multiple porcine populations with high and low backfat androstenone phenotype. BMC genetics, 16, 21.