

# Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

## Cerebellar Development Transcriptome Database

RRID:SCR\_013096

Type: Tool

### Proper Citation

Cerebellar Development Transcriptome Database (RRID:SCR\_013096)

### Resource Information

**URL:** <http://www.cdtdb.brain.riken.jp/CDT/Top.jsp>

**Proper Citation:** Cerebellar Development Transcriptome Database (RRID:SCR\_013096)

**Description:** Transcriptomic information (spatiotemporal gene expression profile data) on the postnatal cerebellar development of mice (C57B/6J & ICR). It is a tool for mining cerebellar genes and gene expression, and provides a portal to relevant bioinformatics links. The mouse cerebellar circuit develops through a series of cellular and morphological events, including neuronal proliferation and migration, axonogenesis, dendritogenesis, and synaptogenesis, all within three weeks after birth, and each event is controlled by a specific gene group whose expression profile must be encoded in the genome. To elucidate the genetic basis of cerebellar circuit development, CDT-DB analyzes spatiotemporal gene expression by using in situ hybridization (ISH) for cellular resolution and by using fluorescence differential display and microarrays (GeneChip) for developmental time series resolution. The CDT-DB not only provides a cross-search function for large amounts of experimental data (ISH brain images, GeneChip graph, RT-PCR gel images), but also includes a portal function by which all registered genes have been provided with hyperlinks to websites of many relevant bioinformatics regarding gene ontology, genome, proteins, pathways, cell functions, and publications. Thus, the CDT-DB is a useful tool for mining potentially important genes based on characteristic expression profiles in particular cell types or during a particular time window in developing mouse brains.

**Abbreviations:** CDT-DB

**Resource Type:** database, data or information resource, atlas

**Defining Citation:** [PMID:18603407](#)

**Keywords:** gene expression, fluorescence, function, gene, gene chip, genome, bioinformatics, brain, cell, cerebellum, development, in situ hybridization, fluorescence differential display, cerebellar development, microarray, mining, mouse, mrna, ontology, pathway, protein, rt-pcr, molecular neuroanatomy resource, transcriptome,

spatiotemporal, cdna microarray, genechip, postnatal, histochemistry, image, postnatal development

**Related Condition:** Brain development, Brain disorder

**Funding:** INCF Japan Node ;  
Japan Society for the Promotion of Science ;  
Japanese Ministry of Education Culture Sports Science and Technology MEXT ;  
Japan Science and Technology Agency

**Availability:** To be used for research and educational purposes only. Any reproduction or use for commercial purposes is prohibited without the prior express written permission of the RIKEN.

**Resource Name:** Cerebellar Development Transcriptome Database

**Resource ID:** SCR\_013096

**Alternate IDs:** nif-0000-00008

**Record Creation Time:** 20220129T080314+0000

**Record Last Update:** 20260810T040556+0000

---

## Ratings and Alerts

No rating or validation information has been found for Cerebellar Development Transcriptome Database.

No alerts have been found for Cerebellar Development Transcriptome Database.

---

## 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 [NIF](#) .

Miller TE, et al. (2014) Lgr5 Marks Post-Mitotic, Lineage Restricted Cerebellar Granule Neurons during Postnatal Development. PloS one, 9(12), e114433.