# **Resource Summary Report**

Generated by NIF on May 16, 2025

## **CanEuCre**

RRID:SCR\_004159

Type: Tool

### **Proper Citation**

CanEuCre (RRID:SCR\_004159)

#### **Resource Information**

URL: http://www.caneucre.org

**Proper Citation:** CanEuCre (RRID:SCR\_004159)

**Description:** Cre expressing mice under the control of promoters with a design focus on the brain. Each promoter is derived from human sequence, but the resulting expression is assessed in the mouse for the activation of a LacZ reporter gene by the Cre activity. Promoters tested as large MaxiPromoters (BACs inserted into the mouse genome) and MiniPromoters (plasmid-based sequences inserted either into the mouse genome or introduced within AAV viruses). The Cre-related project continues from the Pleiades Promoter Project. Here is the list of genes for which icre/ERT2 mice are currently in development: AGTR1, CARTPT, CLDN5, CLVS2, CRH, GABRA6, HTR1A, HTR1B, KCNA4, KDM5C, MKI67, NEUROD6, NKX6-1, NOV, NPY2R, NR2E1, OLIG2, POU4F2, SLITRK6, SOX1, SOX3, SOX9,, SPRY1, VSX2

Abbreviations: CanEuCre

Synonyms: CanEuCre

**Resource Type:** production service resource, material service resource, biomaterial manufacture, service resource

**Keywords:** brain, cre, promoter, expression, transcription, mouse, human, adeno-associated virus (aav)

Funding: GenomeBC

Resource Name: CanEuCre

Resource ID: SCR\_004159

Alternate IDs: nlx\_143587

**Record Creation Time:** 20220129T080223+0000

**Record Last Update:** 20250516T053720+0000

## **Ratings and Alerts**

No rating or validation information has been found for CanEuCre.

No alerts have been found for CanEuCre.

#### **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 <u>NIF</u>.

Bradley A, et al. (2012) The mammalian gene function resource: the International Knockout Mouse Consortium. Mammalian genome: official journal of the International Mammalian Genome Society, 23(9-10), 580.