

Resource Summary Report

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CanEuCre

RRID:SCR_004159

Type: Tool

Proper Citation

CanEuCre (RRID:SCR_004159)

Resource Information

URL: <http://www.caneucre.org>

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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, biomaterial manufacture, service resource, material 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

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 2 mentions in open access literature.

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

Peeters S, et al. (2025) Escape from X-chromosome inactivation at KDM5C is driven by promoter-proximal DNA elements and enhanced by domain context. Human molecular genetics, 34(11), 978.

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.