Resource Summary Report

Generated by NIF on Jul 30, 2026

FUW-tetO-hKLF4

RRID:Addgene_20725
Type: Plasmid

Proper Citation

RRID:Addgene_20725

Plasmid Information

URL: http://www.addgene.org/20725

Proper Citation: RRID:Addgene_20725

Insert Name: KLF4

Organism: Homo sapiens

Bacterial Resistance: Ampicillin

Defining Citation: PMID:18786421

Vector Backbone Description: Backbone Marker:Carlos Lois; Backbone Size:8382; Vector Backbone:FUW; Vector Types:Mammalian Expression, Lentiviral; Bacterial Resistance:Ampicillin

Plasmid Name: FUW-tetO-hKLF4

Record Creation Time: 20220422T222052+0000

Record Last Update: 20260725T074420+0000

Ratings and Alerts

No rating or validation information has been found for FUW-tetO-hKLF4.

No alerts have been found for FUW-tetO-hKLF4.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Cai L, et al. (2025) Transcriptomic insights and feeder-free culturing of porcine expanded potential stem cells from cloned embryos. Stem cell research & therapy, 16(1), 527.

Ozkan B, et al. (2025) Cell-type-specific functionality encoded within the intrinsically disordered regions of OCT4. Nature communications, 16(1), 8647.

Choi H, et al. (2024) Establishment of porcine embryonic stem cells in simplified serum free media and feeder free expansion. Stem cell research & therapy, 15(1), 245.

Roberts GA, et al. (2021) Dissecting OCT4 defines the role of nucleosome binding in pluripotency. Nature cell biology, 23(8), 834.

Ruiz G, et al. (2019) Genes Involved in the Transcriptional Regulation of Pluripotency Are Expressed in Malignant Tumors of the Uterine Cervix and Can Induce Tumorigenic Capacity in a Nontumorigenic Cell Line. Stem cells international, 2019, 7683817.

Nguyen PNN, et al. (2017) miR-524-5p of the primate-specific C19MC miRNA cluster targets TP53IPN1- and EMT-associated genes to regulate cellular reprogramming. Stem cell research & therapy, 8(1), 214.

Cha Y, et al. (2017) Metabolic control of primed human pluripotent stem cell fate and function by the miR-200c-SIRT2 axis. Nature cell biology, 19(5), 445.

Rodriguez-Madoz JR, et al. (2017) Reversible dual inhibitor against G9a and DNMT1 improves human iPSC derivation enhancing MET and facilitating transcription factor engagement to the genome. PloS one, 12(12), e0190275.

Wu J, et al. (2017) Interspecies Chimerism with Mammalian Pluripotent Stem Cells. Cell, 168(3), 473.

Kim SI, et al. (2015) KLF4 N-terminal variance modulates induced reprogramming to pluripotency. Stem cell reports, 4(4), 727.

Soufi A, et al. (2012) Facilitators and impediments of the pluripotency reprogramming factors' initial engagement with the genome. Cell, 151(5), 994.