Resource Summary Report

Generated by RRID on Aug 20, 2026

pMPRAdonor2

RRID:Addgene_49353
Type: Plasmid

Proper Citation

RRID:Addgene_49353

Plasmid Information

URL: http://www.addgene.org/49353

Proper Citation: RRID:Addgene_49353

Insert Name: luc2

Organism: Synthetic

Bacterial Resistance: Ampicillin

Defining Citation: PMID:25177895

Vector Backbone Description: Backbone Marker:Genscript; Backbone Size:2693; Vector Backbone:pUC57; Vector Types:Luciferase; Bacterial Resistance:Ampicillin

Plasmid Name: pMPRAdonor2

Record Creation Time: 20220422T222254+0000

Record Last Update: 20260815T081559+0000

Ratings and Alerts

No rating or validation information has been found for pMPRAdonor2.

No alerts have been found for pMPRAdonor2.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Lee S, et al. (2025) Massively parallel reporter assay investigates shared genetic variants of eight psychiatric disorders. Cell, 188(5), 1409.

Shin T, et al. (2024) Rare variation in non-coding regions with evolutionary signatures contributes to autism spectrum disorder risk. Cell genomics, 4(8), 100609.

??rd T, et al. (2023) Genome-wide census of ATF4 binding sites and functional profiling of trait-associated genetic variants overlapping ATF4 binding motifs. PLoS genetics, 19(10), e1011014.

Shin T, et al. (2023) Rare variation in noncoding regions with evolutionary signatures contributes to autism spectrum disorder risk. medRxiv : the preprint server for health sciences.

Ho D, et al. (2021) Identifying the lungs as a susceptible site for allele-specific regulatory changes associated with type 1 diabetes risk. Communications biology, 4(1), 1072.

Yang X, et al. (2021) A miR-375/YAP axis regulates neuroendocrine differentiation and tumorigenesis in lung carcinoid cells. Scientific reports, 11(1), 10455.

Girskis KM, et al. (2021) Rewiring of human neurodevelopmental gene regulatory programs by human accelerated regions. Neuron, 109(20), 3239.

Richter F, et al. (2020) Genomic analyses implicate noncoding de novo variants in congenital heart disease. Nature genetics, 52(8), 769.

Davis JE, et al. (2020) Dissection of c-AMP Response Element Architecture by Using Genomic and Episomal Massively Parallel Reporter Assays. Cell systems, 11(1), 75.

Mazrooei P, et al. (2019) Cistrome Partitioning Reveals Convergence of Somatic Mutations and Risk Variants on Master Transcription Regulators in Primary Prostate Tumors. Cancer cell, 36(6), 674.

Pashos EE, et al. (2017) Large, Diverse Population Cohorts of hiPSCs and Derived Hepatocyte-like Cells Reveal Functional Genetic Variation at Blood Lipid-Associated Loci. Cell stem cell, 20(4), 558.

Doan RN, et al. (2016) Mutations in Human Accelerated Regions Disrupt Cognition and Social Behavior. Cell, 167(2), 341.

Ernst J, et al. (2016) Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. Nature biotechnology, 34(11), 1180.