

Resource Summary Report

Generated by [RRID](#) on Aug 17, 2026

[pMPRA1](#)

RRID:Addgene_49349

Type: Plasmid

Proper Citation

RRID:Addgene_49349

Plasmid Information

URL: <http://www.addgene.org/49349>

Proper Citation: RRID:Addgene_49349

Bacterial Resistance: Chloramphenicol and Ampicillin

Defining Citation: [PMID:25177895](#)

Vector Backbone Description: Backbone Marker:Promega; Backbone Size:4238; Vector Backbone:pGL4; Vector Types:Mammalian Expression; Bacterial Resistance:Chloramphenicol and Ampicillin

Plasmid Name: pMPRA1

Record Creation Time: 20220422T222254+0000

Record Last Update: 20260815T081558+0000

Ratings and Alerts

No rating or validation information has been found for pMPRA1.

No alerts have been found for pMPRA1.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Comerford M, et al. (2026) Mapping the gene regulatory landscape of archaic hominin introgression in modern Papuans. *PLoS genetics*, 22(3), e1012067.

O'Brien A, et al. (2026) Integrative screening identifies functional variants and VNTRs underlying GWAS signals at the 5p15.33 multi-cancer susceptibility locus. *medRxiv : the preprint server for health sciences*.

Li J, et al. (2025) Modeling and designing enhancers by introducing and harnessing transcription factor binding units. *Nature communications*, 16(1), 1469.

Nishino K, et al. (2025) Functional dissection of metabolic trait-associated gene regulation in steady state and stimulated human skeletal muscle cells. *bioRxiv : the preprint server for biology*.

Zhang P, et al. (2025) Systematic representation and optimization enable the inverse design of cross-species regulatory sequences in bacteria. *Nature communications*, 16(1), 1763.

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.

An M, et al. (2024) Systematic identification of pathogenic variants of non-small cell lung cancer in the promoters of DNA-damage repair genes. *EBioMedicine*, 110, 105480.

Cubillos P, et al. (2024) The growth factor EPIREGULIN promotes basal progenitor cell proliferation in the developing neocortex. *The EMBO journal*, 43(8), 1388.

??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.

Kliesmete Z, et al. (2023) Regulatory and coding sequences of TRNP1 co-evolve with brain size and cortical folding in mammals. *eLife*, 12.

Bhattarai KR, et al. (2023) Functional investigation of inherited noncoding genetic variation impacting the pharmacogenomics of childhood acute lymphoblastic leukemia treatment. *medRxiv : the preprint server for health sciences*.

Noack F, et al. (2023) Joint epigenome profiling reveals cell-type-specific gene regulatory programmes in human cortical organoids. *Nature cell biology*, 25(12), 1873.

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*.

Noack F, et al. (2022) Multimodal profiling of the transcriptional regulatory landscape of the developing mouse cortex identifies Neurog2 as a key epigenome remodeler. *Nature neuroscience*, 25(2), 154.

Vespasiani DM, et al. (2022) Denisovan introgression has shaped the immune system of present-day Papuans. *PLoS genetics*, 18(12), e1010470.

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.

Joslin AC, et al. (2021) A functional genomics pipeline identifies pleiotropy and cross-tissue effects within obesity-associated GWAS loci. *Nature communications*, 12(1), 5253.

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.

Myint L, et al. (2020) A screen of 1,049 schizophrenia and 30 Alzheimer's-associated variants for regulatory potential. *American journal of medical genetics. Part B, Neuropsychiatric genetics : the official publication of the International Society of Psychiatric Genetics*, 183(1), 61.