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.