

Resource Summary Report

Generated by [NIF](#) on Jul 30, 2026

pMB1610_pRR-Puro

RRID:Addgene_65853

Type: Plasmid

Proper Citation

RRID:Addgene_65853

Plasmid Information

URL: <http://www.addgene.org/65853>

Proper Citation: RRID:Addgene_65853

Insert Name: split puromycin N-acetyltransferase coding sequence

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:26190102](#)

Vector Backbone Description: Backbone Marker:Promega; Backbone Size:3705; Vector Backbone:phRL-SV40; Vector Types:Mammalian Expression, CRISPR, TALEN; Bacterial Resistance:Ampicillin

Plasmid Name: pMB1610_pRR-Puro

Record Creation Time: 20220422T222415+0000

Record Last Update: 20260725T075013+0000

Ratings and Alerts

No rating or validation information has been found for pMB1610_pRR-Puro.

No alerts have been found for pMB1610_pRR-Puro.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Schmolka N, et al. (2023) Dissecting the roles of MBD2 isoforms and domains in regulating NuRD complex function during cellular differentiation. *Nature communications*, 14(1), 3848.

Pánek J, et al. (2023) The SMN complex drives structural changes in human snRNAs to enable snRNP assembly. *Nature communications*, 14(1), 6580.

Bademosi AT, et al. (2023) EndophilinA-dependent coupling between activity-induced calcium influx and synaptic autophagy is disrupted by a Parkinson-risk mutation. *Neuron*, 111(9), 1402.

Tabata H, et al. (2022) Erratic and blood vessel-guided migration of astrocyte progenitors in the cerebral cortex. *Nature communications*, 13(1), 6571.

Li X, et al. (2020) High-Resolution In Vivo Identification of miRNA Targets by Halo-Enhanced Ago2 Pull-Down. *Molecular cell*, 79(1), 167.

Villaseñor R, et al. (2020) ChromID identifies the protein interactome at chromatin marks. *Nature biotechnology*, 38(6), 728.

Basilicata MF, et al. (2018) De novo mutations in MSL3 cause an X-linked syndrome marked by impaired histone H4 lysine 16 acetylation. *Nature genetics*, 50(10), 1442.