

Resource Summary Report

Generated by [RRID](#) on Aug 23, 2026

pBABE GFP

RRID:Addgene_10668

Type: Plasmid

Proper Citation

RRID:Addgene_10668

Plasmid Information

URL: <http://www.addgene.org/10668>

Proper Citation: RRID:Addgene_10668

Bacterial Resistance: Ampicillin

Vector Backbone Description: Backbone Size:5000; Vector Backbone:pBABE; Vector Types:Mammalian Expression, Retroviral; Bacterial Resistance:Ampicillin

Comments: Replaced the puromycin resistance gene from pBABE-puro with GFP for cell sorting. HindIII-ClaI GFP ORF from phrGFP-c (Stratagene) was cloned into pBABE-puro. hrGFP =humanized Renilla green fluorescent protein.

Plasmid Name: pBABE GFP

Record Creation Time: 20220422T221517+0000

Record Last Update: 20260815T080102+0000

Ratings and Alerts

No rating or validation information has been found for pBABE GFP.

No alerts have been found for pBABE GFP.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Uible EE, et al. (2026) Scaffolding-dependent CASP1 constrains excessive cell-intrinsic inflammatory signaling in leukemia. *Cell chemical biology*, 33(1), 59.

Newton LM, et al. (2026) CDK9 interacts with a RanGTP-importin-? complex to regulate erythroid enucleation. *Journal of cell science*, 139(12).

Marohl T, et al. (2025) PCSK5M452I is a recessive hypomorph exclusive to MCF10DCIS.com cells. *Molecular cancer research : MCR*.

Liebau RC, et al. (2024) Transcription-Coupled Repair of DNA Interstrand Crosslinks by UVSSA. *bioRxiv : the preprint server for biology*.

Makar AN, et al. (2024) The V-ATPase complex component RNaseK is required for lysosomal hydrolase delivery and autophagosome degradation. *Nature communications*, 15(1), 7743.

Alekseeva NA, et al. (2024) Obtaining Gene-Modified HLA-E-Expressing Feeder Cells for Stimulation of Natural Killer Cells. *Pharmaceutics*, 16(1).

Nagelberg AL, et al. (2024) Integrative genomics identifies SHPRH as a tumor suppressor gene in lung adenocarcinoma that regulates DNA damage response. *British journal of cancer*, 131(3), 534.

Ferrarone JR, et al. (2024) Genome-wide CRISPR screens in spheroid culture reveal that the tumor suppressor LKB1 inhibits growth via the PIKFYVE lipid kinase. *Proceedings of the National Academy of Sciences of the United States of America*, 121(21), e2403685121.

Singh D, et al. (2024) PP2A B55? inhibits epithelial-mesenchymal transition via regulation of Slug expression in non-small cell lung cancer. *Cancer letters*, 598, 217110.

Ferrarone JR, et al. (2023) LKB1 suppresses growth and promotes the internalization of EGFR through the PIKFYVE lipid kinase. *bioRxiv : the preprint server for biology*.

Wang L, et al. (2022) A kinase-independent function of cyclin-dependent kinase 6 promotes outer radial glia expansion and neocortical folding. *Proceedings of the National Academy of Sciences of the United States of America*, 119(38), e2206147119.

Kwanten B, et al. (2022) Target Identification of Small Molecules Using Large-Scale CRISPR-Cas Mutagenesis Scanning of Essential Genes. *Methods in molecular biology (Clifton, N.J.)*, 2377, 43.

Farnsworth DA, et al. (2022) MEK inhibitor resistance in lung adenocarcinoma is associated with addiction to sustained ERK suppression. *NPJ precision oncology*, 6(1), 88.

Yilmaz V, et al. (2022) A novel lineage-tracing mouse model for studying early MmuPV1 infections. *eLife*, 11.

Lee SH, et al. (2022) Inadvertent Transfer of Murine VL30 Retrotransposons to CAR-T Cells. *Advances in cell and gene therapy*, 2022.

Gribble JM, et al. (2021) The human intermediate prolactin receptor is a mammary proto-oncogene. *NPJ breast cancer*, 7(1), 37.

Akimov SS, et al. (2021) Immortalized striatal precursor neurons from Huntington's disease patient-derived iPS cells as a platform for target identification and screening for experimental therapeutics. *Human molecular genetics*, 30(24), 2469.

Xu Z, et al. (2018) Precision Tagging: A Novel Seamless Protein Tagging by Combinational Use of Type II and Type IIS Restriction Endonucleases. *Bio-protocol*, 8(3).

Bisogno LS, et al. (2017) Analysis of post-transcriptional regulation during cancer progression using a donor-derived isogenic model of tumorigenesis. *Methods (San Diego, Calif.)*, 126, 193.

Xu Z, et al. (2017) Highly efficient one-step scarless protein tagging by type IIS restriction endonuclease-mediated precision cloning. *Biochemical and biophysical research communications*, 490(1), 8.