

Resource Summary Report

Generated by [nidm-terms](#) on Aug 10, 2026

BE4

RRID:Addgene_100802

Type: Plasmid

Proper Citation

RRID:Addgene_100802

Plasmid Information

URL: <http://www.addgene.org/100802>

Proper Citation: RRID:Addgene_100802

Insert Name: BE

Organism: Rattus norvegicus

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:28875174](#)

Vector Backbone Description: Backbone Size:3402; Vector Backbone:pCMV; Vector Types:Mammalian Expression; Bacterial Resistance:Ampicillin

Plasmid Name: BE4

Record Creation Time: 20220422T221450+0000

Record Last Update: 20260808T080308+0000

Ratings and Alerts

No rating or validation information has been found for BE4.

No alerts have been found for BE4.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Kaufmann C, et al. (2026) Comprehensive CRISPR/Cas9-based mutagenesis identifies single-amino acid substitutions that abrogate SPEN function in X inactivation. *Nature communications*, 17(1).

Xu N, et al. (2025) Identification and Targeting of POLQ-Associated Hereditary Colorectal Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(15), 3215.

Kleinboehl EW, et al. (2024) Development and testing of a versatile genome editing application reporter (V-GEAR) system. *Molecular therapy. Methods & clinical development*, 32(2), 101253.

Ren CY, et al. (2024) Engineered CBEs based on *Macaca fascicularis* A3A with improved properties for precise genome editing. *Cell reports*, 43(3), 113878.

Jalil S, et al. (2021) Simultaneous high-efficiency base editing and reprogramming of patient fibroblasts. *Stem cell reports*, 16(12), 3064.

Smith CJ, et al. (2020) Enabling large-scale genome editing at repetitive elements by reducing DNA nicking. *Nucleic acids research*, 48(9), 5183.

Sakata RC, et al. (2020) Base editors for simultaneous introduction of C-to-T and A-to-G mutations. *Nature biotechnology*, 38(7), 865.

Webber BR, et al. (2019) Highly efficient multiplex human T cell engineering without double-strand breaks using Cas9 base editors. *Nature communications*, 10(1), 5222.