

Resource Summary Report

Generated by [RRID](#) on Aug 26, 2026

pX600-AAV-CMV::NLS-SaCas9-NLS-3xHA-bGHpA

RRID:Addgene_61592

Type: Plasmid

Proper Citation

RRID:Addgene_61592

Plasmid Information

URL: <http://www.addgene.org/61592>

Proper Citation: RRID:Addgene_61592

Insert Name: hSaCas9

Organism: Other

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:25830891](#)

Vector Backbone Description: Vector Backbone:pAAV; Vector Types:Mammalian Expression, AAV, CRISPR; Bacterial Resistance:Ampicillin

Comments: Note: This plasmid does not have an sgRNA expression cassette. Please refer to the associated publication, as well as the AAV portion of <http://www.addgene.org/crispr/zhang/> , for more information on expressing sgRNAs.

Plasmid Name: pX600-AAV-CMV::NLS-SaCas9-NLS-3xHA-bGHpA

Record Creation Time: 20220422T222353+0000

Record Last Update: 20260815T081744+0000

Ratings and Alerts

No rating or validation information has been found for pX600-AAV-CMV::NLS-SaCas9-NLS-3xHA-bGHpA.

No alerts have been found for pX600-AAV-CMV::NLS-SaCas9-NLS-3xHA-bGHpA.

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 [RRID](#) .

Liu Z, et al. (2025) Regulation of Sleep Amount by CRT1 via Transcription of Crh in Mice. The Journal of neuroscience : the official journal of the Society for Neuroscience, 45(5).

Yan J, et al. (2024) Improving prime editing with an endogenous small RNA-binding protein. Nature, 628(8008), 639.

Escobar M, et al. (2022) Quantification of Genome Editing and Transcriptional Control Capabilities Reveals Hierarchies among Diverse CRISPR/Cas Systems in Human Cells. ACS synthetic biology, 11(10), 3239.

Kim SJ, et al. (2022) Kinase signalling in excitatory neurons regulates sleep quantity and depth. Nature, 612(7940), 512.

Sabatini PV, et al. (2021) tTARGIT AAVs mediate the sensitive and flexible manipulation of intersectional neuronal populations in mice. eLife, 10.

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

Erwood S, et al. (2019) Modeling Niemann-Pick disease type C in a human haploid cell line allows for patient variant characterization and clinical interpretation. Genome research, 29(12), 2010.

Thakore PI, et al. (2018) RNA-guided transcriptional silencing in vivo with S. aureus CRISPR-Cas9 repressors. Nature communications, 9(1), 1674.