

Resource Summary Report

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

[pX330-SpCas9-NG](#)

RRID:Addgene_117919

Type: Plasmid

Proper Citation

RRID:Addgene_117919

Plasmid Information

URL: <http://www.addgene.org/117919>

Proper Citation: RRID:Addgene_117919

Insert Name: SpCas9-NG (L1111R/D1135V/G1218R/E1219F/A1322R/R1335V/T1337R)

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:30166441](#)

Vector Backbone Description: Vector Backbone:pX330; Vector Types:Mammalian Expression; Bacterial Resistance:Ampicillin

Plasmid Name: pX330-SpCas9-NG

Record Creation Time: 20220422T221617+0000

Record Last Update: 20260815T080259+0000

Ratings and Alerts

No rating or validation information has been found for pX330-SpCas9-NG.

No alerts have been found for pX330-SpCas9-NG.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Tan K, et al. (2025) Treatment of Huntington's disease with a pan-HTT-targeting CRISPR nuclease. bioRxiv : the preprint server for biology.

Vasquez CA, et al. (2025) Precision genome editing and in-cell measurements of oxidative DNA damage repair enable functional and mechanistic characterization of cancer-associated MUTYH variants. Nucleic acids research, 53(6).

Hong C, et al. (2024) Genome-wide in-locus epitope tagging of Arabidopsis proteins using prime editors. BMB reports, 57(1), 66.

Kulcsár PI, et al. (2023) A cleavage rule for selection of increased-fidelity SpCas9 variants with high efficiency and no detectable off-targets. Nature communications, 14(1), 5746.

Alowaysi M, et al. (2023) Generation of myoglobin (MB)-knockout human embryonic stem cell (hESC) line (KAIMRCe002-A-1S) using CRISPR/Cas9 technology. Stem cell research, 71, 103158.

Zhao Y, et al. (2023) Debugging and consolidating multiple synthetic chromosomes reveals combinatorial genetic interactions. Cell, 186(24), 5220.

Chen Y, et al. (2022) Multiplex base editing to convert TAG into TAA codons in the human genome. Nature communications, 13(1), 4482.

Sánchez-Rivera FJ, et al. (2022) Base editing sensor libraries for high-throughput engineering and functional analysis of cancer-associated single nucleotide variants. Nature biotechnology, 40(6), 862.

Ye J, et al. (2022) Can SpRY recognize any PAM in human cells? Journal of Zhejiang University. Science. B, 23(5), 382.

Fang Q, et al. (2021) A cost efficient protocol to introduce epitope tags by CRISPR-Cas9 mediated gene knock-in with asymmetric semi-double stranded template. MethodsX, 8, 101365.

Zhao T, et al. (2021) Small-molecule compounds boost genome-editing efficiency of cytosine base editor. Nucleic acids research, 49(15), 8974.

Jang HK, et al. (2021) High-purity production and precise editing of DNA base editing ribonucleoproteins. Science advances, 7(35).

Tang L, et al. (2019) Efficient cleavage resolves PAM preferences of CRISPR-Cas in human cells. Cell regeneration (London, England), 8(2), 44.