

# Resource Summary Report

Generated by [NIF](#) on Jul 29, 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:** 20260725T073612+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 12 mentions in open access literature.

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

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.

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

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.

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

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.

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.