

# Resource Summary Report

Generated by [RRID](#) on Aug 21, 2026

## 5'UTR CGG 99x FMR1

RRID:Addgene\_63089

Type: Plasmid

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### Proper Citation

RRID:Addgene\_63089

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### Plasmid Information

**URL:** <http://www.addgene.org/63089>

**Proper Citation:** RRID:Addgene\_63089

**Insert Name:** expanded CGG repeats (99 repeats) within the 5'UTR of FMR1

**Organism:** Homo sapiens

**Bacterial Resistance:** Ampicillin

**Vector Backbone Description:** Vector Backbone:unknown; Vector Types:Mammalian Expression; Bacterial Resistance:Ampicillin

**Comments:** Should be amplified in STBL3 bacteria and grown at Room temperature to keep the repeats stable. This construct allows translation of CGG repeats into 99 glycine due to a near cognate ATG codon upstream of the repeat in the 5'UTR of FMR1 (an ACG codon that initiates weakly translation). This plasmid should be verified via restriction analysis. Multiple colonies may need to be screened to isolate the correct construct.

**Plasmid Name:** 5'UTR CGG 99x FMR1

**Record Creation Time:** 20220422T222401+0000

**Record Last Update:** 20260815T081758+0000

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### Ratings and Alerts

No rating or validation information has been found for 5'UTR CGG 99x FMR1.

No alerts have been found for 5'UTR CGG 99x FMR1.

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### Data and Source Information

Source: [Addgene](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Tutak K, et al. (2025) Insufficiency of 40S ribosomal proteins, RPS26 and RPS25, negatively affects biosynthesis of polyglycine-containing proteins in fragile-X associated conditions. eLife, 13.

Giesselmann P, et al. (2019) Analysis of short tandem repeat expansions and their methylation state with nanopore sequencing. Nature biotechnology, 37(12), 1478.