

Resource Summary Report

Generated by [dkNET](#) on Aug 17, 2026

pSTARR-seq_fly

RRID:Addgene_71499

Type: Plasmid

Proper Citation

RRID:Addgene_71499

Plasmid Information

URL: <http://www.addgene.org/71499>

Proper Citation: RRID:Addgene_71499

Bacterial Resistance: Chloramphenicol and Ampicillin

Defining Citation: [PMID:23328393](#)

Vector Backbone Description: Backbone Marker:Promega; Vector Backbone:pGL3-Promoter; Vector Types:Insect Expression, flySTARR-seq screening vector; Bacterial Resistance:Chloramphenicol and Ampicillin

Comments: This plasmid was made by replacing the sequence of pGL3-Promoter between BglII and FseI with a fragment containing the core promoter listed above, an mhc16 intron, an ORF (sgGFP, Qbiogene, Inc), a ccdB suicide gene flanked by homology arms (used for cloning the enhancer candidates during library generation), followed by the pGL3's SV40 late polyA-signal.

Plasmid Name: pSTARR-seq_fly

Record Creation Time: 20220422T222440+0000

Record Last Update: 20260815T081911+0000

Ratings and Alerts

No rating or validation information has been found for pSTARR-seq_fly.

No alerts have been found for pSTARR-seq_fly.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Cohen LB, et al. (2025) A genome-wide survey reveals a diverse array of enhancers coordinate the *Drosophila* innate immune response. *bioRxiv : the preprint server for biology*.

Jones BM, et al. (2025) The Fire Ant Social Chromosome Exerts a Major Influence on Genome Regulation. *Molecular biology and evolution*, 42(6).

Gallego Romero I, et al. (2023) Leveraging massively parallel reporter assays for evolutionary questions. *Genome biology*, 24(1), 26.

Holm I, et al. (2021) Comprehensive Genomic Discovery of Non-Coding Transcriptional Enhancers in the African Malaria Vector *Anopheles coluzzii*. *Frontiers in genetics*, 12, 785934.

Neumayr C, et al. (2019) STARR-seq and UMI-STARR-seq: Assessing Enhancer Activities for Genome-Wide-, High-, and Low-Complexity Candidate Libraries. *Current protocols in molecular biology*, 128(1), e105.

Nardini L, et al. (2019) Influence of genetic polymorphism on transcriptional enhancer activity in the malaria vector *Anopheles coluzzii*. *Scientific reports*, 9(1), 15275.