Resource Summary Report

Generated by RRID on Aug 19, 2026

pSTARR-seq_human

RRID:Addgene_71509
Type: Plasmid

Proper Citation

RRID:Addgene_71509

Plasmid Information

URL: http://www.addgene.org/71509

Proper Citation: RRID:Addgene_71509

Bacterial Resistance: Chloramphenicol and Ampicillin

Defining Citation: PMID:23328393

Vector Backbone Description: Backbone Marker:Promega; Vector Backbone:pGL4.10; Vector Types:Mammalian Expression, humanSTARR-seq screening vector; Bacterial Resistance:Chloramphenicol and Ampicillin

Comments: Note: The original human STARR-seq plasmid has been used in the Arnold et al. 2013 publication. It should be replaced for all screens in mammalian cells with the updated version reported by Muerdter et al. 2017 for much improved signal-to-noise, especially for screens with highly complex libraries (e.g. those covering an entire mammalian genome). The improved version is Addgene plasmid # 99296. For enhancer-activity measurements in mammalian cells, please also consider the possibility of a plasmid-induced innate immune response (see Muerdter et al., 2017). The sequence between SacI and AfeI on pGL4 was replaced by the fragment containing the Super Core Promoter 1 (SCP1), a synthetic intron (pIRESpuro3, Clontech; cat. no. 631619) an ORF (sgGFP, Qbiogene, Inc), a ccdB suicide gene flanked by homology arms, and the pGL3's SV40 late polyA-signal.

Plasmid Name: pSTARR-seq_human

Record Creation Time: 20220422T222440+0000

Record Last Update: 20260815T081911+0000

Ratings and Alerts

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

No alerts have been found for pSTARR-seq_human.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Tardaguila M, et al. (2026) Integrating natural and engineered genetic variations to decode regulatory influence on blood traits. Cell reports, 45(2), 116937.

Becker R, et al. (2026) STARR-CRAAVT: A platform to identify cell type-specific regulatory elements for next-generation gene therapy. iScience, 29(4), 115469.

Mishra A, et al. (2024) Identification of functional enhancer variants associated with type I diabetes in CD4+ T cells. Frontiers in immunology, 15, 1387253.

Klagkou E, et al. (2024) An Unbiased Approach to Identifying Cellular Reprogramming-Inducible Enhancers. International journal of molecular sciences, 25(23).

Chan YC, et al. (2023) An unbiased AAV-STARR-seq screen revealing the enhancer activity map of genomic regions in the mouse brain in vivo. Scientific reports, 13(1), 6745.

Gjaltema RAF, et al. (2022) Distal and proximal cis-regulatory elements sense X chromosome dosage and developmental state at the Xist locus. Molecular cell, 82(1), 190.

Kulik M, et al. (2021) Androgen and glucocorticoid receptor direct distinct transcriptional programs by receptor-specific and shared DNA binding sites. Nucleic acids research, 49(7), 3856.

Glaser LV, et al. (2021) Assessing genome-wide dynamic changes in enhancer activity during early mESC differentiation by FAIRE-STARR-seq. Nucleic acids research, 49(21), 12178.

Roberts BS, et al. (2021) Genome-wide strand asymmetry in massively parallel reporter activity favors genic strands. Genome research, 31(5), 866.

Klein JC, et al. (2020) A systematic evaluation of the design and context dependencies of massively parallel reporter assays. Nature methods, 17(11), 1083.

Doni Jayavelu N, et al. (2020) Candidate silencer elements for the human and mouse genomes. Nature communications, 11(1), 1061.

Tippens ND, et al. (2020) Transcription imparts architecture, function and logic to enhancer units. Nature genetics, 52(10), 1067.

van Weerd JH, et al. (2020) Trait-associated noncoding variant regions affect TBX3 regulation and cardiac conduction. eLife, 9.

Malik V, et al. (2019) Pluripotency reprogramming by competent and incompetent POU factors uncovers temporal dependency for Oct4 and Sox2. Nature communications, 10(1), 3477.

Ramisch A, et al. (2019) CRUP: a comprehensive framework to predict condition-specific regulatory units. Genome biology, 20(1), 227.

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.

Wang X, et al. (2018) High-resolution genome-wide functional dissection of transcriptional regulatory regions and nucleotides in human. Nature communications, 9(1), 5380.

Vockley CM, et al. (2016) Direct GR Binding Sites Potentiate Clusters of TF Binding across the Human Genome. Cell, 166(5), 1269.