

Resource Summary Report

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

pQE30-His-T7RNAP

RRID:Addgene_124138

Type: Plasmid

Proper Citation

RRID:Addgene_124138

Plasmid Information

URL: <http://www.addgene.org/124138>

Proper Citation: RRID:Addgene_124138

Insert Name: T7 RNA polymerase

Organism: Enterobacteria phage T7

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:11479568](#)

Vector Backbone Description: Vector Backbone:pQE30; Vector Types:Bacterial Expression; Bacterial Resistance:Ampicillin

Comments: This plasmid is provided in NEB Stable cells from Addgene; however, the depositor originally cloned this plasmid in JM109 cells. It is recommended to screen DNA preps from multiple colonies by Sanger sequencing, as this plasmid may be prone to deletions in the promoter region.

Plasmid Name: pQE30-His-T7RNAP

Record Creation Time: 20220422T221651+0000

Record Last Update: 20260815T080403+0000

Ratings and Alerts

No rating or validation information has been found for pQE30-His-T7RNAP.

No alerts have been found for pQE30-His-T7RNAP.

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 [RRID](#) .

Ansah SO, et al. (2026) Quantifying Mg²⁺ dependence on conformational equilibrium in the two-state 7SK RNA stem-loop 3. bioRxiv : the preprint server for biology.

Yadav S, et al. (2025) ATP Regeneration from Pyruvate in the PURE System. ACS synthetic biology, 14(1), 247.

van der Sijs A, et al. (2024) Broccoli aptamer allows quantitative transcription regulation studies in vitro. PloS one, 19(6), e0304677.

Ngo PHT, et al. (2023) Changes in Coding and Efficiency through Modular Modifications to a One Pot PURE System for In Vitro Transcription and Translation. ACS synthetic biology, 12(12), 3771.

Sobeh AM, et al. (2023) C-terminal determinants for RNA binding motif 7 protein stability and RNA recognition. Biophysical chemistry, 292, 106928.

Pandi A, et al. (2022) A versatile active learning workflow for optimization of genetic and metabolic networks. Nature communications, 13(1), 3876.