

# Resource Summary Report

Generated by [RRID](#) on Sep 1, 2026

## [pGEM-3z/601](#)

RRID:Addgene\_26656

Type: Plasmid

### Proper Citation

RRID:Addgene\_26656

### Plasmid Information

**URL:** <http://www.addgene.org/26656>

**Proper Citation:** RRID:Addgene\_26656

**Bacterial Resistance:** Ampicillin

**Defining Citation:** [PMID:9514715](#)

**Vector Backbone Description:** Backbone Marker:Promega; Backbone Size:2743; Vector Backbone:pGEM-3Z; Vector Types:Bacterial Expression; Bacterial Resistance:Ampicillin

**Comments:** This plasmid contains a 147 bp nucleosome positioning sequence and is referred to as clone"601". Primers that are used by the Widom lab to amplify the 147 bp fragment: Forward: ctggagaatcccgtgccg Reverse: acaggatgtatatctgacacg Please note that there may be discrepancies between Addgene's sequencing results and the depositor's sequence. Potential discrepancies are not a concern according to the depositing scientist because the clones were selected for their ability to bind to histone octamer, not for their specific sequence.

**Plasmid Name:** pGEM-3z/601

**Record Creation Time:** 20220422T222119+0000

**Record Last Update:** 20260829T080309+0000

### Ratings and Alerts

No rating or validation information has been found for pGEM-3z/601.

No alerts have been found for pGEM-3z/601.

### Data and Source Information

## Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Saha A, et al. (2026) Linker histone H1.5 contributes to centromere integrity. *Nucleic acids research*, 54(1).

Li Z, et al. (2026) Protocol for generating endogenous degron tags in essential transcription factors in human iPSCs via CRISPR-Cas9. *STAR protocols*, 7(2), 104602.

Galloy M, et al. (2025) Ubiquitination of the histone variant mH2A1.2 prevents toxic RAD18 accumulation at a subset of genomic loci upon replication stress. *Molecular cell*, 85(16), 3023.

Yadav Y, et al. (2025) Mechanistic insights into DNA binding by BD1 of the TAF1 tandem bromodomain module. *The Biochemical journal*, 482(19), 1415.

Nishide G, et al. (2025) Spatiotemporal dynamics of protamine-DNA condensation revealed by high-speed atomic force microscopy. *Nucleic acids research*, 53(6).

Jung H, et al. (2024) Structural and Biochemical Characterization of the Nucleosome Containing Variants H3.3 and H2A.Z. *Epigenomes*, 8(2).

Lorton BM, et al. (2024) Glutamylation of Npm2 and Nap1 acidic disordered regions increases DNA mimicry and histone chaperone efficiency. *iScience*, 27(4), 109458.

Zhang M, et al. (2024) Angle between DNA linker and nucleosome core particle regulates array compaction revealed by individual-particle cryo-electron tomography. *Nature communications*, 15(1), 4395.

Frisbie VS, et al. (2024) Two DOT1 enzymes cooperatively mediate efficient ubiquitin-independent histone H3 lysine 76 tri-methylation in kinetoplastids. *Nature communications*, 15(1), 2467.

Medeiros SK, et al. (2023) INVESTIGATION OF THE PATHOLOGICAL EFFECTS OF HISTONES, DNA, AND NUCLEOSOMES IN A MURINE MODEL OF SEPSIS. *Shock (Augusta, Ga.)*, 60(2), 291.

Sokolova V, et al. (2023) DNA-translocation-independent role of INO80 remodeler in DNA damage repairs. *The Journal of biological chemistry*, 299(10), 105245.

Safaric B, et al. (2022) The fork protection complex recruits FACT to reorganize nucleosomes during replication. *Nucleic acids research*, 50(3), 1317.

Jack A, et al. (2022) Compartmentalization of telomeres through DNA-scaffolded phase separation. *Developmental cell*, 57(2), 277.

Galloy M, et al. (2021) Approaches to Study Native Chromatin-Modifying Complex Activities and Functions. *Frontiers in cell and developmental biology*, 9, 729338.

Zhang Q, et al. (2021) PALI1 facilitates DNA and nucleosome binding by PRC2 and triggers an allosteric activation of catalysis. *Nature communications*, 12(1), 4592.

Melters DP, et al. (2019) Intrinsic elasticity of nucleosomes is encoded by histone variants and calibrated by their binding partners. *Proceedings of the National Academy of Sciences of the United States of America*, 116(48), 24066.

Chen Z, et al. (2019) High-resolution and high-accuracy topographic and transcriptional maps of the nucleosome barrier. *eLife*, 8.

Würtz M, et al. (2019) DNA accessibility of chromatosomes quantified by automated image analysis of AFM data. *Scientific reports*, 9(1), 12788.

Stumme-Diers MP, et al. (2019) Probing The Structure And Dynamics Of Nucleosomes Using Atomic Force Microscopy Imaging. *Journal of visualized experiments : JoVE*(143).

Stumme-Diers MP, et al. (2018) Nanoscale dynamics of centromere nucleosomes and the critical roles of CENP-A. *Nucleic acids research*, 46(1), 94.