

Resource Summary Report

Generated by [RRID](#) on Aug 22, 2026

[pAG36](#)

RRID:Addgene_35126

Type: Plasmid

Proper Citation

RRID:Addgene_35126

Plasmid Information

URL: <http://www.addgene.org/35126>

Proper Citation: RRID:Addgene_35126

Insert Name: nat1

Organism: Streptomyces noursei

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:10514571](#)

Vector Backbone Description: Vector Backbone:pRS316; Vector Types:Yeast replicating; Bacterial Resistance:Ampicillin

Plasmid Name: pAG36

Record Creation Time: 20220422T222149+0000

Record Last Update: 20260815T081404+0000

Ratings and Alerts

No rating or validation information has been found for pAG36.

No alerts have been found for pAG36.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Zhang S, et al. (2025) Drosophila aux orchestrates the phosphorylation-dependent assembly of the lysosomal V-ATPase in glia and contributes to SNCA/??-synuclein degradation. *Autophagy*, 21(5), 1039.

Stuecker TN, et al. (2025) Improved vectors for retron-mediated CRISPR-Cas9 genome editing in *Saccharomyces cerevisiae*. *G3 (Bethesda, Md.)*, 15(10).

Dutreux F, et al. (2023) Lessons from the meiotic recombination landscape of the ZMM deficient budding yeast *Lachancea waltii*. *PLoS genetics*, 19(1), e1010592.

Rau EM, et al. (2022) Overexpression of Two New Acyl-CoA:Diacylglycerol Acyltransferase 2-Like Acyl-CoA:Sterol Acyltransferases Enhanced Squalene Accumulation in *Aurantiochytrium limacinum*. *Frontiers in microbiology*, 13, 822254.

Peltier E, et al. (2021) Dissection of quantitative trait loci in the *Lachancea waltii* yeast species highlights major hotspots. *G3 (Bethesda, Md.)*, 11(9).

Naseri G, et al. (2019) COMPASS for rapid combinatorial optimization of biochemical pathways based on artificial transcription factors. *Nature communications*, 10(1), 2615.

Hochrein L, et al. (2017) AssemblX: a user-friendly toolkit for rapid and reliable multi-gene assemblies. *Nucleic acids research*, 45(10), e80.