

Resource Summary Report

Generated by [NIF](#) on Sep 21, 2026

pCAG:H2B-EGFP

RRID:Addgene_32599

Type: Plasmid

Proper Citation

RRID:Addgene_32599

Plasmid Information

URL: <http://www.addgene.org/32599>

Proper Citation: RRID:Addgene_32599

Insert Name: H2B-EGFP

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:15619330](#)

Vector Backbone Description: Vector Backbone:pCAGGS; Vector Types:Mammalian Expression; Bacterial Resistance:Ampicillin

Comments: Please note that the plasmid contains a duplication of the H2B-EGFP region as compared to the original depositor sequence. The depositor has confirmed that the plasmid functions as described in the associated publication. The coding sequence for the human histone H2B gene (X57127) was amplified from genomic DNA by PCR using Pfx Polymerase (Invitrogen). The resulting product was cloned into pCR4 TOPO (Invitrogen) to generate pH2B. The H2B fragment was then cloned into plasmids pEGFP-N1, pDsRed2-N1 pDsRedExpress-N1 (BD Biosciences, Inc) in order to generate plasmids pH2B-EGFP, pH2B-DsRed2 and pH2B-DsRedExpress (oligonucleotide sequences are available upon request). The resulting fusions were then re-amplified by PCR and cloned into the XhoI site of pCAGGS [19] to generate pCX-H2B-EGFP, pCX-H2B-DsRed2 and pCX-H2B-DsRedExpress.

Plasmid Name: pCAG:H2B-EGFP

Record Creation Time: 20220422T222141+0000

Record Last Update: 20260919T091709+0000

Ratings and Alerts

No rating or validation information has been found for pCAG:H2B-EGFP.

No alerts have been found for pCAG:H2B-EGFP.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Oikonomou P, et al. (2025) Application and measurement of tissue-scale tension in avian epithelia in vivo to study multiscale mechanics and inter-germ layer coupling. Development (Cambridge, England), 152(16).

Pontes-Quero S, et al. (2017) Dual ifgMosaic: A Versatile Method for Multispectral and Combinatorial Mosaic Gene-Function Analysis. Cell, 170(4), 800.