

Resource Summary Report

Generated by [RRID](#) on Aug 18, 2026

pDule-tfmF A65V S158A

RRID:Addgene_85484

Type: Plasmid

Proper Citation

RRID:Addgene_85484

Plasmid Information

URL: <http://www.addgene.org/85484>

Proper Citation: RRID:Addgene_85484

Insert Name: tri-fluoromethyl-phenylalanine Mj synthetase A65V S158A

Organism: Methanocaldococcus jannaschii

Bacterial Resistance: Tetracycline

Defining Citation: [PMID:20082521](#)

Vector Backbone Description: Backbone Size:5400; Vector Backbone:pDule; Vector Types:Bacterial Expression; Bacterial Resistance:Tetracycline

Plasmid Name: pDule-tfmF A65V S158A

Relevant Mutation: Y32V F108W Q109M I159M with 65Val and 158Ala

Record Creation Time: 20220422T222550+0000

Record Last Update: 20260815T082124+0000

Ratings and Alerts

No rating or validation information has been found for pDule-tfmF A65V S158A.

No alerts have been found for pDule-tfmF A65V S158A.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Liebau J, et al. (2025) 4D structural biology-quantitative dynamics in the eukaryotic RNA exosome complex. Nature communications, 16(1), 7896.

Schweipert M, et al. (2024) The catalytic domain of free or ligand bound histone deacetylase 4 occurs in solution predominantly in closed conformation. Protein science : a publication of the Protein Society, 33(3), e4917.

St-Jacques AD, et al. (2023) Computational remodeling of an enzyme conformational landscape for altered substrate selectivity. Nature communications, 14(1), 6058.

Pagar AD, et al. (2022) Non-Canonical Amino Acid-Based Engineering of (R)-Amine Transaminase. Frontiers in chemistry, 10, 839636.