

Resource Summary Report

Generated by [NIF](#) on Sep 5, 2026

YopH (residues 164-468)

RRID:Addgene_79749

Type: Plasmid

Proper Citation

RRID:Addgene_79749

Plasmid Information

URL: <http://www.addgene.org/79749>

Proper Citation: RRID:Addgene_79749

Insert Name: YopH (residues 164-468)

Organism: Other

Bacterial Resistance: Spectinomycin

Defining Citation: [PMID:30004690](#)

Vector Backbone Description: Backbone Marker:Scott Gradia (Addgene plasmid # 48323); Vector Backbone:pET co-transformation cloning vector (13S-A) ; Vector Types:Bacterial Expression; Bacterial Resistance:Spectinomycin

Comments: This plasmid was generated as part of an open library of human kinase domain constructs for automated bacterial expression. The work can be found here doi: <http://dx.doi.org/10.1101/038711>

Plasmid Name: YopH (residues 164-468)

Record Creation Time: 20220422T222522+0000

Record Last Update: 20260905T080152+0000

Ratings and Alerts

No rating or validation information has been found for YopH (residues 164-468).

No alerts have been found for YopH (residues 164-468).

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 [NIF](#) .

Machner L, et al. (2025) Mechanism of SHP2 activation by bis-Tyr-phosphorylated Gab1. Structure (London, England : 1993).

Baker ZD, et al. (2025) Tyrosine-Mediated Static and Dynamic Quenching of a Receptor Tyrosine Kinase Biosensor Reveals Inhibitor Binding Modes and Kinase Conformations. ACS chemical biology, 20(7), 1683.

Bartošík V, et al. (2024) Structural basis of binding the unique N-terminal domain of microtubule-associated protein 2c to proteins regulating kinases of signaling pathways. The Journal of biological chemistry, 300(8), 107551.

Roy MJ, et al. (2023) Structural mapping of PEAK pseudokinase interactions identifies 14-3-3 as a molecular switch for PEAK3 signaling. Nature communications, 14(1), 3542.

Li F, et al. (2022) Mapping the conformational energy landscape of Abl kinase using ClyA nanopore tweezers. Nature communications, 13(1), 3541.

Woodall NB, et al. (2021) De novo design of tyrosine and serine kinase-driven protein switches. Nature structural & molecular biology, 28(9), 762.

Díaz Galicia ME, et al. (2019) Methods for the recombinant expression of active tyrosine kinase domains: Guidelines and pitfalls. Methods in enzymology, 621, 131.