Resource Summary Report

Generated by RRID on Aug 25, 2026

pHYRS52

RRID:Addgene_31122
Type: Plasmid

Proper Citation

RRID:Addgene_31122

Plasmid Information

URL: http://www.addgene.org/31122

Proper Citation: RRID:Addgene_31122

Insert Name: Ulp1

Organism: Saccharomyces cerevisiae

Bacterial Resistance: Ampicillin

Defining Citation: PMID:19031436

Vector Backbone Description: Backbone Marker:invitrogen; Backbone Size:2894; Vector Backbone:pRsetA; Vector Types:Bacterial Expression; Bacterial Resistance:Ampicillin

Comments: Mossessova E, Lima CD. Mol Cell. 2000 May;5(5):865-76. Note: pFGET19_Ulp1 (#64697) is a new version of pHYRS52(#31122) with kanamycin resistance.

Plasmid Name: pHYRS52

Relevant Mutation: Ulp1(403-621)

Record Creation Time: 20220422T222135+0000

Record Last Update: 20260815T081332+0000

Ratings and Alerts

No rating or validation information has been found for pHYRS52.

No alerts have been found for pHYRS52.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Lud??scher JM, et al. (2026) Structural basis for uracil removal from DNA by human SMUG1. Nature communications, 17(1).

Quintana JI, et al. (2024) Different roles of the heterodimer architecture of galectin-4 in selective recognition of oligosaccharides and lipopolysaccharides having ABH antigens. The Journal of biological chemistry, 300(8), 107577.

Quintana JI, et al. (2024) The impact of glycosylation on the structure, function, and interactions of CD14. Glycobiology, 34(3).

Nelson B, et al. (2023) Bacterial J-Domains with C-Terminal Tags Contact the Substrate Binding Domain of DnaK and Sequester Chaperone Activity. Chembiochem : a European journal of chemical biology, 24(20), e202300261.

Richards A, et al. (2022) Complementary protocols to evaluate inhibitors against the DnaK chaperone network. STAR protocols, 3(2), 101381.

Braffman NR, et al. (2022) Structural basis for an unprecedented enzymatic alkylation in cylindrocyclophane biosynthesis. eLife, 11.

Hosfelt J, et al. (2022) An allosteric inhibitor of bacterial Hsp70 chaperone potentiates antibiotics and mitigates resistance. Cell chemical biology, 29(5), 854.

Nelson B, et al. (2022) Protein Cofactor Mimics Disrupt Essential Chaperone Function in Stressed Mycobacteria. ACS infectious diseases, 8(5), 901.

Maddi ER, et al. (2021) Optimization strategies for expression and purification of soluble N-terminal domain of human centriolar protein SAS-6 in Escherichia coli. Protein expression and purification, 183, 105856.

Yin Y, et al. (2021) Structural basis for aggregate dissolution and refolding by the Mycobacterium tuberculosis ClpB-DnaK bi-chaperone system. Cell reports, 35(8), 109166.

Harnagel A, et al. (2021) Nonredundant functions of Mycobacterium tuberculosis chaperones promote survival under stress. Molecular microbiology, 115(2), 272.

Lopez Quezada L, et al. (2020) Activity-Based Protein Profiling Reveals That Cephalosporins Selectively Active on Non-replicating Mycobacterium tuberculosis Bind Multiple Protein Families and Spare Peptidoglycan Transpeptidases. Frontiers in microbiology, 11, 1248.

Loving HS, et al. (2019) Conformational Dynamics of FERM-Mediated Autoinhibition in Pyk2 Tyrosine Kinase. Biochemistry, 58(36), 3767.

Lupoli TJ, et al. (2016) Reconstitution of a Mycobacterium tuberculosis proteostasis network highlights essential cofactor interactions with chaperone DnaK. Proceedings of the National Academy of Sciences of the United States of America, 113(49), E7947.

Guerrero F, et al. (2015) Tandem SUMO fusion vectors for improving soluble protein expression and purification. Protein expression and purification, 116, 42.