

# PSIPS1

**PDB:**4FU6

## Revision

**Revision Type:**created

**Revised by:**created

**Revision Date:**created

**Entry Clone Accession:**BC044568AT98-b5

**Entry Clone Source:**MGC

**SGC Clone Accession:**JMC049-A09

**Tag:**MHHHHHHSSGRENLYFQG

**Host:**BL21(DE3)-V2R-pRARE2

## Construct

**Prelude:**PWWP domain of PSIP1

Tag not removed

**Sequence:**

mhahhhhhssgrenlyfqqMTRDFKPGDLIFAKMKGYPHWPARVDEVPDGAVKPTNKLPIFFFTHETAFLGPKDIFPYSENKEKYG  
KPNKRKGFNEGWEIDNNPKVKFSSQQATKQSNASSDVEEKEKETSVKEDTDHEEKASNEDVTK

**Vector:**pET28-MHL

## Growth

**Medium:**

**Antibiotics:**

**Procedure:**LEX Bubbling. The target protein was expressed in *E. coli* by inoculating 100 mL of overnight culture grown in Luria-Bertani medium into a 4L of Terrific Broth medium in the presence of 50 mg/mL kanamycin and 30 mg/mL chloramphenicol at 37 degree. When OD600 reached ~3.0, the temperature of the medium was lowered to 16 degree and the culture was induced with 0.4 mM IPTG. The cells were allowed to grow overnight before harvested and flash frozen in liquid nitrogen and stored at -80 degree.

## Purification

**Procedure**

The lysate was centrifuged at 16,000 rpm for 45 minutes and the supernatants were remixed with 8 mL 50% flurry of Ni-NTA beads and incubated at 4 degree on rotary shaker for one hour. The mixture was then centrifuged at 2000 rpm for 5 min and the supernatant discarded. The beads were then washed with 50 mL washing buffer, and finally 25 mL the elution buffer. The protein further purified by a 5mL Hitrap Q HP column and Superdex-75 gel filtration column. Fractions

containing the protein were collected and concentrated with Amicon Ultra-15 centrifugal filter. The purity of the preparation is tested by SDS-PAGE to be greater than 95%.

## **Extraction**

### **Procedure**

Frozen cells from 2L TB culture were thawed and resuspended in 200 mL extraction buffer and 8  $\mu$ L benzonase (Sigma Catalog # E1014, 250U/ $\mu$ L), and lysed using sonicator.

**Concentration:** 25 mg/mL

### **Ligand**

**MassSpec:** protein expected 17487.3, not measured

**Crystallization:** Crystallization was setup using in situ proteolysis method in sitting drops with RedWings and SGC-I screens initially. Diffracting crystals were from initial screen plate for Red Wings F01. Crystal used for structure determination was grown in 2.5M NH<sub>4</sub>SO<sub>4</sub>, 0.1M Tris buffer at pH 8.5. Crystals grew to a mountable size within 1 week

**NMR Spectroscopy:**

**Data Collection:**

**Data Processing:**