

# ARL5:Q15-L176

PDB:2H17

## Revision

**Revision Type:**created

**Revised by:**created

**Revision Date:**created

**Entry Clone Accession:**BC001254

**Entry Clone Source:**MGC AT3-C4

**SGC Clone Accession:**HPC015-C08, ARL5\_40

**Tag:**mgsshhhhhssglvpr\*gs

**Host:**E. coli BL21 (DE3)

## Construct

**Prelude:**

**Sequence:**

mgsshhhhhssglvprgsQEHKVIVGLDNAGKTTILYQFSMNEVVHTSPTIGSNVEEIVINNTRFLMWDIGGQESLRSSWNTYYT  
NTEFVIVVVDSTRERISVTREELYKMLAHEDLRKAGLLIFANKQDVKECMTVAEISQFLKLTSIKDHQWHIQACCALTGEGLCQGL  
EWMSRL

**Vector:**p28a-thrombin-lic

## Growth

**Medium:**Terrific Broth

**Antibiotics:**

**Procedure:**We prepared the seeds by inoculating freshly transforming E. coli cells (BL21 DE3) into 80 mL of Luria-Bertani medium. After growing overnight, all of the seeds were inoculated into 1.8 L of Terrific Broth medium in the presence of 50 µg/mL of kanamycin at 37°C and grown to an OD600 of 3-4. Cells were then induced by isopropyl-1-thio-D-galactopyranoside at the final concentration of 1.5 mM and grown overnight at 20°C in SGC LEX bubbling system.

## Purification

**Procedure**

The supernatant was passed through DE52 (Whatman) column equilibrated with the binding buffer and then loaded onto 3 mL Ni-NTA column (Qiagen) equilibrated with the same binding buffer at 4°C. The Ni-NTA column was washed with 150 mL of the wash buffer (10mM Tris pH7.5, 0.5 M NaCl, 5% glycerol, 30 mM imidazole) and the protein was eluted with 15 mL of the elution buffer (10mM Tris pH 7.5, 0.5 M NaCl, 5% glycerol, 250 mM imidazole). Five molar equivalents of GDP, 5 mM TCEP and 5 mM MgCl were added to the purified protein before concentration. The protein was concentrated using an Amicon Ultra centrifugal filter to the final

volume of 1 mL and the concentration of 10 mg/mL. About 4.5 mg of protein was obtained from 1.8 L of cell culture.

## **Extraction**

### **Procedure**

**Concentration:** 10 mg/mL

**Ligand**

**GDPMassSpec:**

**Crystallization:** Crystallization was setup using sitting drop and 1:1 protein:mother liquor ratio. The crystal used for structure determination was grown in 2.0M sodium formate, 0.1M BTP, pH 7.0 at temperature 291K.

*Structure solved by W.M. Rabeh, M&M last updated by ytong at 20080819 according to data in PolyMorph and M&M of other ARL5 structures*

**NMR Spectroscopy:**

**Data Collection:**

**Data Processing:**