

# KIFC3 ATPase domain

**PDB:**2H58

## Revision

**Revision Type:**created

**Revised by:**created

**Revision Date:**created

**Entry Clone Accession:**GI:12654738

**Entry Clone Source:**MGC

**SGC Clone Accession:**

**Tag:**His-tag integrated at the N-terminal of the protein was cleaved by thrombin protease, resulted in the addition of two residues (GS) attached to the first amino acid of the encoded protein

**Host:**E. coli BL21-CodonPlus (DE-3)-RIL

## Construct

**Prelude:**

**Sequence:**

```
gsKGNIRVIARVRPVTKEGEGPEATNAVTFDADDDSIHLLHKGPVSFELDKVFSPPQASQQDVFQEVQALVTSCIDGFNVCIFAY
GQTGAGKTYTMEGTAENPGIDQRALQLLFSEVQEKASDWEYTTITVSAAEIYNEVLRDLLGKEPQEKLEIRLCPDGSGQLYVPGLTEF
QVQSVDDINKVFEFGHTNRTTEFTNLNEHSSRSHALLIVTVRGVDCSTGLRTTGKLNLDLAGSERVGKSGAEGSRLREAQHINKSL
SALGDVIAALRSRQGHVPPFRNSKLTLYLLQDSLSGDSKTLMMVQVSPVEKNTSETLYSLKFAERVRVEL
```

**Vector:**p28a-LIC

## Growth

**Medium:**

**Antibiotics:**

**Procedure:**We prepared the seeds by inoculating glycerol stock of E. coli cells BL21-CodonPlus (DE-3)-RIL into 100 mL of Luria-Bertani medium. After overnight growth, all of the seeds were inoculated into 1.8 L of Terrific Broth medium in the presence of 50 µg/mL of kanamycin and 50 µg/mL chloramphenicol at 37°C and grown to an OD600 between 3-5. Cells were then induced by isopropyl-1-thio-D-galactopyranoside at the final concentration of 0.5 mM and grown overnight at 18°C in the SGC LEX bubbling system.

## Purification

**Procedure**

The supernatant was passed through DE52 (Whatman) column equilibrated with the binding buffer, and then loaded onto 5 ml HisTrap HP (Amersham) equilibrated with the same binding buffer at 4°C. The HisTrap HP column was washed with 25 ml binding buffer and then 25 ml

binding buffer with 50 mM imidazole, and eluted by linear gradient of imidazole from 50 mM to 500 mM in 50 ml. The eluted protein peak fractions detected by UV280 nm were combined. Thrombin protease was added to the eluted protein and the protease digestion reaction was carried out at 4°C. After 18 hours, almost all protein was His-tag removed as observed on SDS-PAGE. The his-tag removed protein sample was further purified by gel filtration column superdex 75. The Gel filtration buffer contains 20 mM HEPES pH 7.5, 500m M NaCl, 1 mM DTT. Protein peak fractions were combined, ADP (Sigma) 5 times of the protein in molarity, MgCl<sub>2</sub> to the final concentration of 5 mM, and DTT to the final concentration of 5mM were added. The sample was set at room temperature for 30 min to allow the ligand binding before concentration. Protein sample was concentrated using an Amicon Ultra centrifugal filter to the final volume of 0.53 mL. The protein concentration estimated by Bradford to be 69.67 mg/mL. About 36.93 mg of protein was obtained from 1.8 L of cell culture.

## **Extraction**

### **Procedure**

Cultures were centrifuged and the cell pellets were harvested and stored at -80 °C before use. Cells were thawed and suspended in 100 mL the binding buffer (10 mM Tris pH 7.5, 0.5 M NaCl, 5 mM imidazole) with 0.5% CHAPS (Sigma) and 1 mM phenylmethyl sulfonyl fluoride (PMSF) and lysed with microfluidizer. The lysate was centrifuged at 15000 rpm for 30 min and the supernatant was used for subsequent steps of purification. All the extraction steps were carried out at 4°C.

**Concentration:**69.67 mg/mL

### **Ligand**

### **MassSpec:**

**Crystallization:**Purified KIFC3 ATPase domain was crystallized using the sitting drop vapor diffusion method at room temperature. Crystals grew in 2 days when the protein (35 mg/ml) was mixed with the reservoir solution in a 1:1 volume ratio, and the drop was equilibrated against a reservoir solution containing 1.2M sodium citrate, 0.1M Hepes, pH7.5. The crystals were flash frozen with 1.2M sodium citrate, 20% glycerol, 0.1M Hepes, pH7.5 as the cryo solution.

### **NMR Spectroscopy:**

### **Data Collection:**

### **Data Processing:**