

REM2

PDB:3CBQ

Revision

Revision Type:created

Revised by:created

Revision Date:created

Entry Clone Accession:BC035663

Entry Clone Source:MGC AT56-F8

SGC Clone Accession:HPC073-E12

Tag:mhhhhhssgrenlyfq*g

Host:BL21-CodonPlus(DE3)-RIL

Construct

Prelude:

Sequence:

mhhhhhssgrenlyfqgQKDGIFKVMLVGESGVGKSTLAGTFGGLQGDSAHEPENPEDTYERRIMVDKEEVTLVVYDIWEQGDAGG
WLRDHCLQTGDAFLIVFSVTDRRSFSKVPETLLRLRAGRPHHDLPVILVGNKSDLARSREVSLEEGRHLAGTLSCKHIETSAALHHN
TRELFEHAVRQIRLRRGRNHA

Vector:pET28-mhl (GI:134105571)

Growth

Medium:Terrific Broth

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 1.8 L of Terrific Broth medium in the presence of 50 µg/mL kanamycin and 25 µg/mL chloramphenicol at 37 °C. When OD₆₀₀ reached ~3.0, the temperature of the medium was lowered to 15 °C and the culture was induced with 0.5 mM IPTG. The cells were allowed to grow overnight before harvested and flash frozen in liquid nitrogen and stored at -80 °C.

Purification

Procedure

The lysate was centrifuged at 15,000 rpm for 45 minutes and the supernatants were loaded onto 5mL HiTrap HP column charged with Ni²⁺ ion. The column was washed steply using washing buffer containing 30, 60, and 500 mM imidazole. Fractions washed using 500 mM imidazole was collected and pooled together and further purified by a Superdex-75 gel filtration column pre-equilibrated with 20 mM HEPES buffer at pH 7.0, with 10 mM MgCl₂ and 2 mM BME.

Fractions were collected and concentrated with Amicon Ultra-15 centrifugal filter. The purify of the preparation is tested by SDS-PAGE to be around 95%.

Extraction

Procedure

Frozen cells were thawed and resuspended in 150 mL extraction buffer with freshly added 0.5% CHAPS and 2mM BME, and supplemented with protease inhibitor cocktail (SIGMA Catalog # P8849), and 3 μ L benzonase (Sigma Catalog # E1014, 250U/ μ L), and lysed using microfluidizer at 15,000 PSI.

Concentration: 38-40 mg/mL

Ligand

GDP, Mg²⁺+**MassSpec:** Native: 21942.11, expected 21941.61

Crystallization: GDP were added to the concentrated protein to a final concentration of 5mM. Crystallization were set up using SGC-I and Red Wings screen with and without 1:100 different proteases. Crystal were seen for the following conditions: No protease: RW-G12

Chymotrypsin: SGC-B11

Trypsin: RW-B7, RW-A2

Clustered plates like crystals appear in the drop in one week.

Crystal used for structure determination were grown in Red Wings initial screen B07: 20.0% PEG3350, 0.2M KCl, no buffer in the mother liquor. Sitting drop vaporization. Cryo used: 20% PEG 3350 + 20% EG (Last updated YTONG 20080328)

NMR Spectroscopy:

Data Collection:

Data Processing: