

# UPASE2

**PDB:**2XRF

## Revision

**Revision Type:**created

**Revised by:**created

**Revision Date:**created

**Entry Clone Accession:**BC033529

**Entry Clone Source:**Mammalian Gene Collection

**SGC Clone Accession:**UPASE2A-k008

**Tag:**C-terminal hexahistidine tag starting with an additional alanine

**Host:***E.coli* BL21(DE3) R3 pRARE, where R3 denotes a derivative of BL21(DE3) resistant to a strain of T1 bacteriophage (SGC Oxford) and the pRARE plasmid originating from the Rosetta strain (Novagen) supplies tRNAs for rare codons.

## Construct

**Prelude:**

**Sequence:**

MRFVHVKNPYLDLMDDEDILYHLDLGTKTHNLPAMFGDVKFVCVGGSPNRMKAFALFMHKELGFEEAEEDIKDICAGTDRYCMYKTGP  
VLAISHGMGIPISISIMLHELKLLHHARCCDVTIIRIGTSGGIGIAPGTVVITDIAVDSFFKPRFEQVILDNIVTRSTELDKELSEE  
LFNCSKEIPNFP TLVGHTMCTYDFYEGQGRLDGALCSFSREKKLDY LKRAFKAGVRNIEMESTVFAAMCGLCGLKAAVVCVTLLDRL  
DCDQINLPHDVLVEYQQR PQL LISNFIRRR LGLCDahhhhhh

**Vector:**pNIC-CH2

## Growth

**Medium:**

**Antibiotics:**

**Procedure:**Cells from a glycerol stock were grown in 20 ml TB supplemented with 8 g/l glycerol, 100 µg/ml kanamycin and 34 µg/ml chloramphenicol at 30 °C overnight. The overnight culture (15 ml) was used to inoculate 1.5 l TB supplemented with 8 g/l glycerol, 50 µg/ml kanamycin and approximately 200 µl 204 Antifoam A6426 (Sigma). The culture was grown in a LEX bioreactor system (Harbinger Biotechnology) at 37 °C until OD600 reached ~2. The culture was down-tempered to 18 °C over a period of 1 hour before target expression was induced by addition of 0.5 mM IPTG. Expression was allowed to continue overnight and cells were harvested the following morning by centrifugation (4,400 x g, 10 min, 4 °C). The resulting cell pellet (39 g wet cell weight) was resuspended in lysis buffer (1.5 ml/g cell pellet), supplemented with 2000 U Benzonase (Merck) and one tablet of Complete EDTA-free protease inhibitor (Roche Applied Science). The cell suspension was stored at -80 °C.

## Purification

## **Procedure**

### **Columns**

IMAC: Ni-charged 2x1 ml HiTrap Chelating HP (GE Healthcare)

Gel filtration column: HiLoad 16/60 Superdex 200 Prep Grade (GE Healthcare)

### **Procedure**

IMAC columns were equilibrated with IMAC wash1 buffer, and gel filtration columns were equilibrated with GF buffer. Purification of the protein was performed on an ÄKTAexpress system (GE Healthcare). The filtered lysate was loaded onto the Ni-charged HiTrap Chelating column and washed with IMAC wash1 buffer followed by IMAC wash2 buffer. Bound protein was eluted from the IMAC column with IMAC elution buffer and automatically loaded onto the gel filtration column. Fractions containing the target protein were identified by SDS-PAGE, pooled, and fresh TCEP was added to a final concentration of 2 mM. The protein was concentrated using an Amicon Ultra-15 centrifugal filter device (10,000 NMWL; Millipore) to 14,5 mg/ml in a volume of 0.45 ml. The identity of the protein was confirmed by mass spectrometry.

## **Extraction**

### **Procedure**

The cell suspension was quickly thawed in water. Cells were disrupted by sonication (Vibra-Cell, Sonics) at 80% amplitude for 3 min effective time (pulsed 4s on, 4s off) and cell debris was removed by centrifugation (49,000 x g, 20 min, 4 °C). The supernatant was decanted and filtered through a 0.45 µm flask filter.

### **Concentration:**

### **Ligand**

### **MassSpec:**

**Crystallization:** Crystals were obtained by the sitting drop vapour diffusion method in a 96-well plate. 0.1 µl protein solution (14.5 mg/ml) was mixed with 0.1 µl of well solution consisting of 0.1 M tris pH 8, 0.2 M magnesium chloride hexahydrate, and 25% PEG 6000. The plate was incubated at 20 °C and crystals appeared within 5 days. The crystals were quickly transferred to a cryo solution consisting of well solution complemented with 20% glycerol and 0.3 M NaCl, and flash frozen in liquid nitrogen.

### **NMR Spectroscopy:**

**Data Collection:** Diffraction data to 2.3 Å resolution was collected at Bessy, BL14-1.

**Data Processing:** The structure was solved by molecular replacement using apo UPASE1 as template (PDB: 3EUE). The space group was P3<sub>1</sub>21 with cell dimensions a=95.28 Å b=95.28 Å c=186.28 Å. Three subunits were located in the asymmetric unit. Refmac5 and Buster was used for refinement and Coot for model building. Data in the interval 34.4-2.30 Å resolution was used and at the end of the refinement the R values were: R=17% and R<sub>free</sub>=20.6%. Coordinates for the crystal structure were deposited in the Protein Data Bank, accession code 2XRF.