

# MALT1

**PDB:**3BFO

## Revision

**Revision Type:**created

**Revised by:**created

**Revision Date:**created

**Entry Clone Accession:**NP\_006776

**Entry Clone Source:**malt1.BC030143.MGC.AU79-A6.pOTB7

**SGC Clone Accession:**malt1.226.314.128B09 (SDC128B09)

**Tag:**N-terminal: MGSSHHHHHSSGLVPR\*GS (removed)

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

## Construct

**Prelude:**

**Sequence:**

mgsshhhhhhsglvp\*r\*GSKLQICVEPTSQKLMPGSTLVLQCVAVGSPIPHQWFKNELPLTHEKKLYMVPYVDLEHQGTYWCHV  
YNDRDSQDSKKVEIIIDELNNL

**Vector:**pET28a-LIC

## Growth

**Medium:**

**Antibiotics:**

**Procedure:**The protein was expressed in E. coli BL21 (DE3) grown in Terrific Broth (TB) in the presence of 50 µg/mL of kanamycin at 37°C to an OD600 of 7.5. Cells were then induced by isopropyl-1-thio-D-galactopyranoside (IPTG), final concentration 0.05 mM, and incubated overnight at 15°C. The culture was centrifuged and the cell pellets were collected and stored at -80°C.

## Purification

**Procedure:**

**IMAC:** The cleared lysate from a 2 L culture was loaded onto 3 ml TALON metal-affinity resin column (BD Biosciences) at 4°C. The column was washed with 40 ml Wash buffer, and the protein was eluted with 10 ml Elution buffer.

**Tag removal:** 1 Unit of thrombin (Sigma T9681) per milligram of protein was added to the 10 mL sample, stored overnight without shaking at 4°C.

**Gel-filtration:** It was further purified by gel filtration on a HighLoad 16/60 Superdex 200 column (GE Healthcare, Amersham) equilibrated with Gel Filtration buffer and concentrated to 50 mg/ml by ultrafiltration using Amicon Ultra centrifugal filter with 10 kD cutoff and stored at -80 °C.

Protein yield was 12 mg per liter of bacterial culture.

## Extraction

**Procedure:** The cell pellet was defrosted and cells were lysed by sonication, 10 s on, 10 s off at 40% amplitude for 10 min. The lysate was cleared by centrifugation for 45 minutes at 15,500 RPM, 4°C.

**Concentration:** 50 mg/ml

**Ligand:**

**MassSpec:** Mass-spectroscopy by LCMS shows that the product was pure and of correct molecular weight.

**Crystallization:** Purified protein was crystallized using the hanging drop vapor diffusion method. Crystals grew when the protein (50 mg/mL) was mixed with the reservoir solution in a 1:1 volume ratio, and the drop was equilibrated against a reservoir solution containing 30% PEG 550-MME, 0.2 M Ammonium sulfate, and 0.1 M Sodium cacodylate at pH 6.5 in 293 Kelvin.

**NMR Spectroscopy:**

**Data Collection:**

**Data Processing:**