

**Entry Clone Source:** Synthetic

**GenBank GI number:** 4960047

**Vector:** pGEX-6P-1

**Amplified DNA sequence:**

ATGTCCCCTATACTAGGTTATTGGAA  
AATTAAGGGCCTTGTGCAACCCACTC  
GACTTCTTTGGAATATCTTGAAGAA  
AAATATGAAGAGCATTGTATGAGCG  
CGATGAAGGTGATAAAATGGCGAAACA  
AAAAGTTGAATTGGGTTGGAGTT  
CCCAATCTCCTTATTATATTGATGG  
TGATGTTAAATTAACACAGTCTATGG  
CCATCATACTACGTTATATAGCTGACAAG  
CACAACATGTTGGGTGGTTGTCCAAA  
AGAGCGTGCAGAGATTCAATGCTTG  
AAGGAGCGGTTTGGATATTAGATAAC  
GGTGTTCGAGAATTGCATATAGTAA  
AGACTTTGAAACTCTCAAAGTTGATT  
TTCTTAGCAAGCTACCTGAAATGCTG  
AAAATGTTCGAAGATCGTTATGTCA  
TAAAACATATTTAAATGGTGATCATG  
TAAACCCATCCTGACTTCATGTTGTAT  
GACGCTCTTGATGTTGTTTATACAT  
GGACCCAATGTGCCTGGATGCGTTCC  
CAAAATTAGTTGTTTAAAAACGT  
ATTGAAGCTATCCCACAAATTGATAA  
GTACTTGAAATCCAGCAAGTATATAG  
CATGGCCTTGCAGGGCTGGCAAGCC  
ACGTTGGTGGTGGCGACCACCTCC  
AAAATCGGATCTGGAAGTTCTGTTCC  
AGGGGCCCTGGGATCCAAGAAGCGT  
CAGTGTAAAGTTCTTGAGTACAT  
TCCACAAATGAGGATGAACGGAGC  
TGAAAGTGGGAGATATTATTGATATT  
AATGAAGAGGTAGAAGAAGGCTGGT  
GAGTGGAACCCCTGAATAACAAGTTGG  
GACTGTTCCCTCAAATTTGTGAAA  
GAATTAGAGGTAACA

**Final protein sequence (Tag sequence in lowercase):**

mspilgywkikglvqptrlleylee  
kyeehlyerdegdkwrnkkfelglef  
pnlpwyidgdvkltqsmaiiryiadk  
hnlmlggcpkeraeismlegavldiry  
gvsriayskdfetlkvdflsklpeml  
kmfedrlchktylngdhvthpdfmly  
daldvvlymdpmcldafpk1vcfkkr  
ieaipqidkylksskyiawplqgwqa  
tfgggdhpksdlevlfq^GPLGSKK  
RQCKVLFEYIPQNEDELELKVGDIID  
INEEVEEGWWSGTLNNKLGLFPSNFV  
KELEVT

^ PreScission cleavage site

**Tags and additions:** Cleavable N-terminal GST tag.

**Host:** BL21(DE3)

**Growth medium, induction protocol:** 20 ml from a 0.2 L overnight culture containing 75 µg/ml carbenicillin were used to inoculate each of ten 0.6L cultures of TB containing 75 µg/ml carbenicillin. Cultures were grown at 37°C until the OD<sub>600</sub> reached ~1.5 and then cooled before inducing expression overnight with 0.1 mM IPTG at 18°C. The cells were collected by centrifugation and the pellet re-suspended in binding buffer.

**Binding buffer:** PBS, 1% Triton-X100, 100 mM + protease inhibitor cocktail

**Extraction buffer, extraction method:** Re-suspended cells were lysed by sonication. The lysate was centrifuged at 48 000 x g for 60 minutes and the supernatant collected and then snap-frozen in liquid nitrogen.

**Column 1:** Glutathione-affinity beads; GSH-sepharose (GE Healthcare).

11.5 ml of a 50% slurry in 2.5 x 15 cm Econo-column (Bio-Rad), washed with binding buffer.

**Column 1 Buffers:**

**Binding buffer:** PBS, 1% Triton-X100, 100 mM EDTA

**Wash buffer:** 50 mM Tris pH 7.5, 100 mM EDTA, 0.1% Tween20

**Elution buffer:** 100 mM reduced glutathione (pH adjusted to 8.0 with Tris-HCl pH 8.8)

**Column 1 Procedure:** The supernatant was thawed and then glutathione-sepharose beads were added before gentle mixing overnight at 4°C. The beads were then washed with 3 x 50 ml wash buffer using gravity flow through the column. The protein was eluted by gentle mixing after 3 hours with elution buffer and the solution recovered by gravity flow. Additional fractions were collected by eluting with 3 x 5 ml of fresh elution buffer

**Enzymatic treatment:** The N-terminal GST tag was cleaved by treatment with PreScission protease, overnight.

**Column 2:** Size Exclusion Chromatography; Superdex 75 16/60 HiLoad

**Column 2 Buffers:**

**Buffer:** 20 mM Tris, pH 7.5, 150 mM NaCl, 2 mM beta-mercaptoethanol

**Column 2 Procedure:** The protein was concentrated and applied to an S75 16/60 HiLoad gel filtration column equilibrated with 20 mM Tris, pH 7.5, 150 mM NaCl and 2 mM beta-mercaptoethanol using an ÄKTA FPLC system.

**Protein concentration:** The protein was concentrated to 28.2 mg/ml using a Vivaspin 3 kDa cut-off concentrator.

**Mass spectrometry characterization:**

**Measured mass:** 7438.28 Da

LC-ESI-MS TOF gave a measured mass of 7438.28 Da for this construct close to that predicted from the sequence of this protein.

**Crystallisation:** Crystals were grown at 20°C in 150 nl sitting drops from a 1:1 ratio of protein to reservoir solution containing 1.4 M tri-sodium citrate dihydrate, 0.1 M HEPES pH 7.5.

**Data collection:**

**X-ray source:** Diamond I03

**Resolution:** 1.11 Å

Crystals were cryo-protected using the well solution supplemented with 10% glycerol and flash-frozen in liquid nitrogen