

Materials and Method

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Entry Clone Source: MGC
Entry Clone Accession: IMAGE:3686411
SGC Construct ID: TXNL2A-c002
GenBank GI number: gi 95113651
Vector: pNIC28-Bsa4. Details [PDF]; Sequence [FASTA] or [GenBank]
Tag and additions: TEV-cleavable (*), N-terminal histidine tag. Tag sequence: mhhhhhhssgvdlgtlenlyfq*sm. Note: Due to an cloning artefact, a C-terminal histidine tag was added with the sequence: kvkvtdpnsdvdlaaalehhhhh.
Protein sequence: SMAAGAAEAAVAAVEEVGSAGQFEELLRL KAKSLLVVHFWAPWAPQCAQMNEVMAELA KELPQVSFVKLEAEGVPEVSEKYEISSVP TFLFFKNSQKIDRLDGAHAPELTKKVQRH ASSGSFLPSA
Host: BL21(DE3)-R3-pRARE2
Growth medium, induction protocol: Medium: TB supplemented with 50 µg/ml Kanamycin and 34 µg/ml chloramp. 4 liter TB in two 4-L flask were inoculated with 40 ml overnight culture and grown at 37°C until OD ₆₀₀ reached 2.0. The temperature was then decreased to 18°C and the protein expression induced with 0.1 mM IPTG over night. The cells were collected by centrifugation (4000 RPM, 30 minutes) and frozen at -80°C.
Extraction buffer, extraction method: Lysis buffer: 50 mM HEPES pH 7.5, 500 mM NaCl, 10 mM Imidazole, 5% glycerol, 0.5 mM TCEP, 1 mM PMSF and 3 U/ml of Benzonase. The cell pellet was resuspended in a total volume of 250 ml lysis buffer and the cells disrupted by sonication. Nucleic acids and cell debris were removed by adding 0.15% PEI, followed by centrifugation for 60 minutes at 40 000xg. The supernatant was further clarified by filtration (0.20 µm).
Column 1: Ni-Sepharose FF, 4 ml (GE/Amersham Biosciences)
Buffers: Binding buffer: 50 mM HEPES pH 7.5, 500 mM NaCl, 10 mM Imidazole, 5% glycerol, 0.5 mM TCEP. Wash and elution buffers: 50 mM HEPES pH 7.5, 500 mM NaCl, 5% glycerol 10-250 mM imidazole.
Procedure: The cell lysate was applied onto a 4 ml Ni-Sepharose FF column equilibrated with binding buffer. The column was subsequently washed with 10 column volumes of binding buffer and the protein eluted using a stepwise gradient of imidazole. All fractions were collected and analysed by 4-12 % SDS-PAGE.
Column 2: Hiload 16/60 Superdex 200 prep grade 120 ml (GE/Amersham Biosciences)
Buffer: 10 mM HEPES, pH 7.5, 500 mM NaCl, 5% glycerol, 0.5 mM TCEP
Procedure: The fractions containing TXNL2A from the Ni-affinity chromatography were incubated with 0.5 mM TCEP and concentrated in amicon (3K) to 4 ml. The protein was filtered through a 0.20 µm PVDF filter and applied onto a Superdex S200 column at 1.2 ml/min. The eluted proteins were collected in 1.8 ml fractions and analysed by SDS-PAGE.
Enzymatic treatment: TEV cleavage.
Column 3: Ni-Sepharose FF (TEV clean up)
Buffer: 10 mM HEPES, pH 7.5, 500 mM NaCl, 5% glycerol

Procedure: The N-terminal histidine-tag was cleaved with 150 µg of TEV protease per 10 mg protein at 4°C for 16 hours. The TEV cleaved protein was applied to a 0.5 ml Ni-sepharose column and the flow through collected. The column was washed with 5 ml buffer and the flow through and the wash fraction were analysed by SDS-PAGE.

Concentration: The protein was concentrated in Amicon (5 K) to 53.8 mg/ml. The protein concentration was determined spectrophotometrically using the predicted molar extinction coefficient 12490 (M⁻¹ cm⁻¹) predicted mass of 16605.8 Da .

Mass spectrometry characterisation: The mass determined for TXNL2Ap009 was determined with ESI-MS to 16605.8 Da, in agreement with the predicted mass of the protein with an C-terminal histidine tag.

Crystallisation: Crystals of the TXN domain in TXNL2A were grown by vapor diffusion at 20°C, combined with microseeding procedures. Sitting drops consisting of 100 nl protein (28 mg/ml) and 50 nl well solution are equilibrated against well solution containing 1.4 M ammonium citrate pH 7 for 1hr. At this stage, drops were seeded with 20 nl of 10⁻⁵ (v/v) dilution of a microseed suspension from initial needle clusters grown in 1.7 M ammonium citrate pH 7. Seeds were crushed using the Hampton Seed Bead Kit, and diluted into 50µl of precipitant solution. The crystal was transferred to a cryoprotectant composed of 50 % Malonate pH 7.0 before flash-cooling in liquid nitrogen.

Data Collection: Resolution: 1.55 Å; **X-ray source:** Diamond light source I02.