PTPRE

PDB:2JJD

Revision

Revision Type:created
Revised by:created
Revision Date:created
Entry Clone Accession:NM_006504
Entry Clone Source: Origene
SGC Clone Accession:
Tag: Non-cleavable C-terminal His6 tag.
Host:BL21 (DE3)R3 (Phage resistant strain)

Construct

Prelude:
Sequence:

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MSGPKKYFPIPVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEENREKNRYPNILPNDHSRVILSQLDGIPCSDYINA
SYIDGYKEKNKFIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQYWPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCI
QPQLPDGCKAPRLVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHCSAGVGRTGTFIVIDAMMAMMHAEQKVDVFEF
VSRIRNQRPQMVQTDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDKIGLEEEFRKLTNVRIMKENMRTGNLPANMK
KARVIQIIPYDFNRVILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFWRMIWEWKSHTIVMLTEVQEREQDKCYQYW
PTEGSVTHGEITIEIKNDTLSEAISIRDFLVTLNQPQARQ[G]EQVRVVRQFHFHGWPEIGIPAEGKGMIDLIAAVQKQQQQTGNHP
ITVHCSAGAGRTGTFIALSNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQDFIDIFSDYAAHHHHHHHighligh
ted residue in square brackets corresponds to a mutation Glu581Gly at that position.
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Vector: pNIC-CH

Growth

Medium:
Antibiotics:
Procedure:1ml from a 10 ml overnight culture containing 50 µg/ml kanamycin was used to inoculate 1 litre of LB containing 50 µg/ml kanamycin. Cultures were grown at 37°C until the OD600 reached ~0.3 then the temperature was adjusted to 18°C. Expression was induced for overnight using 1 mM IPTG at an OD600 of 0.8. The cells were collected by centrifugation and the pellet resuspended in binding buffer and frozen. Binding buffer: 50mM HEPES pH 7.5; 500 mM NaCl; 5 mM imidazole, 5% glycerol; 0.5 mM TCEP.

Purification

Procedure
Column 1: Ion exchange - Nucleic acid removal. DEAE cellulose (DE52, Whatman), 10 g of resin in 2.5 x 20 cm column. The resin was hydrated in 2.5M NaCl, then washed with 20 ml

binding buffer prior to loading the sample.Buffers: 50mM HEPES pH 7.5; 500 mM NaCl; 5 mM imidazole, 5% glycerol; 0.5 mM TCEPProcedure: Supernatant was applied by gravity flow, followed by a wash with 100 ml binding buffer. The column flow-through was collected.Column 2: Ni-affinity. Ni-NTA (Qiagen), 5 ml of 50% slurry in 1.5 x 10 cm column, washed with binding buffer.Buffers : Binding buffer: 50 mM HEPES pH 7.5, 500 mM NaCl, 5% Glycerol, 0.5 mM TCEP; Wash buffer: 50 mM HEPES pH 7.5, 500 mM NaCl, 30 mM Imidazole, 5% glycerol, 0.5 mM TCEP; Elution buffer: 50 mM HEPES pH 7.5, 500 mM NaCl, 50 to 250 mM Imidazole , 5% Glycerol, 0.5 mM TCEP.Procedure: The flowthrough from column 1 was loaded by gravity flow on the Ni-NTA column. The column was then washed with 100 ml wash buffer at gravity flow. The protein was eluted by gravity flow by applying 5-ml portions of elution buffer with increasing concentration of imidazole (50 mM, 100 mM, 150 and 250 mM); fractions were collected until essentially all protein was eluted.Enzymatic treatment : noneColumn 3: Size Exclusion Chromatography. Superdex S200 16/60 HiLoadBuffers: 50 mM Tris-HCl, pH 7.5; 250 mM NaCl; 10 mM DTTProcedure: PTPRE was concentrated and applied to a S200 16/60 HiLoad gel filtration column equilibrated in 50 mM Tris-HCl, pH 7.5; 250 mM NaCl; 10 mM DTT using either an ÄKTAprime or ÄKTAexpress system.

Extraction

Procedure
Frozen pellets were thawed and cells lysed using a high pressure cell disrupter. The lysate was centrifuged at 17,000 rpm for 30 minutes and the supernatant collected for purification.
Concentration: Protein was concentrated to 10.7 mg/ml using an Amicon 30 kDa cut-off concentrator.
Ligand
MassSpec:LC -ESI -MS TOF gave a measured mass of 69378 for this construct. Predicted mass 69580. Sequencing indicated a base change at position 1427bp from ATG changing A to G (Glu581 to Gly). No human EST has been reported in Genbank suggesting this may be a PCR error. The discrepancy in mass was interpreted as a loss of the N-terminal methionine during expression and the Glu to Gly change.
Crystallization: Crystals were grown at 20°C from a 1:1 ratio of protein to reservoir solution, where the reservoir solution was 1.6 M $MgSO_4$, 0.1 M MES pH 6.5.
NMR Spectroscopy:
Data Collection: Crystals were cryo-protected using 2.25M Li_2SO_4. X-ray source: Diffraction data were collected at the SLS beamline SAX10 at a single wavelength.Resolution: 3.2 Å resolution limit.
Data Processing: