

# SEC14L4

**PDB:**4TLG

## Revision

**Revision Type:**created

**Revised by:**created

**Revision Date:**created

**Entry Clone Accession:** BC139912

**Entry Clone Source:**GeneScript

**SGC Clone Accession:**

**Tag:**N-terminal, TEV protease cleavable hexahistidine tag

**Host:**

## Construct

**Prelude:**

**Sequence:**

"MHSHHHHSSGVDLGTENLYFQSMSSRVGDLSPQQQEALARFRENLDLLPILPNADDYFLLRWLRARNFDLQKSEDMRLRRHMEFRK  
QQDLDNIVTWQPPEVIQLYDSGGLCGYDEGCPVYFNIIGSLDPKGLLLSASKQDMIRKRIKVCELLLHECELQTQKLGRKIEALM  
VFDMEGLSLKHLWKPAVEVYQQFFSILEANYPETLKNLIVIRAPKLPVAFNLVKSFMSEETRRKIVILGDNWKQELTKFISPDQLP  
VEFGGTMTDPDGNPKCLTKINYGGEVPKSYLCEQVRLQYEHTRSVGRGSSLQVENEILFPGCVLRWQFASDGGDIGFGVFLKTKMG  
EQQSAREMTEVLPSQRYNAHMPEDGSLTCLQAGVYVLRFDNTYSRMHAKKLSYTVLEVLLPKASEETLQSLKAMRPSPTQ"

MHSHHHHSSGVDLGTENLYFQ\*SM is the purification tag plus TEV protease recognition site  
\*.

**Vector:**pNIC28-Bsa4

## Growth

**Medium:**

**Antibiotics:**

**Procedure:**

## Purification

**Buffers**

**Procedure**

**Buffers Used:**

Binding/Lysis Buffer: 50 mM Hepes (pH 7.5), 500 mM NaCl, 5% Glycerol, 20 mM Imidazole  
pH 7.5, 0.01mM TCEP

Wash Buffer: 50 mM Hepes (pH 7.5), 500 mM NaCl, 5% Glycerol, 40 mM Imidazole pH 7.5,  
0.01mM TCEP

Elution Buffer: 50 mM Hepes (pH 7.5), 500 mM NaCl, 5% Glycerol, 250 mM Imidazole pH 7.5,

0.01mM TCEP

Gel Filtration Buffer: 10 mM Hepes (pH 7.5), 500 mM NaCl, 5% Glycerol, 0.01mM TCEP

### **Cell Lysis**

Cell pellets were dissolved in approximately 50ml lysis buffer and broken by passing through the homogeniser (x6) at a constant pressure of 15KPa. The cell debris was pelleted at 16,000 RPM and the supernatant used for further purification.

### **Column 1**

Ni-NTA (5.0 ml volume in a gravity-flow column).

The clarified cell extract was incubated with 5.0 ml pre-equilibrated 50% Ni<sub>2</sub>NTA bead solution for 1 hour at 4°C with rotation after which it was passed through a glass column. The column was then washed with 30ml Binding Buffer (2 x 15ml) and 50 ml Wash Buffer (2 x 15 ml). The protein was eluted with 25 ml of Elution Buffer in 5 x 5 ml fractions.

### **Column 2**

Superdex s200 16/60 Gel Filtration.

A pool of the fractions (BB2+WB1+WB2+E1) was concentrated to a volume of 5 ml using a 10 kDa mwco concentrator and applied directly to the size exclusion chromatography column, s200 (pre-equilibrated in GF buffer). at 1.0 ml/min. 1.0 ml fractions were collected.

### **Enzymatic treatment and purification**

The N-terminal His6- tag was cleaved by incubating overnight with TEV (20°C). Cleaved protein was purified by batch binding on 1ml pre-equilibrated 50% Ni-NTA bead solution. The column was then washed with 2x1ml Gel Filtration buffer, 2x1ml Binding buffer, 2x1ml Wash buffer, and finally 2x1ml of Elution buffer.

## **Extraction**

### **Buffers**

#### **Procedure**

#### **Expression strain**

BL21(DE3)-R3-pRARE2

A glycerol stock was used to inoculate 2X60 ml of TB media containing 50mg/ml kanamycin and 50 µg/ml chloramphenicol, which was placed in a 37°C shaker overnight. The next day this starter culture was used to inoculate 12L of TB media (10 ml starter culture used per 1L) containing 50 µg/ml kanamycin. When the OD600 reached approximately 1.0 the temperature was reduced to 18°C and after a further 30 minutes the cells were induced by the addition of 0.1 mM IPTG. Expression was continued overnight.

### **Cell harvest**

Cells were harvested by centrifugation at 16,000 RPM after which the supernatant was poured out and the cell pellet either placed in a -80°C freezer or used directly for purification.

**Concentration:** To set up plates the sample was concentrated to 15.23 mg/ml using a 10 kDa mwco concentrator.

### **Ligand**

**MassSpec:** Expected mass: 46731.0 Da

Measured mass: 47649.9592 Da

**Crystallization:** Crystals were grown by vapour diffusion in sitting drop at 20°C. A sitting drop consisting of 100 nl protein and 50nl well solution was equilibrated against well solution containing 0.2M Magnesium Chloride -- 0.1M tris pH 8.5 -- 25%(w/v) PEG 3350.

**NMR Spectroscopy:**

**Data Collection:**Resolution: 1.77 Å

X-ray source: Diamond Light Source beamline IO4

**Data Processing:**