

Target ID: GLOD4A
Entry Clone ID: GLOD4A-s001
Allele ID: GLOD4A-a001
Construct ID: GLOD4A-c001
Clone ID: GLOD4A-k001
Expression ID: GLOD4A-e014
Purification ID: GLOD4A-p002
Entry clone source: MGC
Entry clone accession: IMAGE:4186251
Vector: pNIC28-Bsa4
E.coli strain: BL21(DE3)-R3-pRARE2
Tags and additions: N-terminal, TEV protease cleavable hexahistidine tag

Coding DNA sequence:

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ATGGCTGCTCGCAGAGCTCTGCACTT
CGTATTCAAAGTGGGAAACCGCTTCC
AGACGGCGCGTTTTCTATCGGGACGTC
CTGGGGATGAAGGTTCTGCGGCATGA
GGAATTTGAAGAAGGCTGCAAAGCTG
CCTGTAATGGGCCTTATGATGGGAAA
TGGAGTAAAACAATGGTGGGATTTGG
GCCTGAGGATGATCATTTTGTTCGAG
AACTGACTTACAATTATGGCGTCGGA
GACTACAAGCTTGGCAATGACTTTAT
GGGAATCACGCTCGCTTCTAGCCAGG
CTGTCAGCAACGCCAGGAAGCTGGAG
TGGCCACTGACGGAAGTTGCAGAAGG
TGTTTTTGAAACCGAGGCCCCGGGAG
GATATAAGTTCTATTTGCAGAATCGC
AGTCTGCCTCAGTCAGATCCTGTATT
AAAAGTAACTCTAGCAGTGTCTGATC
TTCAAAAGTCCTTGAATACTGGTGT
AATCTACTGGGAATGAAAATTTATGA
AAAAGATGAAGAAAAGCAAAGGGCTT
TGCTGGGCTATGCTGATAACCAAGTGT
AAGCTGGAGCTACAGGGCGTCAAGGG
TGGGGTGGACCATGCAGCAGCTTTTG
GAAGAATTGCCTTCTCTTGCCCCCAG
AAAGAGTTGCCAGACTTAGAAGACTT
GATGAAAAGGGAGAACCAGAAGATTC
TGACTCCCCTGGTGAGCCTGGACACC
CCAGGGAAAGCAACAGTACAGGTGGT
CATTCTGGCCGACCCTGACGGACATG
AAATTTGCTTTGTCTGGGGATGAAGCA
TTTCGAGAACTTTCTAAGATGGATCC
AGAGGGAAGCAAATTGTTGGATGATG
CAATGGCAGCAGATAAAAGTGACGAG
TGGTTTGCCAAACACAATAAACCCAA
AGCTTCAGGTAA
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Final protein sequence:

MHHHHHSSGVDLGTENLYFQ*SM
RRALHFVFKVGNRFQTARFYRDVLGM
KVL RHEEFEEGCKAACNGPYDGKWSK
TMVGFGPEDDHFVAELTYNYGVGDYK
LGNDFMGITLASSQAVSNARKLEWPL
TEVAEGVFETEAPGGYKFYLNRSPL
QSDPVLKVTLAVSDLQKSLNYWCNLL
GMKIYENDEEKQRALLGYADNQCKLE
LQGVKGGVDHAAAFGRIAFSCPQKEL
PDLEDLMKRENQKILTPLVSLDTPGK
ATVQVVILADPDGHEICFVGDEAFRE
LSKMDPEGSNCWIDSKGGYGSEFELR
RQACGRTRAPPPPLRSGC

MHHHHHSSGVDLGTENLYFQ*SM is the purification tag plus TEV protease recognition site (*).

Expression

Expression strain: BL21(DE3)-R3-pRARE2

A glycerol stock was used to inoculate 2X60 ml of TB media containing 50 mg/ml kanamycin and 50 μ g/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 μ g/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.

Purification

Buffers Used:

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

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

Elution Buffer: 50 mM Hepes (pH 7.5), 500 mM NaCl, 5% Glycerol, 250 mM Imidazole pH 7.5, 0.01 mM TCEP

Gel Filtration Buffer: 10 mM Hepes (pH 7.5), 500 mM NaCl, 5% Glycerol, 0.01 mM 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_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 50ml Binding Buffer (2 x 25ml) and 50 ml Wash Buffer (2 x 25 ml). The protein was eluted with 50 ml of

Elution Buffer in 5 x 5 ml fractions.

Column 2

Superdex s200 16/60 Gel Filtration.

Elution fraction 1 and 2 were then pooled and concentrated to 5 ml (10 kDa mwco concentrator) and applied to the GF column (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 Wash buffer. Uncut fractions isolated and combined.

Concentration

To set up plates the sample was concentrated to 11.52 mg/ml using a 10 kDa mwco concentrator.

Mass spectrometry characterisation

Expected mass: 368599.0 Da

Measured mass: 36859.3347 Da

Crystallization

Crystals were grown by vapour diffusion in sitting drop at 4°C. A sitting drop consisting of 75 nl protein and 75nl well solution was equilibrated against well solution containing 0.2M Magnesium Chloride -- 0.1M HEPES pH 7.5 -- 25%(w/v) PEG 3350.

Data collection

Resolution: 1.89 Å

X-ray source: Diamond Light Source beamline IO3