

Entry Clone Source: MGC

Entry Clone Accession: gi|3504538

Vector: pNIC28-Bsa4 Details [[PDF](#)]; Sequence [[FASTA](#)] or [[GenBank](#)]

Amplified DNA sequence:

```
CATATGCACCATCATCATCATCATCATTC
TTCTGGTAGATCTGGTACCGAGA
ACCTGTACTTCCAATCCATGACAGAT
CAGGCCTTGTGACACTAACCAACAAA
CGATGCCTACGCCAAAGGTGCCCTGG
TCCTGGGATCATCTCTGAAACAGCAC
AGGACCACCAGGAGGCTGGCGTGC
CGCCACCCCTCAGGTCTCAGACTCCA
TGAGAAAAGTTTAGAGACAGTCTTT
GATGAAGTCATCATGGTAGATGTCTT
GGACAGTGGCGATTCTGCTCATCTAA
CCTTAATGAAGAGGCCAGAGTTGGGT
GTCACGCTGACAAAGCTCCACTGCTG
GTCGCTTACACAGTATTCAAATGTG
TATTGATGGATGCAAGATACTCTGGTC
CTAGCAAATATTGATGATCTTTGA
CAGAGAAGAATTGTCAGCAGCACCAG
ACCCAGGGTGGCCTGACTGCTTCAAT
TCCGGAGTCTCGTTATCAGCCTTC
AGTGAAACATACAATCAGCTGTTGC
ATCTTGCTCTGAGCAAGGTAGTTTT
GATGGTGGGACCAAGGCATACTGAA
CACATTTTAGCAGCTGGCAACAA
CAGATATCAGAAAACACCTGCCGTTT
ATTTATAACCTAACGAGCATCTCTAT
ATACTCCTACCTCCGGCATTAAAG
TGTGTTGGTGCAGTGCCTAAAGTTGTG
CATTTCTGGGACGAGTCACCCATG
GAATTATACTTATGATCCAAACAA
AAAGTGTCAAAAGTGAGGCCATGAT
CCCAACATGACTCATCCAGAGTTCT
CATCCTGTGGTGGAACATCTTACCA
CCAACGTTTACCTCTGCTTCAATGA
CAGTAAAGGTGGATACGGATCCGAA
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Final protein sequence (Tag sequence in lowercase):

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mhhhhhhssgvdlgtenlyfq^smTD
QAFVTLTTNDAYAKGALVLGSSLKQH
RTTRRLVVLATPQVSDSMRKVLETVF
DEVIMVDVLDGDSAHLTLMKRPELG
VTLTKLHCWSLTQYSKCVFMDADTLV
LANIDDLFDREELSAAPDPGPDCFN
SGVFVYQPSVETYNQLLHLASEQGSF
DGGDQGILNTFFSSWATTDIRKHLF
IYNLSSIISYLPAFKVGASAKVV
HFLGRVKPWNYTYDPKTKSVKSEAH
PNMTHPEFLILWWNIFTTNVLPLLQ
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^ TEV cleavage site

Tags and additions: Cleavable N-terminal His6 tag.

Host: BL21 (DE3)R3-pRARE2 (Phage resistant strain)

Growth medium, induction protocol: A glycerol stock was used to inoculate 50 ml of TB media containing 50 µg/ml kanamycin and 34 µg/ml chloramphenicol, which was placed in a 37°C shaker overnight. The next day this starter culture was used to inoculate 6L of TB media (7.5 ml starter culture used per 1L) containing 50 µg/ml kanamycin. When the OD₆₀₀ reached approximately 0.8 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. The expression was continued overnight.

Binding buffer: 50 mM Hepes pH 7.4, 500 mM NaCl, 5% Glycerol, 10 mM Imidazole pH 7.4, 0.5 mM TCEP, 1 tablet per 50 ml protease inhibitor cocktail EDTA-free (Roche)

Extraction buffer, extraction method: Cell pellets were dissolved in approximately 150ml lysis buffer and broken by passing through a high pressure homogenizer at 15,000 psi for 4 cycles. The cell debris was pelleted at 35,000 x g and the supernatant used for further purification

Column 1: Ni-NTA (2.5 ml volume in a gravity-flow column).

Column 1 Buffers:

Binding buffer: 50 mM Hepes pH 7.4, 500 mM NaCl, 5% Glycerol, 10 mM Imidazole pH 7.4, 0.5 mM TCEP

Wash buffer: 50 mM Hepes pH 7.4, 500 mM NaCl, 5% Glycerol, 40 mM Imidazole pH 7.4, 0.5 mM TCEP

Elution buffer: Elution Buffer: 50 mM Hepes pH 7.4, 500 mM NaCl, 5% Glycerol, 250 mM Imidazole pH 7.4, 0.5 mM TCEP

Column 1 Procedure: The clarified cell extract was incubated with 2.5 ml of Ni-NTA pre-equilibrated with lysis buffer for 1 hour at 4°C with rotation after which it was passed through a glass column. The column was then washed with Binding Buffer (100 ml) and Wash Buffer (50 ml). The protein was eluted with 25ml of Elution Buffer in 5ml fractions

Column 2: Superdex 75 16/60 Gel Filtration

Column 2 Buffers:

GF Buffer: 10 mM Hepes pH 7.4, 500 mM NaCl, 0.5 mM TCEP, 5% Glycerol.

Column 2 Procedure: The elution buffer fractions from column 1 were pooled and concentrated to 2ml with a 10 kDa mwco spin concentrator and injected onto an s75 16/60 column (pre-equilibrated in GF Buffer) at 1.0 ml/min. 1 ml fractions were collected. The protein eluted at between 50 ml and 55 ml volume.

Column 3: Ni-NTA rebind

Column 3 Procedure: Protein fractions eluted at 50-55 ml from S75 gel filtration were pooled and incubated with 1:20 mol:mol TEV protease overnight at 4°C. Then protein plus TEV was passed through a column containing 0.5 ml Ni-NTA pre-equilibrated with GF Buffer. Column was washed 1ml of GF Buffer. Flow-through and wash were pooled.

Protein concentration: 9.95 mg/ml using Millipore 10k mwco concentrators.

Mass spectrometry characterization:

Measured mass: 29584.9 Da

Expected mass: 29582.8 Da

Crystallisation: Prior to crystallization, protein was pre-incubated with 1mM MnCl₂ and 1mM 1'-deoxy-glucose. Crystals were grown by vapour diffusion in sitting drop at 20°C. 100 nl protein and 50 nl well solution was equilibrated against well solution containing 0.1M HEPES

pH 7.5 and 1.4M sodium citrate tribasic. Crystals were mounted in the presence of 25% (v/v) ethylene glycol and flash-cooled in liquid nitrogen.

Data collection:

X-ray source: FRE superbright, single wavelength

Resolution: 2.0Å