

Product datasheet for **SC310877**

ELMO1 (NM_001039459) Human Untagged Clone

Product data:

| | |
|---------------------------|--|
| Product Type: | Expression Plasmids |
| Product Name: | ELMO1 (NM_001039459) Human Untagged Clone |
| Tag: | Tag Free |
| Symbol: | ELMO1 |
| Synonyms: | CED-12; CED12; ELMO-1 |
| Mammalian Cell Selection: | Neomycin |
| Vector: | pCMV6-Entry (PS100001) |
| E. coli Selection: | Kanamycin (25 ug/mL) |
| Fully Sequenced ORF: | >SC310877 representing NM_001039459. Blue=Insert sequence Red=Cloning site Green=Tag(s) |

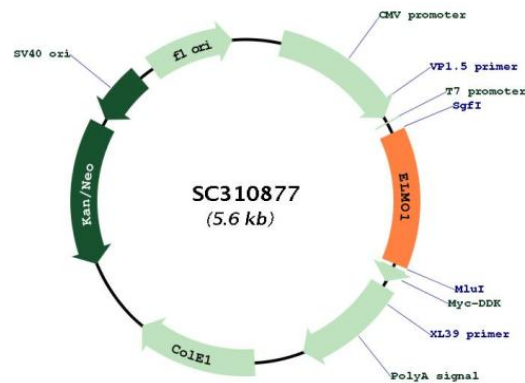
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GCTCGTTT TAGTGAACCGTCAGAATTTTGT AATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCC GCGATCGCC
ATGCAGGTGGTGAAGGAGCAGGTTATGAGAGCACTTACAACCAAGCCTAGCTCCCTGGACCAGTTCAAG
AGCAAACCTGCAGAACCTGAGCTACACTGAGATCCTGAAAATCCGCCAGTCCGAGAGGATGAACCAGGAA
GATTTCCAGTCCCGCCGATTTTGGAACTAAAGGAGAAGATTCAGCCAGAAATCTTAGAGCTGATCAAA
CAGCAACGCTGAACCGCCTTGTTGGAAGGGACCTGCTTAGGAACTCAATGCCCGCGGAGGCAAGAC
AAGTTTTGGTATTGTCGGCTTTTCGCAAATCACAAGTCTGCATTACGGAGACTTAGAAGAGATCCT
CAGGGAGAAGTGCCACGATTCCTTG CAGGACAACTGCCGGTGCAGATATCAAAGCCGTGGTGACG
GGAAAGGACTGCCCTCATATGAAAGAGAAAGGTGCCCTTAAACAAAACAAGGAGGTGCTTGAACCGCT
TTCTCCATCTTGATGACTCAAACCTGCCAACTGAACCTCATCGCTCCTGACAAGCATGAGTACTGTATC
TGGACGGATGGACTGAATGCGCTACTCGGGAAGGACATGATGAGCGACCTGACGCGGAATGACCTGGAC
ACCCTGCTCAGCATGAAATCAAGCTCCGCCTCCTGGACCTGGAAAACATCCAGATCCCTGACGCACCT
CCGCCGATTCCCAAGGAGCCCAGCAACTATGACTTCGTCTATGACTGTAACTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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Restriction Sites: Sgfl-Mlul



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Plasmid Map:



ACCN: NM_001039459

Insert Size: 744 bp

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

OTI Annotation: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

Components: The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

Reconstitution Method:

1. Centrifuge at 5,000xg for 5min.
2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.
3. Close the tube and incubate for 10 minutes at room temperature.
4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.
5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.

RefSeq: [NM_001039459.2](#)

| | |
|-------------------|-----------------------------|
| RefSeq Size: | 3590 bp |
| RefSeq ORF: | 744 bp |
| Locus ID: | 9844 |
| UniProt ID: | Q92556 |
| Cytogenetics: | 7p14.2-p14.1 |
| Protein Pathways: | Chemokine signaling pathway |
| MW: | 28.7 kDa |

Gene Summary: This gene encodes a member of the engulfment and cell motility protein family. These proteins interact with dedicator of cytokinesis proteins to promote phagocytosis and cell migration. Increased expression of this gene and dedicator of cytokinesis 1 may promote glioma cell invasion, and single nucleotide polymorphisms in this gene may be associated with diabetic nephropathy. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Aug 2013]

Transcript Variant: This variant (3) represents use of an alternate promoter and differs in the 5' UTR and 5' coding region, compared to variant 1. These differences cause translation initiation at a downstream AUG and result in an isoform (2) with a shorter N-terminus, compared to isoform 1. Both variants 2 and 3 encode the same isoform (2). Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.