

Product datasheet for SC308365

ELOB (NM_207013) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: ELOB (NM_207013) Human Untagged Clone

Tag: Tag Free Symbol: ELOB

Synonyms: SIII; TCEB2

Mammalian Cell None

Selection:

Vector: pCMV6-XL4

E. coli Selection: Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene ORF sequence for NM_207013 edited

CTGTAA

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5' Read Nucleotide Sequence: >OriGene 5' read for NM_207013 unedited

TTTTTTTTCGTTTCGTTATCCAAAACCCCCCCCGTTAGCATTTGTAATACGATTACTAT AGGCGGCCGCGAATTCGCACGAGGTCGAGGGGTATAGCAGCAGCCGCGATGGACGTGTT CCTCATGATCCGGCGCCACAAGACCACCATCTTCACGGACGCCAAGGAGTCCAGCACGGT GTTCGAACTGAAGCGCATCGTCGAGGGCATCCTCAAGCGGCCTCCTGACGAGCAGCGGCT GTACAAGGATGACCAACTCTTGGATGATGGCAAGACACTGGGCGAGTGTGGCTTCACCAG TCAAACAGCACGGCCACAGGCCCAGCCACAGTGGGGCTGGCCTTCCGGGCAGATGACAC CTTTGAGGCCCTGTGCATCGAGCCGTTTTCCAGCCCGCCAGAGCTGCCCGATGTGATGAA GCCCCAGGACTCGGGAAGCAGTGCCAATGAACAAGCCGTGCACCTGCATGTCCACTCCCA GACGATGGCCAAGAACAGAACACAAGCTGGAGCCAGTGTCCTGGTTTGACAGCATGTTC GAGGGAAGTGGCTGCCCCTTACCACCACCTTTAATAAACAGTCTACAGACCCAAAAAAA AAAAAAAAAAAAAACTCGACTCTAGATTGCGGCCGCGGGCATAGCTGTTTCCTGAACAG AACCCGGGGTGGCATCCCTGTGACCCCTCCCCATGCCTTTCCTGGCCCTGGAAGTTGCCA CTCCAATGCCCACCAGCCTTGTCCTAATAAAATAAGTTGCATCATTTTGTCTGACTAAGG GTCCTTCTATATATTATGGGGTGAGGGGGGGGGGGGTTCTTGAACCAAGCCCCAATTTTGG TCTAAACCTCTTGTCGGCTCTCGTCGCGGTCTTTGGTTACCCCCATTGCA

Restriction Sites: Notl-Notl ACCN: NM_207013

Insert Size: 600 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: There is 1 nucleotide difference between the OriGene clone and the NCBI reference ORF.

These result in the substitution of 1 aa and insertion of 1 aa.

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: <u>NM 207013.1, NP 996896.1</u>

 RefSeq Size:
 609 bp

 RefSeq ORF:
 486 bp

 Locus ID:
 6923

 UniProt ID:
 Q15370

 Cytogenetics:
 16p13.3



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Protein Families: Druggable Genome, Transcription Factors

Protein Pathways: Pathways in cancer, Renal cell carcinoma, Ubiquitin mediated proteolysis

Gene Summary: This gene encodes the protein elongin B, which is a subunit of the transcription factor B (SIII)

complex. The SIII complex is composed of elongins A/A2, B and C. It activates elongation by RNA polymerase II by suppressing transient pausing of the polymerase at many sites within transcription units. Elongin A functions as the transcriptionally active component of the SIII complex, whereas elongins B and C are regulatory subunits. Elongin A2 is specifically expressed in the testis, and capable of forming a stable complex with elongins B and C. The von Hippel-Lindau tumor suppressor protein binds to elongins B and C, and thereby inhibits transcription elongation. Two alternatively spliced transcript variants encoding different isoforms have been described for this gene. Pseudogenes have been identified on

chromosomes 11 and 13. [provided by RefSeq, Aug 2008]

Transcript Variant: This variant (2) lacks a segment in the 3' region, resulting in a downstream stop codon, compared to variant 1. The resulting isoform (b) has a longer C-terminus, compared to isoform a. 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.