

## Product datasheet for **SC301297**

### STEAP3 (NM\_001008410) Human Untagged Clone

#### Product data:

|                           |  |
|---------------------------|--|
| Product Type:             | Expression Plasmids                              |
| Product Name:             | STEAP3 (NM_001008410) Human Untagged Clone       |
| Tag:                      | Tag Free   |
| Symbol:                   | STEAP3   |
| Synonyms:                 | AHMIO2; dudlin-2; dudulin-2; pHyde; STMP3; TSAP6 |
| Mammalian Cell Selection: | Neomycin   |
| Vector:                   | pCMV6-Entry (PS100001)                           |
| E. coli Selection:        | Kanamycin (25 ug/mL)                             |



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**Fully Sequenced ORF:** >SC301297 representing NM\_001008410.  
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

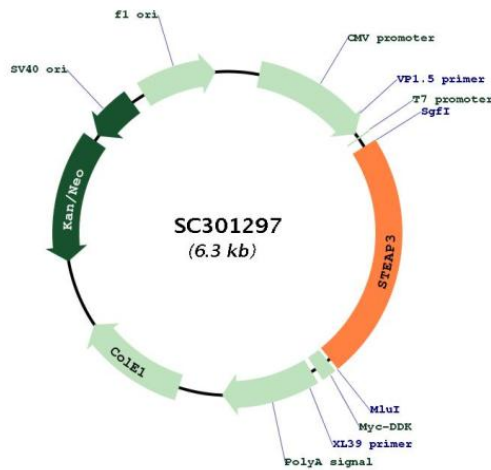
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TTCCCGATGAGCCCCCAAAGTGGGCATCCTGGGTAGCGGGACTTTGCCCGCTCCCTGGCCACACGC
CTGGTGGGCTCTGGCTTCAAAGTGGTGGTGGGAGCCGCAACCCCAAACGCACAGCCAGGCTGTTTCCC
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CGGGAGCACTACTCTTCACTGTGCACTCTCAGTGACCAGCTGGCGGGCAAGATCCTGGTGGATGTGAGC
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TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
  
```

**Restriction Sites:**

SgfI-MluI

**Plasmid Map:**



**ACCN:**

NM\_001008410

|                               |   |
|-------------------------------|---|
| <b>Insert Size:</b>           | 1467 bp   |
| <b>OTI Disclaimer:</b>        | 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).  |
| <b>OTI Annotation:</b>        | 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.  |
| <b>Components:</b>            | 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).  |
| <b>Reconstitution Method:</b> | <ol style="list-style-type: none"><li>1. Centrifuge at 5,000xg for 5min.</li><li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li><li>3. Close the tube and incubate for 10 minutes at room temperature.</li><li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li><li>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.</li></ol>   |
| <b>RefSeq:</b>                | <a href="#">NM_001008410.1</a>  |
| <b>RefSeq Size:</b>           | 3870 bp   |
| <b>RefSeq ORF:</b>            | 1467 bp   |
| <b>Locus ID:</b>              | 55240   |
| <b>UniProt ID:</b>            | <a href="#">Q658P3</a>  |
| <b>Cytogenetics:</b>          | 2q14.2  |
| <b>Protein Families:</b>      | Transmembrane   |
| <b>Protein Pathways:</b>      | p53 signaling pathway   |
| <b>MW:</b>                    | 54.6 kDa  |
| <b>Gene Summary:</b>          | <p>This gene encodes a multipass membrane protein that functions as an iron transporter. The encoded protein can reduce both iron (Fe<sup>3+</sup>) and copper (Cu<sup>2+</sup>) cations. This protein may mediate downstream responses to p53, including promoting apoptosis. Deficiency in this gene can cause anemia. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Aug 2015]</p> <p>Transcript Variant: This variant (3) lacks an exon in the 5' region and initiates translation at a downstream start codon compared to variant 1. The resulting isoform (b) is shorter at the N-terminus compared to isoform a. Variants 2 and 3 both encode the same isoform (b).</p> <p>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.</p> |