

## **Product datasheet for SC334360**

ZNF534 (NM 001291368) Human Untagged Clone

## **Product data:**

**Product Type:** Expression Plasmids

**Product Name:** ZNF534 (NM\_001291368) Human Untagged Clone

Tag:Tag FreeSymbol:ZNF534Synonyms:KRBO3

Selection:

**Mammalian Cell** 

Neomycin

Vector:pCMV6-Entry (PS100001)E. coli Selection:Kanamycin (25 ug/mL)

Fully Sequenced ORF: >NCBI ORF sequence for NM\_001291368, the custom clone sequence may differ by one or

more nucleotides

Restriction Sites: Sgfl-Mlul

**ACCN:** NM 001291368

**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).

**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).



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**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 001291368.1</u>, <u>NP 001278297.1</u>

 RefSeq Size:
 1085 bp

 RefSeq ORF:
 582 bp

 Locus ID:
 147658

 Cytogenetics:
 19q13.41

**Gene Summary:** May be involved in transcriptional regulation.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (3) uses an alternate 3' exon in the 3' UTR and 3' coding region compared to variant 1. The encoded isoform (3) is shorter and distinct C-terminus compared to isoform 1. 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.