

## Product datasheet for **SC309948**

### MAP4K4 (NM\_145687) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	MAP4K4 (NM_145687) Human Untagged Clone
Tag:	Tag Free
Symbol:	MAP4K4
Synonyms:	FLH21957; HEL-S-31; HGK; MEKKK4; NIK
Vector:	<u>pCMV6 series</u>
Fully Sequenced ORF:	>NCBI ORF sequence for NM_145687, the custom clone sequence may differ by one or more nucleotides

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ATGGCGAACGACTCCCCTGCAAAAAGTCTGGTGGACATCGACCTCCTCCCTGCGGGAT
CCTGCTGGGATTTTTGAGCTGGTGAAGTGGTTGGAAATGGCACCTATGGACAAGTCTAT
AAGGGTCGACATGTTAAAACGGGTGAGTGGCAGCCATCAAAGTTATGGATGTCAGT
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AACATTGCAACATATTATGGTGTCTTCATCAAAAAGAGCCCTCCAGGACATGATGACCA
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GCCTGTGATGAGAACCAGATGCCACCTATGATTACAGAAGTGATCTTTGGTCTTTGGC
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GCACTGTTTCTCATTCCCAGAAACCCTCCTCCCGGCTGAAGTCAAAAAATGGTGAAG
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CACCCGACGACTCGCAGCAGCCGCCACCACCGCAGCAGGAAAGGAGCAAGCCAAGCTTC
CATGCTCCCGAGCCAAAGCCACTACGAGCCTGCTGACCGAGCGGAGAGGTGGAAGAT
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CATCCCGCCCTGCAGAGACCAGCGGAGCCACAGGTTCTGTGAGAACAACATCTCGCTCC
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ACAGATGGAAATGGAGCTTCTGGTGTGCTATGAAGATGAGGGGGTTTATGTAACACATAT
GGAAGGATCACCAGGATGTAGTTCTACAGTGGGAGAGATGCCTACATCAGTAGCATAT
ATTCGATCCAATCAGACAATGGGCTGGGAGAGAAAGCCATAGAGATCCGATCTGTGGAA
ACTGGTCACTTGGATGGTGTGTTTCATGCACAAAAGGGCTCAAAGACTAAAATTCTTGTGT
GAACGCAATGACAAGGTGTTCTTTGCCCTCTGTTCCGGTCTGGTGGCAGCAGTCAGGTTAT
TTCATGACCTTAGGCAGGACTTCTCTTCTGAGCTGGTAG
    
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- Restriction Sites:** Please inquire
- ACCN:** NM\_145687
- 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\\_145687.2](#), [NP\\_663720.1](#)

**RefSeq Size:** 7171 bp

**RefSeq ORF:** 3639 bp

**Locus ID:** 9448

**UniProt ID:** [O95819](#)

**Cytogenetics:** 2q11.2

**Domains:** pkinase, CNH, TyrKc, S\_TKc

**Protein Families:** Druggable Genome, Protein Kinase

**Protein Pathways:** MAPK signaling pathway

**Gene Summary:** The protein encoded by this gene is a member of the serine/threonine protein kinase family. This kinase has been shown to specifically activate MAPK8/JNK. The activation of MAPK8 by this kinase is found to be inhibited by the dominant-negative mutants of MAP3K7/TAK1, MAP2K4/MKK4, and MAP2K7/MKK7, which suggests that this kinase may function through the MAP3K7-MAP2K4-MAP2K7 kinase cascade, and mediate the TNF-alpha signaling pathway. Alternatively spliced transcript variants encoding different isoforms have been identified. [provided by RefSeq, Jul 2008]

**Transcript Variant:** This variant (3) lacks an alternate in-frame exon but includes a different in-frame exon in the central coding region, compared to variant 2. The encoded isoform (3) is shorter than isoform 2. The 5' UTR of this variant is incomplete due to a lack of 5'-complete transcripts representing this variant, and the presence of splicing ambiguity in the 5' UTR.

**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.