

## **Product datasheet for MC209719**

## Map2k7 (NM 011944) Mouse Untagged Clone

**Product data:** 

**Product Type:** Expression Plasmids

Product Name: Map2k7 (NM 011944) Mouse Untagged Clone

Tag: Tag Free Symbol: Map2k7

**Synonyms:** 5930412N11Rik; JNKK 2; Jnkk2; MAPKK 7; Mapkk7; MEK 7; Mek7; Mkk7; Prkmk7; sek2

Mammalian Cell

Selection:

Neomycin

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

Fully Sequenced ORF: >MC209719 representing NM\_011944

Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC

ATGGCGGCGTCCTCCCTGGAGCAGAAGCTGTCCCGCCTGGAAGCCAAGCTGAAGCAGGAGAACCGTGAGG

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATTACAAGGATGACGACGATAAGGTTTAA

GGGGACTTCCAGTCATTTGTCAAAGACTGCCTTACTAAAGATCACAGGAAGAGCCAAAGTATAATAAGC TACTTGAACACAGCTTCATCAAGCACTATGAGATACTCGAGGTGGATGTCGCGTCCTGGTTTAAGGATGT CATGGCGAAGACCGAGTCCCCAAGGACTAGTGGAGTCCTGAGTCAGCACCATCTGCCCTTCTTCAGGTAG



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## Map2k7 (NM\_011944) Mouse Untagged Clone - MC209719

**Restriction Sites:** Sgfl-Mlul

**ACCN:** NM\_011944

**Insert Size:** 1260 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).

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 011944.3, NP 036074.2</u>

 RefSeq Size:
 3515 bp

 RefSeq ORF:
 1260 bp

 Locus ID:
 26400

 UniProt ID:
 Q8CE90

**Cytogenetics:** 8 A1.1



## **Gene Summary:**

Dual specificity protein kinase which acts as an essential component of the MAP kinase signal transduction pathway. Essential component of the stress-activated protein kinase/c-Jun Nterminal kinase (SAP/JNK) signaling pathway. With MAP2K4/MKK4, is the one of the only known kinase to directly activate the stress-activated protein kinase/c-Jun N-terminal kinases MAPK8/JNK1, MAPK9/JNK2 and MAPK10/JNK3. MAP2K4/MKK4 and MAP2K7/MKK7 both activate the JNKs by phosphorylation, but they differ in their preference for the phosphorylation site in the Thr-Pro-Tyr motif. MAP2K4/MKK4 shows preference for phosphorylation of the Tyr residue and MAP2K7/MKK7 for the Thr residue. The monophosphorylation of JNKs on the Thr residue is sufficient to increase JNK activity indicating that MAP2K7/MKK7 is important to trigger JNK activity, while the additional phosphorylation of the Tyr residue by MAP2K4/MKK4 ensures optimal JNK activation. Has a specific role in JNK signal transduction pathway activated by proinflammatory cytokines. The MKK/JNK signaling pathway is also involved in mitochondrial death signaling pathway, including the release cytochrome c, leading to apoptosis. Part of a non-canonical MAPK signaling pathway, composed of the upstream MAP3K12 kinase and downstream MAP kinases MAPK1/ERK2 and MAPK3/ERK1, that enhances the AP-1-mediated transcription of APP in response to APOE (PubMed:28111074).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (2) lacks an alternate in-frame exon in the 5' coding region and retains the last intron compared to variant 1. The resulting isoform (2) lacks an alternate internal segment and has a 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.