

Product datasheet for **MC223083**

Mapk8ip3 (NM_001163449) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Mapk8ip3 (NM_001163449) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Mapk8ip3
Synonyms:	BB120594; D17Wsu15e; JIP-3; Jip3; JSAP1; JSAP1a; JSAP1b; JSAP1c; JSAP1d; mKIAA1066; Syd2
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
Fully Sequenced ORF:	>MC223083 representing NM_001163449 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGCC**

ATGATGGAGATCCAGATGGACGAGGGAGGAGGAGTGGTGGTGTACCAAGACGACTACTGCTCGGGCTCGG
TCATGTCCGAGCGTGTGTCCGGCCTGGCGGGCTCCATCTACCGCAGTTCGAGCGCCTCATTCACTGCTA
TGACGAGGAGGTGGTCAAGGAGCTCATGCCGCTGGTGGTGAACGTGCTGGAGAACCTTGACTCGGTGCTG
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GACAAAATCCCCATGGCCAGCGCCGACGCTTACACGGTGGAGATGGCCCGAGTGCTCATGGAACGCA



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ACCAGTACAAGGAACGCCTCATGGAGCTGCAGGAGGCTGTGAGGTGGACTGAAATGATCAGAGCATCAAG
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GCAGGTGCTACACCCCTGAGTGA
    
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ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:

Sgfl-MluI

ACCN:

NM_001163449

Insert Size:

3945 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: [NM_001163449.1](#), [NP_001156921.1](#)

RefSeq Size: 5510 bp

RefSeq ORF: 3945 bp

Locus ID: 30957

UniProt ID: [Q9ESN9](#)

Cytogenetics: 17 12.53 cM

Gene Summary: The JNK-interacting protein (JIP) group of scaffold proteins selectively mediates JNK signaling by aggregating specific components of the MAPK cascade to form a functional JNK signaling module. May function as a regulator of vesicle transport, through interactions with the JNK-signaling components and motor proteins (PubMed:10523642, PubMed:10629060). Promotes neuronal axon elongation in a kinesin- and JNK-dependent manner (PubMed:23576431, PubMed:25944905, PubMed:28259553). Activates cofilin at axon tips via local activation of JNK, thereby regulating filopodial dynamics and enhancing axon elongation (PubMed:23576431, PubMed:25944905, PubMed:28259553). Its binding to kinesin heavy chains (KHC), promotes kinesin-1 motility along microtubules and is essential for axon elongation and regeneration (PubMed:23576431, PubMed:25944905, PubMed:28259553). Regulates cortical neuronal migration by mediating NTRK2/TRKB anterograde axonal transport during brain development (PubMed:23576431, PubMed:25944905, PubMed:28259553). Acts as an adapter that bridges the interaction between NTRK2/TRKB and KLC1 and drives NTRK2/TRKB axonal but not dendritic anterograde transport, which is essential for subsequent BDNF-triggered signaling and filopodia formation (PubMed:23576431, PubMed:25944905, PubMed:28259553).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (4) contains an alternate in-frame exon and uses an alternate in-frame splice site in the 5' coding region compared to variant 1. This results in a shorter protein (isoform d) 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.