

Product datasheet for **SC315755**

JNK3 (MAPK10) (NM_138980) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	JNK3 (MAPK10) (NM_138980) Human Untagged Clone
Tag:	Tag Free
Symbol:	MAPK10
Synonyms:	JNK3; JNK3A; p54bSAPK; p493F12; PRKM10; SAPK1b
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC315755 representing NM_138980. Blue=Insert sequence Red=Cloning site Green=Tag(s)

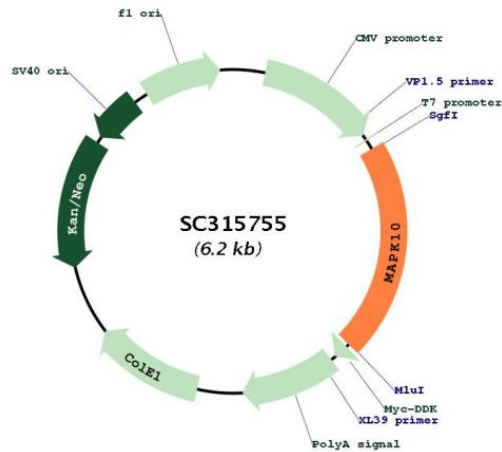
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CTGGAAGCCTCGGCAGGACCCCTGGGTTGTTGCAGGTGA
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TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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Restriction Sites: SgfI-MluI

Plasmid Map:



ACCN: NM_138980

Insert Size: 1281 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).

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_138980.3](#)

RefSeq Size: 7058 bp

RefSeq ORF: 1281 bp

Locus ID: 5602

UniProt ID:	<u>P53779</u>
Cytogenetics:	4q21.3
Domains:	pkinase
Protein Families:	Druggable Genome, Protein Kinase
Protein Pathways:	Adipocytokine signaling pathway, Colorectal cancer, Epithelial cell signaling in Helicobacter pylori infection, ErbB signaling pathway, Fc epsilon RI signaling pathway, Focal adhesion, GnRH signaling pathway, Insulin signaling pathway, MAPK signaling pathway, Neurotrophin signaling pathway, NOD-like receptor signaling pathway, Pancreatic cancer, Pathways in cancer, Progesterone-mediated oocyte maturation, RIG-I-like receptor signaling pathway, Toll-like receptor signaling pathway, Type II diabetes mellitus, Wnt signaling pathway
MW:	48.1 kDa
Gene Summary:	<p>The protein encoded by this gene is a member of the MAP kinase family. MAP kinases act as integration points for multiple biochemical signals, and thus are involved in a wide variety of cellular processes, such as proliferation, differentiation, transcription regulation and development. This kinase is specifically expressed in a subset of neurons in the nervous system, and is activated by threonine and tyrosine phosphorylation. Targeted deletion of this gene in mice suggests that it may have a role in stress-induced neuronal apoptosis. Alternatively spliced transcript variants encoding different isoforms have been described for this gene. A recent study provided evidence for translational readthrough in this gene, and expression of an additional C-terminally extended isoform via the use of an alternative in-frame translation termination codon. [provided by RefSeq, Dec 2017]</p> <p>Transcript Variant: This variant (3) uses an alternate acceptor splice site in the 5' region, which results in translation initiation from an in-frame, downstream start codon compared to variant 1. The encoded isoform (3) has a shorter N-terminus compared to isoform 1.</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>