



<b>OTI Disclaimer:</b>	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).
<b>OTI Annotation:</b>	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.
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"> <li>1. Centrifuge at 5,000xg for 5min.</li> <li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>3. Close the tube and incubate for 10 minutes at room temperature.</li> <li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
<b>Note:</b>	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
<b>RefSeq:</b>	<a href="#">NM_002745.4</a> , <a href="#">NP_002736.3</a>
<b>RefSeq Size:</b>	5916 bp
<b>RefSeq ORF:</b>	1083 bp
<b>Locus ID:</b>	5594
<b>UniProt ID:</b>	<a href="#">P28482</a>
<b>Cytogenetics:</b>	22q11.22
<b>Protein Families:</b>	Druggable Genome, Protein Kinase
<b>Protein Pathways:</b>	Acute myeloid leukemia, Adherens junction, Alzheimer's disease, Axon guidance, B cell receptor signaling pathway, Bladder cancer, Chemokine signaling pathway, Chronic myeloid leukemia, Colorectal cancer, Dorso-ventral axis formation, Endometrial cancer, ErbB signaling pathway, Fc epsilon RI signaling pathway, Fc gamma R-mediated phagocytosis, Focal adhesion, Gap junction, Glioma, GnRH signaling pathway, Insulin signaling pathway, Long-term depression, Long-term potentiation, MAPK signaling pathway, Melanogenesis, Melanoma, mTOR signaling pathway, Natural killer cell mediated cytotoxicity, Neurotrophin signaling pathway, NOD-like receptor signaling pathway, Non-small cell lung cancer, Oocyte meiosis, Pancreatic cancer, Pathways in cancer, Prion diseases, Progesterone-mediated oocyte maturation, Prostate cancer, Regulation of actin cytoskeleton, Renal cell carcinoma, T cell receptor signaling pathway, TGF-beta signaling pathway, Thyroid cancer, Toll-like receptor signaling pathway, Type II diabetes mellitus, Vascular smooth muscle contraction, VEGF signaling pathway

**Gene Summary:**

This gene encodes a member of the MAP kinase family. MAP kinases, also known as extracellular signal-regulated kinases (ERKs), act as an integration point for multiple biochemical signals, and are involved in a wide variety of cellular processes such as proliferation, differentiation, transcription regulation and development. The activation of this kinase requires its phosphorylation by upstream kinases. Upon activation, this kinase translocates to the nucleus of the stimulated cells, where it phosphorylates nuclear targets. One study also suggests that this protein acts as a transcriptional repressor independent of its kinase activity. The encoded protein has been identified as a moonlighting protein based on its ability to perform mechanistically distinct functions. Two alternatively spliced transcript variants encoding the same protein, but differing in the UTRs, have been reported for this gene. [provided by RefSeq, Jan 2014]

Transcript Variant: This variant (1) represents the longer transcript. Both variants 1 and 2 encode the same protein. 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.