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Product datasheet for SC323455

MAPKAP Kinase 3 (MAPKAPK3) (NM_004635) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	MAPKAP Kinase 3 (MAPKAPK3) (NM_004635) Human Untagged Clone
Tag:	Tag Free
Symbol:	MAPKAP Kinase 3
Synonyms:	3PK; MAPKAP-K3; MAPKAP3; MAPKAPK-3; MDPT3; MK-3; MK3
Mammalian Cell Selection:	None
Vector:	pCMV6-XL5
E. coli Selection:	Ampicillin (100 ug/mL)

Fully Sequenced ORF:

>OriGene ORF within SC323455 sequence for NM_004635 edited (data generated by NextGen Sequencing)

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ATGGATGGTGAAACAGCAGAGGAGCAGGGGGGCCCTGTGCCCCCGCCAGTTGCACCCGGC
GGACCCGGCTTGGGCGGTGCTCCGGGGGGGCGGCGGGAGCCCAAGAAGTACGCAGTGACC
GACGACTACCAGTTGTCCAAGCAGGTGCTGGGCCTGGGTGTGAACGGCAAAGTGCTGGAG
TGCTTCCATCGGCGCACTGGACAGAAGTGTGCCCTGATGCTCCTGTATGACAGCCCCAAG
GCCCGGCAGGAGGTAGACCATCACTGGCAGGCTTCTGGCGGCCCCCATATTGTCTGCATC
CTGGATGTGTATGAGAACATGCACCATGGCAAGCGCTGTCTCCTCATCATCATGGAATGC
ATGGAAGGTGGTGAGTTGTTCAGCAGGATTCAGGAGCGTGGCGACCAGGCTTTCACTGAG
AGAGAAGCTGCAGAGATAATGCGGGATATTGGCACTGCCATCCAGTTTCTGCACAGCCAT
AACATTGCCCACCGAGATGTCAAGCCTGAAAACCTACTCTACACATCTAAGGAGAAAGAC
GCAGTGCTTAAGCTCACCGATTTTGGCTTTGCTAAGGAGACCACCCAAAATGCCCTGCAG
ACACCCTGCTATACTCCCTATTATGTGGCCCCTGAGGTCCTGGGTCCAGAGAAGTATGAC
AAGTCATGTGACATGTGGTCCCTGGGTGTCATCATGTACATCCTCCTTTGTGGCTTCCCA
CCCTTCTACTCCAACACGGGCCAGGCCATCTCCCCGGGGATGAAGAGGAGGATTCGCCTG
GGCCAGTACGGCTTCCCCAATCCTGAGTGGTCAGAAGTCTCTGAGGATGCCAAGCAGCTG
ATCCGCCTCCTGTTGAAGACAGACCCCACAGAGAGGCTGACCATCACTCAGTTCATGAAC
CACCCCTGGATCAACCAATCGATGGTAGTGCCACAGACCCCACTCCACACGGCCCGAGTG
CTGCAGGAGGACAAAGACCACTGGGACGAAGTCAAGGAGGAGATGACCAGTGCCTTGGCC
ACTATGCGGGTAGACTACGACCAGGTGAAGATCAAGGACCTGAAGACCTCTAACAACCGG
CTCCTCAACAAGAGGAGAAAAAAGCAGGCAGGCAGCTCCTCTGCCTCACAGGGCTGCAAC
AACCAGTAG

Clone variation with respect to NM_004635.4
218 a=>t
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5' Read Nucleotide Sequence:

>OriGene 5' read for mutant NM_004635 unedited
ACGCCCGTCCAGCAACGGGCGGAGGCGTCACGGAGGGAGGACACACAAGAGAGCCCGTTAGCGAACCGTC
AGAACACCGTAATACGACACACCACAGGGCGGCCGCGAACACGGCACCAGCACCCGCGACCGCCTCTCCC
GCCCCTCGCCGGCACCTCAGCAAGGCGCCACTAGAAGCGCCAGGCTGGGGCCGCCTCTGAGCGCCCCGCG
GGGGCCATGGATGGTGAAACAGCAGAGGAGCAGGGGGGCCCTGTGCCCCCGCCAGTCGCACCCGGCGGAC
CCGGCTTGGGCGGTGCTCCGGGGGGGCGGCGGGGAGCCCAAGAAGTACGCAGTGACCGACGACTACCAGT
TGTCCCAAGCAGGTGCTGGGGCCTGGGGTGTGAACGGCAAAGTGCTTGGAGTTGCTTTCCTTCGCCCCAC
TGGGACAAAATTGTGCCCTGAATGCTTCTTGTTTAACACCCCCAAGGCCGGGCAGGAGGTAAACAATCAC
TGCCGGGCTTTGGGCGGCCCCATTTTTGCTGCCTTCTGGAAGTTTTTGAAAAAACATGCCCATGGGCAGC
CCCTGCTTCTTATCCTTATGGGATGGATGGAAAGGGGGGAATTTTGTCAACAAGATTCAAGGGCGTGGCC
AACAGGCTTTTACTGAAAAAAAAACTGCAGAGATAATGCGGGAAATTGGCACTCTGCATCCCGTTTCGCA
CAGCCATAAAAATGCCCACCCAAATGTGTAAGCCCTGAAAACCTACTCTTCCACATCTTAAGGAGAAAAA
AAGCAGTGCTTAAGCCTCACCCGAATTTGGGCTTTTGCTAAGAGACCCACCAAATGCCCTGCAAACCCCC
TGCTATACTCCTATATGTGCCCTGAGTTCTGGTCAGAAAGTTGACAGTCATGTGACATGTGTCCTTGTGT
CACATGTACTCTCTGTGCTTCCACCTCTACTCACACGCCAGCACTCTCCCAG

Kinase Domain Sequence:

>SC323455 kinase domain raw sequence. By performing BLASTX analysis with this sequence against NCBI refernce protein database, you can confirm the presence of the kinase-deficient mutation
TAGCAGGTGCTGGGCCTGGGTKGACGGCAAAGTGCTGGAGTGCTTCCATCGGCGCACTGGACAGAAGTGT
GCCCTGATGCTCCTGTATGACAGCCCCAAGGCCCGGCAGGAGGTAGACCATCACTGGCAGGCTTCTGGCG
GCCCCCATATTGTCTGCATCCTGGATGTGTATGAGAACATGCACCATGGCAAGCGCTGTCTCCTCATCAT
CATGGAATGCATGGAAGGTGGTGAGTTGTTCAGCAGGATTCAGGA

Restriction Sites: Please inquire

ACCN: NM_004635

Insert Size: 2560 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 kinase-deficient mutant clone was generated by created by site-directed mutagenesis from the corresponding wild-type clone. See details in "Application of active and kinase-deficient kinome collection for identification of kinases regulating hedgehog signaling." Cell. 2008 May p536-548.

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_004635.3, NP_004626.1

RefSeq Size:	2500 bp
RefSeq ORF:	1149 bp
Locus ID:	7867
UniProt ID:	Q16644
Cytogenetics:	3p21.2
Domains:	pkinase, TyrKc, S_TKc
Protein Families:	Druggable Genome, Protein Kinase
Protein Pathways:	MAPK signaling pathway, VEGF signaling pathway
Gene Summary:	This gene encodes a member of the Ser/Thr protein kinase family. This kinase functions as a mitogen-activated protein kinase (MAP kinase)- activated protein kinase. MAP kinases are also known as extracellular signal-regulated kinases (ERKs), act as an integration point for multiple biochemical signals. This kinase was shown to be activated by growth inducers and stress stimulation of cells. In vitro studies demonstrated that ERK, p38 MAP kinase and Jun N-terminal kinase were all able to phosphorylate and activate this kinase, which suggested the role of this kinase as an integrative element of signaling in both mitogen and stress responses. This kinase was reported to interact with, phosphorylate and repress the activity of E47, which is a basic helix-loop-helix transcription factor known to be involved in the regulation of tissue-specific gene expression and cell differentiation. Alternate splicing results in multiple transcript variants that encode the same protein. [provided by RefSeq, Sep 2011] Transcript Variant: This variant (3) differs in the 5' UTR compared to variant 1. Variants 1, 2 and 3 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.