

Product datasheet for MC215924

Dapk3 (NM_001190473) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Dapk3 (NM_001190473) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Dapk3
Synonyms:	dlk; ZIPK
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin

OriGene Technologies, Inc.

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ORIGENE Dapk3 (NM_001190473) Mouse Untagged Clone – MC215924	
Fully Sequenced ORF:	>MC215924 representing NM_001190473 Red=Cloning site Blue=ORF Orange=Stop codon
	TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCC <mark>GCGATCGC</mark> C
	ATGTCCACATTCAGGCAAGAGGATGTTGAGGACCATTATGAGATGGGAGAGGAGCTTGGCAGTGGCCAAT TTGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACGGGCATGGAGTATGCAGCCAAGTTCATCAAGAAGCG GCGCCTGCCATCCAGCCGGCGCGGTGTGAGCCGGGAGGAGGATCGAACGCGAGGTGAGCATCCTGCGCGCGAG ATCCGCCACCCCAACATCATAACACTGCATGCATGACGCGGAGGAGCAACAAGAACAAGACAAGATGTGGTGCTGATCCTGG AGCTGGTGTCCGGTGGCGAGCTTTTCGACTTCCTGGCCGAGAAAGAA
	AGEGGAEEGAEGEGEEGEEGEEEGEEEGEEGAGAAAEEEGAEEAGAAGA
Restriction Sites:	SgfI-RsrII
ACCN:	NM_001190473
Insert Size:	1347 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 Metho	 d: 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.

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	Dapk3 (NM_001190473) Mouse Untagged Clone – MC215924
RefSeq:	<u>NM 001190473.1, NP 001177402.1</u>
RefSeq Size:	1676 bp
RefSeq ORF:	1347 bp
Locus ID:	13144
UniProt ID:	<u>054784</u>
Cytogenetics:	10 39.72 cM
Gene Summary:	Serine/threonine kinase which is involved in the regulation of apoptosis, autophagy, transcription, translation and actin cytoskeleton reorganization. Regulates both type I (caspase-dependent) apoptotic and type II (caspase-independent) autophagic cell deaths signal, depending on the cellular setting. Involved in formation of promyelocytic leukemia protein nuclear body (PML-NB). Involved in apoptosis involving PAWR which mediates cytoplasmic relocation; in vitro phosphorylates PAWR (By similarity). Phosphorylates MYL12B

in non-muscle cells leading to reorganization of actin cytoskeleton such as in regulation of cell polarity and cell migration. Positively regulates canonical Wnt/beta-catenin signaling through interaction with NLK and TCF7L2; disrupts the NLK-TCF7L2 complex thereby influencing the phosphorylation of TCF7L2 by NLK. Phosphorylates STAT3 and enhances its transcriptional activity. Enhances transcription from AR-responsive promoters in a hormone- and kinase-dependent manner. Phosphorylates histone H3 on 'Thr-11' at centromeres during mitosis (By similarity). Phosphorylates RPL13A on 'Ser-77' upon interferon-gamma activation which is causing RPL13A release from the ribosome, RPL13A association with the GAIT complex and its subsequent involvement in transcript-selective translation inhibition.[UniProtKB/Swiss-Prot

Transcript Variant: This variant (3) differs in the 5' UTR and coding sequence compared to variant 1. The resulting isoform (b) is shorter at the N-terminus compared to isoform a. Variants 2 and 3 both encode the same isoform (b). Sequence Note: This RefSeq record was created from genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on

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Function]

transcript alignments.