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Product datasheet for MC226958

Stk11 (NM_001301854) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Stk11 (NM_001301854) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Stk11
Synonyms:	AA408040; Lkb1; Par-4; R75140
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC226958 representing NM_001301854 Red=Cloning site Blue=ORF Orange=Stop codon TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCCGCGATCGCC ATGTATATGGTGATGGAGTACTGCGTATGTGGCATGCAGGAGATGCTGGACAGTGTGCCGGAGAAGCGCT TCCCTGTGTGCCAAGCTCATGGGTACTTCCGCCAGCTGATTGACGGCCTGGAATACCTACACAGCCAGGG CATTGTTCACAAGGACATCAAGCCGGGCAACCTGCTACTCACCACCAATGGCACACTCAAGATCTCCGAC CTCGGTGTTGCCGAGGCCCTGCACCCTTTCGCTGTGGATGACACCTGCCGGACAAGCCAGGGCTCCCCGG CCTTCCAGCCTCCTGAGATTGCCAATGGACTGGACACCTTTTCAGGTTTCAAGGTGGACATCTGGTCAGC TGGGGTCACACTTTACAACATCACCACGGGCCTGTACCCATTTGAGGGGGACAATATCTACAAGCTCTTT GAGAACATTGGGAGAGGAGACTTCACCATCCCTTGTGACTGCGGCCCACCACTCTCTGACCTACTCCGAG GGATGTTGGAGTATGAGCCGGCCAAGAGGTTCTCCATCCGACAGATTAGGCAGCACAGCTGGTTCCGGAA GAAACACCCTCTGGCTGAGGCGCTCGTACCTATCCCACCAAGCCCAGACACTAAGGACCGCTGGCGCAGT ATGACTGTAGTGCCCTACCTGGAGGACCTGCATGGCCGTGCGGAGGAGGAGGAGGAGGAAGACTTGTTTG ACATTGAGGACGGCATTATCTACACCCAGGACTTCACAGTGCCTGGACAGGTCCTGGAAGAGGAAGTGGG TCAGAATGGACAGAGCCACAGTTTGCCCAAGGCTGTTTGTGTGAATGGCACAGAGCCCCAGCTCAGCAGC AAGGTGAAGCCAGAAGGCCGACCTGGCACCGCCAACCCTGCGCGCAAGGTGTGCTCCAGCAACAAGATCC GCCGGCTCTCGGCCTGCAAGCAGCAGTGA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_001301854

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Insert Size:	939 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:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	NM_001301854.1, NP_001288783.1
RefSeq Size:	2378 bp
RefSeq ORF:	939 bp
Locus ID:	20869
UniProt ID:	Q9WTK7
Cytogenetics:	10 C1
Gene Summary:	This gene encodes a member of the serine/threonine kinase family. The encoded protein, a known tumor suppressor, activates (via phosphorylation) adenine monophosphate-activated protein kinase (AMPK) and AMPK-related kinase proteins. This upstream regulation of the AMPK pathway is thought to regulate a number of different processes, including cell metabolism, cell polarity, apoptosis and DNA damage response. Mutations in a similar gene in human have been associated with Peutz-Jeghers syndrome. Alternative splicing results in multiple transcript variants, including the S isoform which plays a potential role in spermiogenesis. [provided by RefSeq, Sep 2014] Transcript Variant: This variant (3) uses an alternate splice site in the 5' terminal exon, and initiates translation at a downstream in-frame start codon, compared to variant 1. The resulting protein (isoform 3) has a shorter N-terminus, compared to isoform L. 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.