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Product datasheet for SC301640

FTS (AKTIP) (NM_001012398) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	FTS (AKTIP) (NM_001012398) Human Untagged Clone
Tag:	Tag Free
Symbol:	FTS
Synonyms:	FT1; FTS
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC301640 representing NM_001012398. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGAACCCTTTCTGGAGCATGTCTACAAGCTCTGTACGCAAACGATCTGAAGGTGAAGAGAAGACATTA ACAGGGGACGTGAAAACCAGTCCTCCACGAACTGCACCAAAGAAACAGCTGCCTTCTATTCCCAAAAAT GCTTTGCCCATAACTAAGCCTACATCTCCTGCCCCAGCAGCACAGTCAACAAATGGCACGCATGCGTCC TATGGACCCTTCTACCTGGAATACTCTCTTCTTGCAGAATTTACCTTGGTTGTGAAGCAGAAGCTACCA GGCGTCTATGTGCAGCCATCTTATCGCTCTGCATTAATGTGGTTTGGAGTAATATTCATACGGCATGGA CTTTACCAAGATGGCGTATTTAAGTTTACAGTTTACATCCCTGATAACTATCCAGATGGTGACTGTCCA CGCTTGGTGTTCGATATTCCTGTCTTTCACCCGCTAGTTGATCCCACCTCAGGTGAGCTGGATGTGAAG AGAGCATTTGCAAAATGGAGGCGGAACCATAATCATATTTGGCAGGTATTAATGTATGCAAGGAGAGTT TTCTACAAGATTGATACAGCAAGCCCCCTGAACCCAGAGGCTGCAGTACTGTATGAAAAAGATATTCAG CTTTTTAAAAGTAAAGTTGTTGACAGTGTTAAGGTGTGCACTGCTCGTTTGTTTGACCAACCTAAAATA GAAGACCCCTATGCAATTAGCTTTTCTCCATGGAATCCTTCTGTACATGATGAAGCCAGAGAAAAGATG CTGACTCAGAAAAAGCCTGAAGAACAGCACAATAAAAGTGTTCATGTTGCTGGCCTGTCATGGGTAAAG CCTGGCTCAGTACAGCCTTTCAGTAAAGAAGAGAAAACAGTGGCGACTTAA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	SgfI-MluI
ACCN:	NM_001012398
Insert Size:	879 bp

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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_001012398.2
RefSeq Size:	2525 bp
RefSeq ORF:	879 bp
Locus ID:	64400
UniProt ID:	Q9H8T0
Cytogenetics:	16q12.2
MW:	33.1 kDa
Gene Summary:	The mouse homolog of this gene produces fused toes and thymic hyperplasia in heterozygous mutant animals while homozygous mutants die in early development. This gene may play a role in apoptosis as these morphological abnormalities are caused by altered patterns of programmed cell death. The protein encoded by this gene is similar to the ubiquitin ligase domain of other ubiquitin-conjugating enzymes but lacks the conserved cysteine residue that enables those enzymes to conjugate ubiquitin to the target protein. This protein interacts directly with serine/threonine kinase protein kinase B (PKB)/Akt and modulates PKB activity by enhancing the phosphorylation of PKB's regulatory sites. Alternative splicing results in two transcript variants encoding the same protein. [provided by RefSeq, Jul 2008] Transcript Variant: This variant (1) encodes isoform 1. 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.

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