

Product datasheet for MC226736

Casp3 (NM_001284409) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Casp3 (NM_001284409) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Casp3
Synonyms:	A830040C14Rik; AC-; AC-3; Casp; CASP-3; Caspase-3; CC3; CPP; CPP-32; CPP32; Lice; mld; mldy; SCA-1; Ya; Yama
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
Fully Sequenced ORF:	>MC226736 representing NM_001284409 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGCC**

ATGGAGAACAACAAACCTCAGTGGATTCAAATCCATTAATAATTTGAAGTAAAGACCATACATGGGA
GCAAGTCAGTGGACTCTGGGATCTATCTGGACAGTAGTTACAAAATGGATTATCCTGAAATGGGCATATG
CATAATAATTAATAAAGAACTCCATAAGAGCACTGGAATGTCATCTCGCTCTGGTACGGATGTGGAC
GCAGCCAACCTCAGAGAGACATTCATGGCCTGAAATACCAAGTCAGGAATAAAAATGATCTTACTCGT
AAGACATTTTGAATTAATGGATAGTGTCTAAGGAAGATCATAGCAAAGGAGCAGCTTTGTGTGTGT
GATTCTAAGCCATGGTGATGAAGGGTCATTTATGGGACAAATGGGCCTGTTGAACTGAAAAAGTTGACT
AGCTTCTTCAGAGGCGACTACTGCCGGAGTCTGACTGGAAGCCGAAACTCTTCATCATTAGGCCTGCC
GGGTACGGAGCTGGACTGTGGCATTGAGACAGACAGTGGGACTGATGAGGAGATGGCTTGCCAGAAGAT
ACCGGTGGAGGCTGACTTCTGTATGCTTACTCTACAGCACCTGGTTACTATTCTGGAGAAATCAAAG
GACGGTCTGTGGTTATCCAGTCCCTTTCAGCATGCTGAAGCTGTACGGCACAAGCTAGAATTTATGC
ACATTCTCACTCGGTAAACAGGAAGTGGCAACGGAATTCGAGTCTTCTCCCTGGACTCCACTTTCCA
CGCAAAGAAACAGATCCCGTGTATTGTGCCATGCTCACGAAAGAACTGACTTTTATCAC**TAG**

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001284409
Insert Size:	834 bp



[View online »](#)

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:	<ol style="list-style-type: none">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:	<u>NM_001284409.1</u> , <u>NP_001271338.1</u>
RefSeq Size:	2610 bp
RefSeq ORF:	834 bp
Locus ID:	12367
UniProt ID:	<u>P70677</u>
Cytogenetics:	8 26.39 cM
Gene Summary:	<p>This gene encodes a protein that belongs to a highly conserved family of cysteinyl aspartate-specific proteases that function as essential regulators of programmed cell death through apoptosis. Members of this family contain an N-terminal pro-domain and require cleavage at specific aspartate residues to become mature. The protein encoded by this gene belongs to a subgroup of cysteinyl aspartate-specific proteases that are activated by initiator caspases and that perform the proteolytic cleavage of apoptotic target proteins. Mice defective for this gene exhibit a variety of phenotypes including reduced neuronal apoptosis resulting in hyperplasias, hearing loss, attenuated osteogenic differentiation of bone marrow stromal stem cells, and pre- and post-natal lethality. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2015]</p> <p>Transcript Variant: This variant (1) represents the longer transcript. Both variants 1 and 2 encode the same protein. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p>