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Product datasheet for SC309463

Caspase 1 (CASP1) (NM_033294) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Caspase 1 (CASP1) (NM_033294) Human Untagged Clone
Tag:	Tag Free
Symbol:	Caspase 1
Synonyms:	ICE; IL1BC; P45
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-AC (PS100020)
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF sequence for NM_033294 edited ATGGCCGACAAGGTCCTGAAGGAGAAGAGAAAGCTGTTTATCCGTTCCATGGGTGAAGCT CCTCAGGCAGTGCAGGACAACCCAGCTATGCCCACATCCTCAGGCTCAGAAGGGAATGTC AAGCTTTGCTCCCTAGAAGAAGCTCAAAGGATATGGAAACAAAAGTCGGCAGAGATTTAT CCAATAATGGACAAGTCAAGCCGCACACGTCTTGCTCTCATTATCTGCAATGAAGAATTT GACAGTATTCCTAGAAGAACTGGAGCTGAGGTTGACATCACAGGCATGACAATGCTGCTA CAAAATCTGGGGTACAGCGTAGATGTGAAAAAAAATCTCACTGCTTCGGACATGACTACA GAGCTGGAGGCATTTGCACACCGCCCAGAGCACAAGACCTCTGACAGCACGTTCCTGGTG TTCATGTCTCATGGTATTCGGGAAGGCATTTGTGGGAAGAAACACTCTGAGCAAGTCCCA GATATACTACAACTCAATGCAATCTTTAACATGTTGAATACCAAGAACTGCCCAAGTTTG AAGGACAAACCGAAGGTGATCATCATCCAGGCCTGCCGTGGTGATAATGTTTCTTGGAGA CATCCCACAATGGGCTCTGTTTTTATTGGAAGACTCATTGAACATATGCAAGAATATGCC TGTTCCTGTGATGTGGAGGAAATTTTCCGCAAGGTTCGATTTTCATTTGAGCAGCCAGAT GGTAGAGCGCAGATGCCCACCACTGAAAGAGTGACTTTGACAAGATGTTTCTACCTCTTC CCAGGACATTAA
Restriction Sites:	Please inquire
ACCN:	NM_033294
Insert Size:	800 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).

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OTI Annotation:	The ORF of this clone has been fully sequenced and found to be a perfect match to NM_033294.2.
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_033294.2, NP_150636.1
RefSeq Size:	941 bp
RefSeq ORF:	792 bp
Locus ID:	834
UniProt ID:	P29466
Cytogenetics:	11q22.3
Protein Families:	Druggable Genome, Protease
Protein Pathways:	Amyotrophic lateral sclerosis (ALS), Cytosolic DNA-sensing pathway, NOD-like receptor signaling pathway
Gene Summary:	This gene encodes a protein which is a member of the cysteine-aspartic acid protease (caspase) family. Sequential activation of caspases plays a central role in the execution-phase of cell apoptosis. Caspases exist as inactive proenzymes which undergo proteolytic processing at conserved aspartic residues to produce 2 subunits, large and small, that dimerize to form the active enzyme. This gene was identified by its ability to proteolytically cleave and activate the inactive precursor of interleukin-1, a cytokine involved in the processes such as inflammation, septic shock, and wound healing. This gene has been shown to induce cell apoptosis and may function in various developmental stages. Studies of a similar gene in mouse suggest a role in the pathogenesis of Huntington disease. Alternative splicing results in transcript variants encoding distinct isoforms. [provided by RefSeq, Mar 2012] Transcript Variant: This variant (delta) has multiple differences in the coding region but the translation remains in frame, compared to variant alpha. Variant delta encodes a protein lacking two internal segments, compared to the isoform alpha. Isoform delta lacks apoptosis-inducing activity. 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.