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Product datasheet for MC226994

Cops5 (NM_001277101) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Cops5 (NM_001277101) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Cops5
Synonyms:	AI303502; CSN5; Jab1; Mov34; Sgn5
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC226994 representing NM_001277101 Red=Cloning site Blue=ORF Orange=Stop codon TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCCGCGATCGCC ATGTCGCTGCGCCGCCGCCGCGCCCCAGCGCGCGAATGGTCTGGACCAACGTCACCTCCGGTCTCAAGTG TCATGGCTGCCTTGAGAGTCTATCACCACTACTTTAAATACTGCAAAATCTCAGCATTGGCTCTACTGAA AATGGTGATGCATGCCAGGTCAGGAGGCAACTTGGAAGTGATGGGTTTGATGCTCGGGAAAGTCGACGGC GAGACCATGATCATCATGGACAGTTTCGCTTTGCCTGTAGAGGGCACAGAAACTCGAGTAAATGCTCAAG CTGCTGCGTATGAGTATATGGCTGCATACATAGAAAATGCCAAACAGGTTGGCCGCCTTGAGAATGCAAT CGGTTGGTATCATAGCCACCCTGGTTATGGCTGCTGGCTCTCCGGGATTGATGTTAGTACACAGATGCTG AACCAGCAGTTTCAAGAACCATTTGTAGCAGTGGTGATTGATCCAACCAGAACAATCTCTGCAGGAAAAG TGAATCTTGGCGCCTTTAGGACATATCCAAAGGGCTACAAACCTCCTGATGAAGGACCTTCTGAGTACCA GACTATCCCACTTAATAAAATAGAAGATTTTGGCGTGCACTGCAAACAATATTATGCCTTAGAAGTCTCA TATTTCAAATCATCTTTGGATCGTAAACTACTTGAGCTTTTGTGGAATAAATACTGGGTGAATACCCTGA GTTCCTCTAGCTTGCTTACTAATGCAGACTACACCACAGGCCAGGTGTTTGATTTGTCTGAGAAGTTAGA GCAGTCGGAAGCCCAACTGGGACGTGGCAGTTTCATGTTGGGCTTAGAAACACATGACCGCAAGTCGGAA GACAAACTTGCCAAAGCTACTAGAGACAGCTGTAAAACCACCATAGAAGCCATCCATGGACTGATGTCTC AGGTTATTAAGGATAAACTGTTTAATCAGATTAACGTTGCTTAG ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_001277101

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Insert Size:	954 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_001277101.1, NP_001264030.1
RefSeq Size:	1482 bp
RefSeq ORF:	954 bp
Locus ID:	26754
UniProt ID:	O35864
Cytogenetics:	1 2.29 cM

Gene Summary:

Probable protease subunit of the COP9 signalosome complex (CSN), a complex involved in various cellular and developmental processes. The CSN complex is an essential regulator of the ubiquitin (Ubl) conjugation pathway by mediating the deneddylation of the cullin subunits of the SCF-type E3 ligase complexes, leading to decrease the Ubl ligase activity of SCF-type complexes such as SCF, CSA or DDB2. Promotes the proteasomal degradation of BRSK2. The complex is also involved in phosphorylation of p53/TP53, c-jun/JUN, IkappaBalpha/NFKBIA, ITPK1 and IRF8, possibly via its association with CK2 and PKD kinases. CSN-dependent phosphorylation of TP53 and JUN promotes and protects degradation by the Ubl system, respectively. In the complex, it probably acts as the catalytic center that mediates the cleavage of Nedd8 from cullins. It however has no metalloprotease activity by itself and requires the other subunits of the CSN complex. Interacts directly with a large number of proteins that are regulated by the CSN complex, confirming a key role in the complex.[UniProtKB/Swiss-Prot Function]
Transcript Variant: This variant (2) differs in the 5' UTR, lacks a portion of the 5' coding region, and initiates translation at an alternate start codon, compared to variant 1. The encoded isoform (2) is shorter and has a distinct N-terminus, compared to isoform 1. 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.