

Product datasheet for SC211952

CEE (GET4) (NM_015949) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	CEE (GET4) (NM_015949) Human 3' UTR Clone
Symbol:	CEE
Synonyms:	C7orf20; CEE; CGI-20; TRC35
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_015949
Insert Size:	1044 bp
Insert Sequence:	<p>>SC211952 3'UTR clone of NM_015949</p> <p>The sequence shown below is from the reference sequence of NM_015949. The complete sequence of this clone may contain minor differences, such as SNPs.</p> <p>Blue=Stop Codon Red=Cloning site</p>

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GGCAAGTTGGACGCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAACGATCGCC
AGCGACGGCAGCCCCATCGAGCTGGACTGAACTGGCCAGGCCACGTGGAGACACCACGGTCGACGACGG
CTGGAGGGACGTTTCAGAGGCGAGTCTGGGTGGCTCCTCGCCTTGGGGGCTCCTGGCCCTGAGGCTGG
CGGTGGCCGCATGCCGGCGGTGTCTGTTTCTGTGCGGCGGCTCAGGGTGGCGGGCTGCTGCTCACTG
TGCTGCTGGGACCAAGAGTGGGGCGTCCCCCTGCTGGCCGCCGCTCCCCGAGATTGACCCACAAT
AAAGCACAGGCCCTTACCGCGGCGTCACCCCTCTCCCACTCCTTTGTTCTGGGTCTTTTCGGGAGGGCTGA
TGGGCAGCACAGGAGGCCGTCCTCGGGGGGCTGCGCACATCACGCTCCTTGCCGGGCGTCCGGCACAG
CTGCGGTACCAAAGCAGGTGCTGGCCCTCGGACCTGAGAGCCCAGCCAGGGCCCATGTGGTCTGCAAAA
TGGGAGCGGTGTTTTGAACACGGGGTCATTCTGCAGTCAGGACGAACCGGTCCCCGTCGACAGCGGA
GTGCAGTGCCCTGCGCCACATCCTCACGCTCGGTGGAGGACGCGTGCGGCGGGACGGTGCCTACGGG
TACTTGCAGCTGTGTCCCATGTGGCATCCCAGAGCTGCGCCCTGCTGGTCTCTGTGAGCGCCACGCTGC
TGTGCTGGAAATGCCGCTTTAAAAAGGGATACCGTGGGACTCTGCCGCTCTTTTCATAACGCAATATT
TATTTGTATTGGGTGATGATTGATTCTTTTCGACCTAACATTTTGGGTTTAAACCAATAACCGGTCCAG
GAGTGAGCAGCTCCGTTCTGTGAGATGCTACTCAAATGTTACCAGAACGATGACAAAAGGGGAGACGC
TCTATTTTTTACAGTTAAATGACAGTTGTAGATTGATACGCAGTTGTGCATGGGAAGGGGAAACGCAC
AGCTTTATTTACTGTAAAGTGGAATTTAGGAAGGCTTGTGTGAACCGTTGCGCATAAATAAACCCCTT
CTACCGGGC
AGCGGACCGACTTACGCGTAAGCGGCCGCGGCATCTAGATTGGAAGAAAATGACCGACCAAGCGACGCC
CAACCTGCCATCACGAGATTTGATTCCACCGCCGC
  
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Restriction Sites: SgfI-RsrII



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OTI Disclaimer:	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).
Components:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.
RefSeq:	NM_015949.3
Summary:	As part of a cytosolic protein quality control complex, the BAG6/BAT3 complex, maintains misfolded and hydrophobic patches-containing proteins in a soluble state and participates to their proper delivery to the endoplasmic reticulum or alternatively can promote their sorting to the proteasome where they undergo degradation (PubMed:20676083, PubMed:21636303, PubMed:21743475, PubMed:28104892). The BAG6/BAT3 complex is involved in the post-translational delivery of tail-anchored/type II transmembrane proteins to the endoplasmic reticulum membrane. Recruited to ribosomes, it interacts with the transmembrane region of newly synthesized tail-anchored proteins and together with SGTA and ASNA1 mediates their delivery to the endoplasmic reticulum (PubMed:20676083, PubMed:28104892, PubMed:25535373). Client proteins that cannot be properly delivered to the endoplasmic reticulum are ubiquitinated and sorted to the proteasome (PubMed:28104892). Similarly, the BAG6/BAT3 complex also functions as a sorting platform for proteins of the secretory pathway that are mislocalized to the cytosol either delivering them to the proteasome for degradation or to the endoplasmic reticulum (PubMed:21743475). The BAG6/BAT3 complex also plays a role in the endoplasmic reticulum-associated degradation (ERAD), a quality control mechanism that eliminates unwanted proteins of the endoplasmic reticulum through their retrotranslocation to the cytosol and their targeting to the proteasome. It maintains these retrotranslocated proteins in an unfolded yet soluble state condition in the cytosol to ensure their proper delivery to the proteasome (PubMed:21636303).[UniProtKB/Swiss-Prot Function]
Locus ID:	51608
MW:	39.1