

Product datasheet for **MC218385**

Get4 (NM_001163316) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Get4 (NM_001163316) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Get4
Synonyms:	1110007L15Rik; AW412535; Cee
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC218385 representing NM_001163316 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGCC**

ATGTCTCAGAGCAAACATGCAGAGGCCCGGAGCTTATGTACTCAGGAGCATTGCTCTTCTCAGTCATG
GCCAGCAGAACAGTGCAGCTGACCTGTCCATGCTGGTCCCGAATCCCTGGAAAAGGCCGAGGTGGACGT
AGCTGATGAGCTTTTGGAAAATCTGGCTAAAGTGTTTCAGTTTGATGGATCCAAATTCCTGAACGAGTA
GCTTTTGTGTCCAGAGCCCTGAAGTGGTCCAGTGGAGGGTCTGGGAACTGGGCCATCCTCGACTCCACC
AGCTGCTGGCCCTCACATTATGGAAAGAGCAAAATTAAGTGTGAGTCTCGGTATCACTTTCTGCCTCCAG
TGATGGCGAGGGCTGCGCCAACATGCTGGTTCGAGTACTCTACTGCCGAGGCTCCGAAGTGAGGTGGAC
ATGTTCTGTGGCTCAGGCTGTGCTACAGTTTCTCTGTTTAAAAAATAAGAACAGTGCCTGGTGGTCTTTA
CAACGTACACACAGAAGCATCCATCCATCGAGGATGGGCCGCCCTTTGTTGAGCCCTGCTCAATTTTCAT
CTGGTTTCTGCTGCTGGCCGTGGACGGTGGCAAGCTGGCTGTCTTACGGTGTGTGCGAGCAGTACCAG
CCGTCCCTGCGGAGGGACCCCATGTACAACGAGTACCTCGACAGGATCGGACAACCTTCTTTCGGTGTGC
CGCCAAAGCAGACATCCTCCTATGGAGGCTTGTAGGGAACCTGCTGAGCAGCCTCATGGGCTCCTCAGA
GCAGGAAGAGGGGAAGAGAGCCAGGATGACAGCAGCCCCATCGAGCTGGACTGA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	Sgfl-MluI
ACCN:	NM_001163316
Insert Size:	825 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).
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_001163316.1</u> , <u>NP_001156788.1</u>
RefSeq Size:	1915 bp
RefSeq ORF:	825 bp
Locus ID:	67604
UniProt ID:	<u>Q9D1H7</u>
Cytogenetics:	5 G2
Gene Summary:	<p>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. 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. Client proteins that cannot be properly delivered to the endoplasmic reticulum are ubiquitinated and sorted to the proteasome. 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. 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.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) differs in the 5' UTR, lacks a portion of the 5' coding region, and initiates translation at a downstream start codon, compared to variant 1. The encoded isoform (2) is shorter than isoform 1.</p>