

## Product datasheet for MC226143

### Eif3k (NM\_001285942) Mouse Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	Eif3k (NM_001285942) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Eif3k
Synonyms:	1200009C21Rik; Eif3s12
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC226143 representing NM_001285942 Red=Cloning site Blue=ORF Orange=Stop codon

TTTGTAAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
 GCC**CGATCGCC**

ATGGCGATGTTTGAGCAGATGAGAGCGAACGTGGGCAAGTTGCTCAAGGGTATCGACAGGTACCAAGTTCA  
 ACCCAGCCTTCTTCCAGACCACAGTCACTGCCAGATTCTGCTGAAAGCCCTACCAACCTGCCCCACAC  
 CGACTTCACTCTGTGTAATGTATGATCGACAGGCACATCAAGAAGAGCGGCCCATCCGGCAGATCTTG  
 TACCTCGGGGACCTGCTGGAGACCTGCCACTTTCAAGCCTTCTGGCAAGCCCTGGATGAGAACATGGACC  
 TTCTGGAAGGCATAACTGGCTTTGAAGACTCTGTCCGAAAATTTATCTGCCACGTGGTGGGCATCACGTA  
 CCAGCACATCGACCGCTGGCTGCTGGCCGAGATGCTCGGAGACCTGACTGACAACAGCTGAAGGTGTGG  
 ATGAGCAAGTACGGCTGGAGCGCTGACGAGTCAGGGCAGGTCTTCATCTGCAGCCAGGAAGAGGCATTA  
 AGCCCAAGAACATCGTGGAGAAGATTGACTTTGACAGTGTGTCCAGCATCATGGCCTCCTCCAG**TAA**

**ACGCGT**ACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	SgfI-MluI
ACCN:	NM_001285942
Insert Size:	558 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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<b>OTI Annotation:</b>	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"> <li>1. Centrifuge at 5,000xg for 5min.</li> <li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>3. Close the tube and incubate for 10 minutes at room temperature.</li> <li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
<b>Note:</b>	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
<b>RefSeq:</b>	<a href="#">NM_001285942.1</a> , <a href="#">NP_001272871.1</a>
<b>RefSeq Size:</b>	767 bp
<b>RefSeq ORF:</b>	558 bp
<b>Locus ID:</b>	73830
<b>UniProt ID:</b>	<a href="#">Q9DBZ5</a>
<b>Cytogenetics:</b>	7 B1
<b>Gene Summary:</b>	<p>Component of the eukaryotic translation initiation factor 3 (eIF-3) complex, which is required for several steps in the initiation of protein synthesis. The eIF-3 complex associates with the 40S ribosome and facilitates the recruitment of eIF-1, eIF-1A, eIF-2:GTP:methionyl-tRNA<sup>i</sup> and eIF-5 to form the 43S pre-initiation complex (43S PIC). The eIF-3 complex stimulates mRNA recruitment to the 43S PIC and scanning of the mRNA for AUG recognition. The eIF-3 complex is also required for disassembly and recycling of post-termination ribosomal complexes and subsequently prevents premature joining of the 40S and 60S ribosomal subunits prior to initiation. The eIF-3 complex specifically targets and initiates translation of a subset of mRNAs involved in cell proliferation, including cell cycling, differentiation and apoptosis, and uses different modes of RNA stem-loop binding to exert either translational activation or repression.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) lacks an alternate in-frame exon compared to variant 1. The resulting isoform (2) has the same N- and C-termini but is shorter compared to isoform 1.</p> <p>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.</p>