

## Product datasheet for **SC325662**

### EIF4E (NM\_001130679) Human Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** EIF4E (NM\_001130679) Human Untagged Clone  
**Tag:** Tag Free  
**Symbol:** EIF4E  
**Synonyms:** AUTS19; CBP; eIF-4E; EIF4E1; EIF4EL1; EIF4F  
**Mammalian Cell Selection:** None  
**Vector:** [pCMV6-XL5](#)  
**E. coli Selection:** Ampicillin (100 ug/mL)

**Fully Sequenced ORF:** >OriGene ORF sequence for NM\_001130679 edited  
ATGGCGACTGTCTGAACCGGAAACCACCCCTACTCCTAATCCCCGACTACAGAAGAGGAG  
AAAACGGAAATCTAATCAGGAGGTTGCTAACCCAGAACACTATATTAACATCCCCCTACAG  
AACAGATGGGCACTCTGGTTTTTTAAAAATGATAAAAGCAAACTTGGCAAGCAAACCTG  
CGGCTGATCTCCAAGTTTGATACTGTTGAAGACTTTTGGGCTCTGTACAACCATATCCAG  
TTGTCTAGTAATTTAATGCCTGGCTGTGACTACTCACTTTTTAAGGATGGTATTGAGCCT  
ATGTGGGAAGATGAGAAAAACAAACGGGGAGGACGATGGCTAATTACATTGAACAAACAG  
CAGAGACGAAGTGACCTCGATCGCTTTTGGCTAGAGACAAGATGGGATCTTGCTATGTTG  
CCCAGTTGGTCTCAAATTTCTGGCCTCAAGTGATCCTCCCACTTCAGCCTCCCAAAGTG  
CTGGAATTACAGTCTCTGTGCCTTATTGGAGAATCTTTGATGACTACAGTGATGATGTA  
TGTGGCGCTGTTGTTAATGTTAGAGCTAAAGGTGATAAGATAGCAATATGGACTACTGAA  
TGTGAAAACAGAGAAGCTGTTACACATATAGGGAGGGTATACAAGGAAAGTTAGGACTT  
CCTCAAAGATAGTGATTGGTTATCAGTCCCACGCAGACACAGCTACTAAGAGCGGCTCC  
ACCACTAAAAATAGGTTTGTGTTAA

**Restriction Sites:** Please inquire

**ACCN:** NM\_001130679

**Insert Size:** 3300 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>	This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.
<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>RefSeq:</b>	<a href="#">NM_001130679.1</a> , <a href="#">NP_001124151.1</a>
<b>RefSeq Size:</b>	4842 bp
<b>RefSeq ORF:</b>	747 bp
<b>Locus ID:</b>	1977
<b>UniProt ID:</b>	<a href="#">P06730</a>
<b>Cytogenetics:</b>	4q23
<b>Protein Pathways:</b>	Insulin signaling pathway, mTOR signaling pathway
<b>Gene Summary:</b>	<p>The protein encoded by this gene is a component of the eukaryotic translation initiation factor 4F complex, which recognizes the 7-methylguanosine cap structure at the 5' end of messenger RNAs. The encoded protein aids in translation initiation by recruiting ribosomes to the 5'-cap structure. Association of this protein with the 4F complex is the rate-limiting step in translation initiation. This gene acts as a proto-oncogene, and its expression and activation is associated with transformation and tumorigenesis. Several pseudogenes of this gene are found on other chromosomes. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2015]</p> <p>Transcript Variant: This variant (2) contains an alternate in-frame exon in the 3' coding region compared to variant 1. It encodes isoform 2, which is longer than isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data because transcript sequence consistent with the reference genome assembly was not available for all regions of the RefSeq transcript. The extent of this transcript is supported by transcript alignments.</p>