OriGene Technologies, Inc.
9620 Medical Center Drive, Ste 200
Rockville, MD 20850, US
Phone: +1-888-267-4436
https://www.origene.com
techsupport@origene.com
EU: info-de@origene.com
CN: techsupport@origene.cn

Product datasheet for SC109192

EIF4G1 (NM_004953) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	EIF4G1 (NM_004953) Human Untagged Clone
Tag:	Tag Free
Symbol:	EIF4G1
Synonyms:	EIF-4G1; EIF4F; EIF4G; EIF4GI; P220; PARK18
Mammalian Cell Selection:	None
Vector:	pCMV6-XL6
E. coli Selection:	Ampicillin (100 ug/mL)

Fully Sequenced ORF:

>OriGene ORF within SC109192 sequence for NM_004953 edited (data generated by NextGen Sequencing)

ATGTCTGGGGCCCGCACTGCCTCCACACCCACCCCTCCCCAGACGGGAGGCGGTCTGGAG
CCTCAAGCTAATGGGGAGACGCCCCAGGTTGCTGTCATTGTCCGGCCAGATGACCGGTCA
CAGGGAGCAATCATTGCTGACCGGCCAGGGCTGCCTGGCCCAGAGCATAGCCCTTCAGAA
TCCCAGCCTTCGTCGCCTTCTCCGACCCCATCACCATCCCCAGTCTTGGAACCGGGGTCT
GAGCCTAATCTCGCAGTCCTCTCTATTCCTGGGGACACTATGACAACTATACAAATGTCT
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CCCACTCCTCTCGCCGAACCCATACTGGAAGTAGAAGTGACACTTAGCAAACCGGTTCCA
GAATCTGAGTTTTCTTCCAGTCCTCTCCAGGCTCCCACCCCTTTGGCATCTCACACAGTG
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AGCCCAGAGCTTGCTCCTCCCCCAGCTTGCCCCTCCGAATCCCCTGTGCCCATTGCTCCA
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CCAGTCAGTGAGCCAGAGGAGCAGGCCAAGGAGGTGACAGCATCAGTGGCGCCCCCCACC
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CAGAATTTGGAGGCAGCAGCAGCCACTCAAGTGGCAGTATCTGTGCCAAAGAGGAGACGG
AAAATTAAGGAGCTAAATAAGAAGGAGGCTGTTGGAGACCTTCTGGATGCCTTCAAGGAG
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CTACAAGGCATAAATTGTGGCCCAGACTTCACTCCATCCTTTGCCAACCTTGGCCGGACA
ACCCTTAGCACCCGTGGGCCCCCAAGGGGTGGGCCAGGTGGGGAGCTGCCCCGTGGGCCN

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NNGGCTGGCCTGGGACCCCGGCGCTCTCAGCAGGGACCCCGAAAAGAACCACGCAAGATC
ATTGCCACAGTGTTAATGACCGAAGATATAAAACTGAACAAAGCAGAGAAAGCCTGGAAA
CCCAGCAGCAAGCGGACGGCGGCTGATAAGGATCGAGGGGAAGAAGATGCTGATGGCAGC
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AAGGAGGATGCCTTCTACAGTTGGGAGAGTAGCAAGGACCCCGCTGAGCAGCAGGGCAAG
GGTGTGGCCCTTAAATCTGTCACAGCCTTCTTCAAGTGGCTCCGTGAAGCAGAGGAGGAG
TCTGACCACAACTGA

Clone variation with respect to NM_004953.4
706 a=>g;1500 g=>n;1501 c=>n;1502 a=>n

5' Read Nucleotide Sequence:

>OriGene 5' read for NM_004953 unedited
CCGCCCCGTTGNCGCAAAGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGC
TCATTTAGGTGACACTATAGAATACAAGCTACTTGTTCTTTTTGCAGCGGCCGCGAATTC
GGCACGAGGCGAGATCCAAACCAAGGAGGAAAGGATATCACAGAGGAGATCATGTCTGGG
GCCCGCACTGCCTCCACACCCACCCCTCCCCAGACGGGAGGCGGTCTGGAGCCTCAAGCT
AATGGGGAGACGCCCCAGGTTGCTGTCATTGTCCGGCCAGATGACCGGTCACAGGGAGCA
ATCATTGCTGACCGGCCAGGGCTGCCTGGCCCAGAGCATAGCCCTTCAGAATCCCAGCCT
TCGTCGCCTTCTCCGACCCCATCACCATCCCCAGTCTTGGAACCGGGGTCTGAGCCTAAT
CTCGCAGTCCTCTCTATTCCTGGGGACACTATGACAACTATACAAATGTCTGTAGAAGAA
TCAACCCCCATCTCCCGTGAAACTGGGGAGCCATATCGCCTCTCTCCAGAACCCACTCCT
CTCGCCGAACCCATACTGGAAGTAGAAGTGACACTTAGCAAACCGGTTCCAGAATCTGAG
TTNTCTTCCAGTCCTCTCCAGGCTCCCACCCCTTTGGCATCTCACACAGTGGAAATTCAT
GAGCCTAATGGCATGGTCCCATCTGAAGATCTGGAACCCAGAGTGGAGTCAAGCCCAGAG
CTTGCTCCTCCCCAGCTTGCCCCTNCGATCCCCTGTGCCCATTGCTCCACTGCCCACCTG
NAGACTGCTCACGGAGCCCNCTCGCACCAGCTGNGGACTTAAGCCAGTCAGTGAGCCAGA
GGAGCAGCCAGGNNAGTGACAGCATCAGTGGNGCCCCCACCATCCCTNTGNTACTCAGTA
CGGNNTCTTAGCTACTTCCACTCAGAGGGAGGATGGGAAACAAANAAANAGGANAAGGNN
ACCNGGAAANCNNGAACCTGAT

3' Read Nucleotide Sequence:

>OriGene 3' read for NM_004953 unedited
TANGATCGAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAATGAA
TTCATGTTTAATAATTACAGGCACCGTGCCCCCCCTTCCCCCTGCCCAGGCAACAACAGG
GGTGGTACAGGGGCTGGGGCATATGCCCCCAGCAGCGAGGACGGGAGTCCCGAGAGTGAT
TTTCAAAAAATATAATAAAGGACCCCAGGGGCAGGCGTTGGGGCCCCTCCCCACCCCAAG
ACACACCAAATTTCAAGACTTTATATATAATATATCTCTGTGCCCCAGGGGGAGGAAAGG
GACACCTGGCGGCATCCTGGAGGGGGGCCCAAGGAGCCCCAAGCCATCCTGCCTCTTCAA
CCACTTTATTAGTTTAAACACATTAACACTAAAGGGACCCACTGGCACCGCCGCTGGTGG
CGCCCCCCTGGAGTCCAAGGGGGTATCCGGGCCATCTGTGTGTCCCTGGGGCTTCCAGTT
CCCGGGCCCCCCAAACCTTCATTGGGGGCAAACCCCTTCTCTTGCTTCCGGAACCCCCTG
AAAAAGCTGTGACAATTTAAAGGCACACCCTTTGCCTGGTTGTTAAGGGGGGTCTTGCTT
CTCTCCCCACCTGTGAAAGGGATTCTCCTTTAACCAATTCTCTTTTTAAAAGGGGTCAAA
AAAAATCCCCCCAAAGGGGGGGGGGGTGTGCCTAAGGGTAACTAAAAGGGCCTCGAGGGC
GTAAAAAGCCCCTTGTTCCCTTTTTGTTCGGACACAAGGGTTTTTTTGGGAACCTTTCCT
TGTAGCTTTATTACCTCGGAGCCCCCCCGCCGGGGGGGATTTACCAAAAATATTCGAAAA
AATAAAACGCCCCCTACGGGGGTGAGTACCAC

Restriction Sites: NotI-NotI

ACCN: NM_004953

Insert Size: 5000 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).

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.
RefSeq:	NM_004953.2, NP_004944.2
RefSeq Size:	5045 bp
RefSeq ORF:	4212 bp
Locus ID:	1981
UniProt ID:	Q04637
Cytogenetics:	3q27.1
Domains:	eIF5C, MIF4G, MA3
Protein Pathways:	Viral myocarditis
Gene Summary:	The protein encoded by this gene is a component of the multi-subunit protein complex EIF4F. This complex facilitates the recruitment of mRNA to the ribosome, which is a rate-limiting step during the initiation phase of protein synthesis. The recognition of the mRNA cap and the ATP-dependent unwinding of 5'-terminal secondary structure is catalyzed by factors in this complex. The subunit encoded by this gene is a large scaffolding protein that contains binding sites for other members of the EIF4F complex. A domain at its N-terminus can also interact with the poly(A)-binding protein, which may mediate the circularization of mRNA during translation. Alternative splicing results in multiple transcript variants, some of which are derived from alternative promoter usage. [provided by RefSeq, Aug 2010] Transcript Variant: This variant (5) differs in the 5' UTR, lacks a portion of the 5' coding region, and uses a downstream start codon, compared to variant 1. The resulting isoform (4) is shorter at the 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.