

Product datasheet for SC304538

THG1L (NM_017872) Human Untagged Clone

Product data:

OriGene Technologies, Inc.

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| Product Type: | Expression Plasmids |
|------------------------------|--|
| Product Name: | THG1L (NM_017872) Human Untagged Clone |
| Tag: | Tag Free |
| Symbol: | THG1L |
| Synonyms: | hTHG1; ICF45; IHG-1; IHG1; SCAR28; THG1 |
| Mammalian Cell Selection: | Neomycin |
| Vector: | pCMV6-Entry (PS100001) |
| E. coli Selection: | Kanamycin (25 ug/mL) |
| Fully Sequenced ORF: | >SC304538 representing NM_017872. Blue=Insert sequence <mark>Red</mark> =Cloning site Green=Tag(s) |
| | GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGTGGGGCGCCTGTAAAGTTAAGGTTCACGATTCCTTGGCCACCATTTCCATCACTCTGAGACGGTAC CTGAGATTGGGGGCGACCATGGCAAAAAGCAAGTTCGAGTACGTGAGGGACTTCGAGGCTGACGACACC TGCCTGGCACACTGCTGGGTGGTAGTGCGGCTGGACGGCCGGAATTTCCATCGGTTTGCTGAGAAGCAC AACTTTGCAAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATGTGCGCAGACTGTGATGGAA GAACTAGAGGATATTGTGATCGCGTATGGACAGAGTGATGAGTACAGCTTTGGTTCAAGCGGAAAACC AATTGGTTTAAAAGAAGAGCCAGTAAGTTCATGACTCACGTGGGCCTCCCAGTTTGCCTCCAGCTATGTG TTTTATTGGCGGGATTACTTTGAGGACCAGCCCCTTCTGTATCCCCCAGGCTTTGACGAAAGACCG GTGTATCCCAGCAACCAGACTTTAAAGGACTACCTCAGCTGGCGACAAGCAGATTGTCACATCAATAT CTTTATAATACAGTTTTCTGGGCACTTATACAACAATCTGGACTAACACCAGTACAACACCAAGGAGAGA TTACAGGGAACTCTTGCAGCAGACAAGAATGAGATTTTGTTTTCTGAATTCAACACATCAACTAATAAT GAGCTGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAGAAGGTGGATGAAGTGATGACAAAAGAA ATTAAGCTGCCAACAGAAATGGAAAGGAACATCCAGCAGTGGACGAAGGTGATGAACAAAGCAGCTGA TTCACGCGATGTATACGGAAGGAAAAAGAATGGCAGTGGACGAAGGTGGATGAAGTGACAAAAGAA ATTAAGCTGCCAACAGAAATGGAAGGAAAAAAGATGGCAGTGACCCGGACCAGGACAAAGCCAGTGGCC TTGCACTGCCGATATCATCGGGGATGCTTTCTGGAAGGAA |
| Restriction Sites: | Sgfl-Mlul |
| ACCN: | NM_017872 |
| Insert Size: | 897 bp |



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| GRIGENE THG1L (NM_017872) Human Untagged Clone – SC304538 | |
|--|--|
| 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). |
| OTI Annotation: | 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. |
| 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: | Centrifuge at 5,000xg for 5min. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. Close the tube and incubate for 10 minutes at room temperature. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 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 017872.4</u> |
| RefSeq Size: | 2932 bp |
| RefSeq ORF: | 897 bp |
| Locus ID: | 54974 |
| UniProt ID: | <u>Q9NWX6</u> |
| Cytogenetics: | 5q33.3 |
| MW: | 34.8 kDa |
| Gene Summary: | The protein encoded by this gene is a mitochondrial protein that is induced by high levels of glucose and is associated with diabetic nephropathy. The encoded protein appears to increase mitochondrial biogenesis, which could lead to renal fibrosis. Another function of this protein is that of a guanyltransferase, adding GMP to the 5' end of tRNA(His). Several transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Dec 2015] Transcript Variant: This variant (1) represents the longest transcript and encodes the longest |

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.

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