

Product datasheet for **SC116137**

COG5 (NM_006348) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	COG5 (NM_006348) Human Untagged Clone
Tag:	Tag Free
Symbol:	COG5
Synonyms:	CDG2I; GOLTC1; GTC90
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL6</u>
E. coli Selection:	Ampicillin (100 ug/mL)



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Fully Sequenced ORF: >OriGene ORF within SC116137 sequence for NM_006348 edited (data generated by NextGen Sequencing)

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ATGGGCTGGGTGGGCGGGCGGGCCGGGATTCTGCGTCACCACCTGGGCGGAGCCGTTCT
GCTGCTGACGACATCAACCCGGCACCTGCCAACATGGAAGGTGGCGGGCAGCGTCGCT
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GCAACTGGGATTGAGTCGTTGGAAGGTGTTCTTCAAGATGATGCAGACGAGAATTGGGGCT
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TAA
    
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Clone variation with respect to NM_006348.3
 988 t=>c;1782 t=>g

5' Read Nucleotide Sequence:

>OriGene 5' read for NM_006348 unedited
 CTTATTACCCGCCGTCGNCGCTAAGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAA
 GCAGAGCTCATTTAGGTGACACTATAGAATACAAGCTACTTGTCTTTTTGCAGCGGCCG
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 CGTTCGGTGCCACCTTCTTCTGGCTAGGGCAGCAGCCAGCCAGGGGGCGCGGCC
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 TGACGACATCAACCCGGCACCTGCCAATGGAAGGTGGGCGGCGCAGCGTCGCTGTAGC
 TGGCCTCGGAGCTCGAGGCTCTGGAGCGGCTGCAGCTACAGTCCGGAACTTCTGCAGGA
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 TGGATTGAGTCGTTNAAAGTTGCTTCANATGAGCAAACCAGAATTGGGCCTTACAGGG
 AGCTGTG

3' Read Nucleotide Sequence:

>OriGene 3' read for NM_006348 unedited
 CTANATCGAGTTTTTTTTTTTTTTTTTTTTGGGATATGTGTTAACTGCCAACTATGAATG
 GGTTAGCACAAAGTGGAGATGAACAAAGATTTTCATGTCATTACTGAAGAGCAGACATAGC
 CTTTTGAAGCAGCTGAACCATTATGGGATAAACTGGTGCAAATCTTTGCCTTCTCTACT
 TCTCACTGATTGAACATAAGCTTCCAGGGCTCCCCTGATGAGGAGGAGCCTGTCTTTTT
 AGATGGATGGTCATCCAGCCACTGAGAGAAGCGTGTGTGGGACCACTCTGCCCTCTGGAA
 AGGAGATTTCAAGTTCAGCGGGTCTCTCGTGAACAAAACTGAATAATGATGCTGAACGG
 AATCACATCCCCAATGCAGGACTACTGGCTACATGTTCACTTGCCTGGAAGAGCAGAGG
 TCTGAATGATCTCAGCATCCGATAGGACTTTCTAAATCAGATACTCGTCTACAGAATGG
 ACCCACAGCCAACTCCATCTGTGCAAAAATCAGCAGCAAGTCGCATTTTCCACCTTACC
 AAGAGGCTTATGAGACTGGCATGGCGGATAAAAAGTTCAACAGCTCTTTGGGCAATAGC
 CTCAGTGTGTCAAAGACNAAATCCAAGCATTCAAAGTGTNTAATAGTCACTATAAC
 TCTGGCAATGAAACCTTGTAGCTCCCTCATGTACAGAGGACAAGGAACATCCGGTTTTTC
 TGAGCTGGGTAATGACCCAAAAAGTCTTCTGATGCAGGGTGATGGATATGGCCCTAAT
 AGCTCTNCACAGAAGTGGATAAAGTTTGCACCAGATTTTCCATAAGAGCATGAATAGCC
 TTTAGAGCTGAAATTTAGTTT

Restriction Sites:

NotI-NotI

ACCN:

NM_006348

Insert Size:

3200 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_006348.2](#), [NP_006339.2](#)

RefSeq Size: 3604 bp

RefSeq ORF: 2583 bp

Locus ID: 10466

UniProt ID: [Q9UP83](#)

Cytogenetics: 7q22.3

Gene Summary: The protein encoded by this gene is one of eight proteins (Cog1-8) which form a Golgi-localized complex (COG) required for normal Golgi morphology and function. The encoded protein is organized with conserved oligomeric Golgi complex components 6, 7 and 8 into a sub-complex referred to as lobe B. Alternative splicing results in multiple transcript variants. Mutations in this gene result in congenital disorder of glycosylation type 2I.[provided by RefSeq, Jan 2011]

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.