

Product datasheet for SC206055

COPG2 (NM_012133) Human 3' UTR Clone

Product data:

OriGene Technologies, Inc.

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Product Type:	3' UTR Clones
Product Name:	COPG2 (NM_012133) Human 3' UTR Clone
Symbol:	COPG2
Synonyms:	2-COP; gamma-2-COP
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_012133
Insert Size:	468 bp
Insert Sequence:	<pre>>SC206055 3'UTR clone of NM_012133 The sequence shown below is from the reference sequence of NM_012133. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC GTAGATGTTATCTTAGCTTCGTTGGATAAATGCTTACTGGACAAGAGGAAACTGATGCACACTACATG GTCAGTGGGCTTTTAGGCTAGTGGCATCAGTTCCCAGAATCAGACTTTGAAGATGAATGA</pre>
Restriction Sites:	Sgfl-Mlul
OTI Disclaimer:	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).
Components:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.



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RefSeq:	<u>NM 012133.6</u>
Summary:	The coatomer is a cytosolic protein complex that binds to dilysine motifs and reversibly associates with Golgi non-clathrin-coated vesicles, which further mediate biosynthetic protein transport from the ER, via the Golgi up to the trans Golgi network. Coatomer complex is required for budding from Golgi membranes, and is essential for the retrograde Golgi-to-ER transport of dilysine-tagged proteins. In mammals, the coatomer can only be recruited by membranes associated to ADP-ribosylation factors (ARFs), which are small GTP-binding proteins; the complex also influences the Golgi structural integrity, as well as the processing, activity, and endocytic recycling of LDL receptors (By similarity).[UniProtKB/Swiss-Prot Function]
Locus ID:	26958
MW:	17.6

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