

Product datasheet for RC225371L3V

OriGene Technologies, Inc.

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COMT (NM 001135162) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type: Lentiviral Particles

Product Name: COMT (NM_001135162) Human Tagged ORF Clone Lentiviral Particle

Symbol:

HEL-S-98n Synonyms:

Mammalian Cell Puromycin

Selection:

Vector: pLenti-C-Myc-DDK-P2A-Puro (PS100092)

Tag: Myc-DDK

NM 001135162 ACCN:

ORF Size: 813 bp

ORF Nucleotide

The ORF insert of this clone is exactly the same as(RC225371).

OTI Disclaimer:

Cytogenetics:

Sequence:

The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing

variants is recommended prior to use. More info

OTI Annotation: This clone was engineered to express the complete ORF with an expression tag. Expression

varies depending on the nature of the gene.

RefSeq: NM 001135162.1, NP 001128634.1

RefSeq Size: 2279 bp RefSeq ORF: 816 bp Locus ID: 1312 **UniProt ID:** P21964

22q11.21 **Protein Families:** Druggable Genome, Transmembrane

Protein Pathways: Metabolic pathways, Tyrosine metabolism





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MW: 30 kDa

Gene Summary:

Catechol-O-methyltransferase catalyzes the transfer of a methyl group from S-adenosylmethionine to catecholamines, including the neurotransmitters dopamine, epinephrine, and norepinephrine. This O-methylation results in one of the major degradative pathways of the catecholamine transmitters. In addition to its role in the metabolism of endogenous substances, COMT is important in the metabolism of catechol drugs used in the treatment of hypertension, asthma, and Parkinson disease. COMT is found in two forms in tissues, a soluble form (S-COMT) and a membrane-bound form (MB-COMT). The differences between S-COMT and MB-COMT reside within the N-termini. Several transcript variants are formed through the use of alternative translation initiation sites and promoters. [provided by RefSeq, Sep 2008]