

Product datasheet for SC332384

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PCYT2 (NM_001256435) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: PCYT2 (NM_001256435) Human Untagged Clone

Tag: Tag Free Symbol: PCYT2

Synonyms: ET; SPG82

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF: >SC332384 representing NM_001256435.

Blue=Insert sequence Red=Cloning site Green=Tag(s)

GCGGCACAGCCCCTGGGGGAGCGCGATGGTGACTTCTAA

Restriction Sites: Sgfl-Mlul

ACCN: NM 001256435

Insert Size: 936 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: <u>NM 001256435.2</u>

 RefSeq Size:
 3525 bp

 RefSeq ORF:
 936 bp

 Locus ID:
 5833

 UniProt ID:
 Q99447

 Cytogenetics:
 17q25.3

Protein Pathways: Glycerophospholipid metabolism, Metabolic pathways

MW: 35.2 kDa

Gene Summary: This gene encodes an enzyme that catalyzes the formation of CDP-ethanolamine from CTP

and phosphoethanolamine in the Kennedy pathway of phospholipid synthesis. Alternative

splicing results in multiple transcript variants. [provided by RefSeq, May 2010] Transcript Variant: This variant (4) uses an alternate splice site in its 5' UTR, uses a

downstream in-frame start codon, and lacks an alternate in-frame exon in the central coding

region, compared to variant 1. The encoded isoform (4) is shorter at the N-terminus,

compared to isoform 1. Both variants 4 and 5 encode the same isoform (4). 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.