

## Product datasheet for **SC336242**

### CDT2 (DTL) (NM\_001286229) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	CDT2 (DTL) (NM_001286229) Human Untagged Clone
Tag:	Tag Free
Symbol:	DTL
Synonyms:	CDT2; DCAF2; L2DTL; RAMP
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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**Fully Sequenced ORF:** >SC336242 representing NM\_001286229.  
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

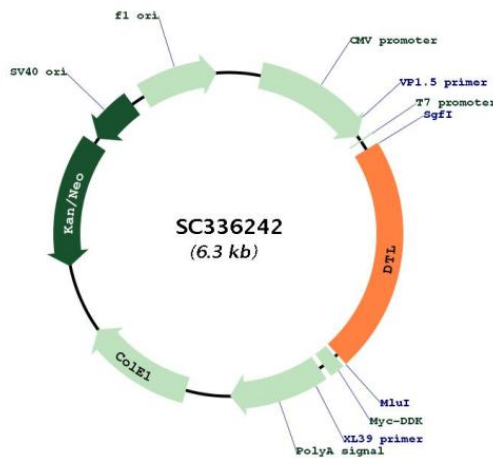
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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAATACGACTCACTATAGGGCGGCCGGGAATTCGTGACTG
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ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
  
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**Restriction Sites:**

SgfI-MluI

**Plasmid Map:**



**ACCN:** NM\_001286229

**Insert Size:** 1380 bp

<b>OTI Disclaimer:</b>	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).
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"><li>1. Centrifuge at 5,000xg for 5min.</li><li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li><li>3. Close the tube and incubate for 10 minutes at room temperature.</li><li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li><li>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.</li></ol>
<b>RefSeq:</b>	<a href="#">NM_001286229.1</a>
<b>RefSeq Size:</b>	4381 bp
<b>RefSeq ORF:</b>	1380 bp
<b>Locus ID:</b>	51514
<b>UniProt ID:</b>	<a href="#">Q9NZJ0</a>
<b>Cytogenetics:</b>	1q32.3
<b>Protein Families:</b>	Druggable Genome
<b>MW:</b>	49.4 kDa

**Gene Summary:**

Substrate-specific adapter of a DCX (DDB1-CUL4-X-box) E3 ubiquitin-protein ligase complex required for cell cycle control, DNA damage response and translesion DNA synthesis. The DCX(DTL) complex, also named CRL4(CDT2) complex, mediates the polyubiquitination and subsequent degradation of CDT1, CDKN1A/p21(CIP1), FBH1, KMT5A and SDE2 (PubMed:16861906, PubMed:16949367, PubMed:16964240, PubMed:17085480, PubMed:18703516, PubMed:18794347, PubMed:18794348, PubMed:19332548, PubMed:20129063, PubMed:23478441, PubMed:23478445, PubMed:23677613, PubMed:27906959). CDT1 degradation in response to DNA damage is necessary to ensure proper cell cycle regulation of DNA replication (PubMed:16861906, PubMed:16949367, PubMed:17085480). CDKN1A/p21(CIP1) degradation during S phase or following UV irradiation is essential to control replication licensing (PubMed:18794348, PubMed:19332548). KMT5A degradation is also important for a proper regulation of mechanisms such as TGF-beta signaling, cell cycle progression, DNA repair and cell migration (PubMed:23478445). Most substrates require their interaction with PCNA for their polyubiquitination: substrates interact with PCNA via their PIP-box, and those containing the 'K+4' motif in the PIP box, recruit the DCX(DTL) complex, leading to their degradation. In undamaged proliferating cells, the DCX(DTL) complex also promotes the 'Lys-164' monoubiquitination of PCNA, thereby being involved in PCNA-dependent translesion DNA synthesis (PubMed:20129063, PubMed:23478441, PubMed:23478445, PubMed:23677613). The DDB1-CUL4A-DTL E3 ligase complex regulates the circadian clock function by mediating the ubiquitination and degradation of CRY1 (PubMed:26431207).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) differs in the 5' UTR and lacks an exon in the coding region compared to variant 1. These differences result in the use of an alternate AUG, compared to variant 1. The encoded isoform (2) is shorter and has a distinct N-terminus compared to 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.