

Product datasheet for **SC326700**

ABCB5 (NM_001163993) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	ABCB5 (NM_001163993) Human Untagged Clone
Tag:	Tag Free
Symbol:	ABCB5
Synonyms:	ABCB5alpha; ABCB5beta; EST422562
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC326700 representing NM_001163993. Blue=Insert sequence Red=Cloning site Green=Tag(s)

GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG
 GATCCGGTACCGAGGAGATCTGCCGCC**GCGATCGCC**
 ATGGTGGATGAGAATGACATCAGAGCTTTAAATGTGCGGCATTATCGAGACCATATTGGAGTGGTTAGT
 CAAGAGCCTGTTTGTTCGGGACCACCATCAGTAACAATATCAAGTATGGACGAGATGATGTGACTGAT
 GAAGAGATGGAGAGAGCAGCAAGGGAAGCAAATGCGTATGATTTTATCATGGAGTTTCCTAATAAATTT
 AATACATTGGTAGGGGAAAAAGGAGCTCAAATGAGTGGAGGGCAGAAACAGAGGATCGCAATTGCTCGT
 GCCTTAGTTCGAAACCCAAGATTCTGATTTTAGATGAGGCTACGTCTGCCCTGGATTAGAAAGCAAG
 TCAGCTGTTCAAGCTGCACTGGAGAAGAAAAA**TAA**
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
 TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites:	SgfI-MluI
ACCN:	NM_001163993
Insert Size:	381 bp


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OTI Disclaimer: Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery.

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 TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

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_001163993.2](#)

RefSeq Size: 1724 bp

RefSeq ORF: 381 bp

Locus ID: 340273

UniProt ID: [Q2M3G0](#)

Cytogenetics: 7p21.1

Protein Families: Druggable Genome, Transmembrane

Protein Pathways: ABC transporters

MW: 14.1 kDa

Gene Summary:

ABCB5 belongs to the ATP-binding cassette (ABC) transporter superfamily of integral membrane proteins. These proteins participate in ATP-dependent transmembrane transport of structurally diverse molecules ranging from small ions, sugars, and peptides to more complex organic molecules (Chen et al., 2005 [PubMed 15760339]).[supplied by OMIM, Mar 2008]

Transcript Variant: This variant (4) differs in the 5' and 3' UTRs and has multiple coding region differences, compared to variant 1. These differences cause translation initiation at a downstream AUG and result in an isoform (4) with a shorter N-terminus and a shorter and distinct C-terminus, compared to variant 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.