

Product datasheet for **SC331966**

ATP7B (NM_001243182) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	ATP7B (NM_001243182) Human Untagged Clone
Tag:	Tag Free
Symbol:	ATP7B
Synonyms:	PWD; WC1; WD; WND
Vector:	pCMV6-Entry (PS100001)
Fully Sequenced ORF:	>SC331966 representing NM_001243182. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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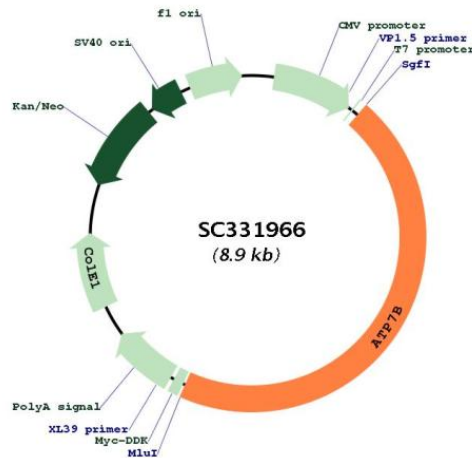
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Restriction Sites:

Sgfl-MluI

Plasmid Map:



ACCN:	NM_001243182
Insert Size:	4065 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:	<ol style="list-style-type: none">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_001243182.1</u>
RefSeq Size:	6322 bp
RefSeq ORF:	4065 bp
Locus ID:	540
UniProt ID:	<u>P35670</u>
Cytogenetics:	13q14.3
Protein Families:	Druggable Genome, Transmembrane
MW:	145.8 kDa
Gene Summary:	<p>This gene is a member of the P-type cation transport ATPase family and encodes a protein with several membrane-spanning domains, an ATPase consensus sequence, a hinge domain, a phosphorylation site, and at least 2 putative copper-binding sites. This protein is a monomer, and functions as a copper-transporting ATPase which exports copper out of the cells, such as the efflux of hepatic copper into the bile. Alternate transcriptional splice variants, encoding different isoforms with distinct cellular localizations, have been characterized. Mutations in this gene have been associated with Wilson disease which is characterized by copper accumulation. [provided by RefSeq, Dec 2019]</p> <p>Transcript Variant: This variant (3) lacks an in-frame segment in the coding region, compared to variant 1. The resulting isoform (c) lacks an internal segment, compared to isoform a.</p> <p>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.</p>