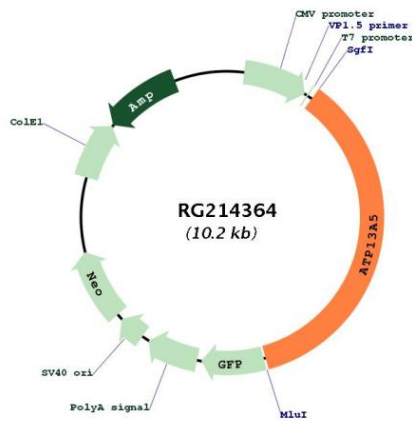


OTI Disclaimer:	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially 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.
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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	NM_198505.4
RefSeq Size:	3657 bp
RefSeq ORF:	3657 bp
Locus ID:	344905
UniProt ID:	Q4VNC0
Cytogenetics:	3q29
Protein Families:	Transmembrane

Gene Summary:

This gene encodes a member of the P5 subfamily of P-type transport ATPases. P-type ATPases form a large superfamily of cation and lipid pumps that transport inorganic cations and other substrates across cell membranes. P5 ATPases are localized to membranes of the endoplasmic reticulum (ER) and serve many important functions including transport of cargo proteins to the Golgi, glycosylation and cell wall biosynthesis, control of protein insertion orientation, 3-hydroxy-3-methylglutaryl-CoA reductase (HMGR) degradation, and sensitivity to unfolded protein response (UPR) activators. The encoded protein is organized into three cytoplasmic domains (A, P, and N) and two membrane-embedded domains (T and S). The N-domain binds ATP and serves as a built-in protein kinase, which phosphorylates the P-domain. The A-domain is an intrinsic protein phosphatase, which dephosphorylates the P-domain once during each catalytic cycle. [provided by RefSeq, Jul 2017]

Product images:



Circular map for RG214364