

Specifications:

Gene:	<i>mTcirg1</i>
Accession:	NP_058617
Insert size:	2518bp
Concentration:	10µg at 0.2µg/µL

mTCIRG1 cDNA Plasmid

**Tcirg1 T cell, immune regulator
1, ATPase, H⁺ transporting,
lysosomal V0 protein A3 [*Mus
musculus* (house mouse)]**

Also known as: oc; Stv1; Vph1;
Atp6i; OPTB1; TIRC7; ATP6a3; OC-
116; ATP6N1C

Summary:

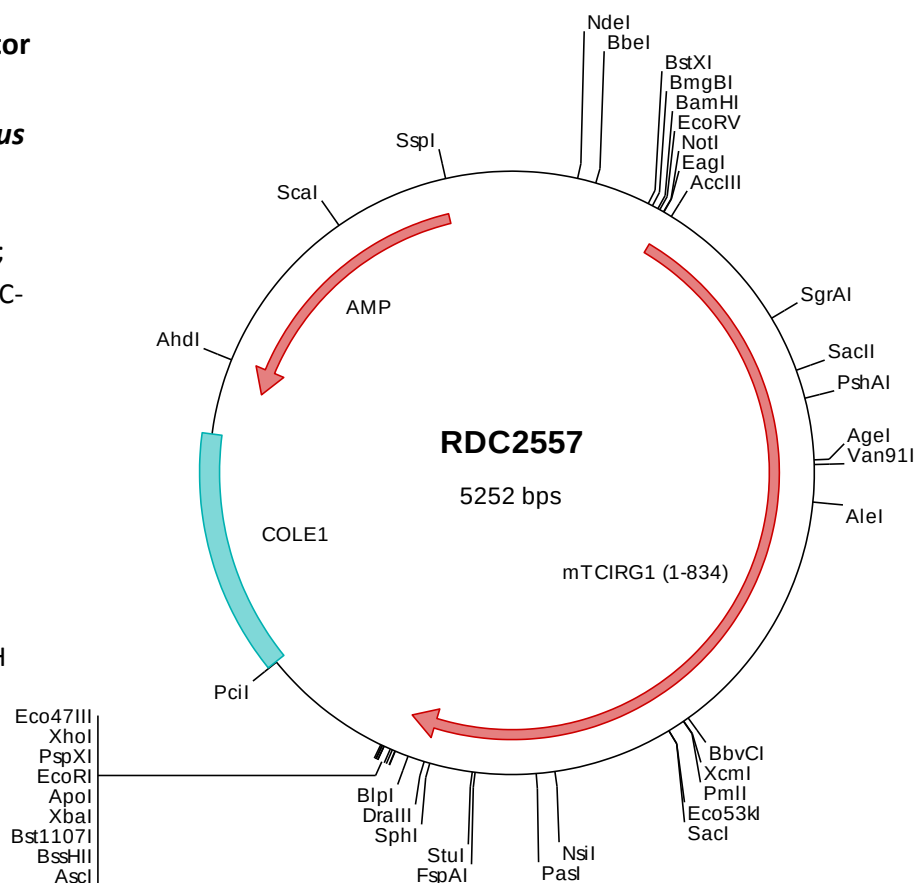
TCIRG1 is a subunit of a large protein complex known as a vacuolar H⁺-ATPase (V-ATPase). The protein complex acts as a pump to move protons across the membrane. This movement of protons helps regulate the pH of cells and their surrounding environment. V-ATPase dependent organelle acidification is necessary for such intracellular processes as protein sorting, zymogen activation, and receptor-mediated endocytosis. Mutations in TCORG1 are associated with infantile malignant osteopetrosis.

Description

This shuttle vector contains the complete ORF for the gene of interest, along with a Kozak consensus sequence for optimal translation initiation. It is inserted NotI to AscI. The gene insert is flanked with convenient multiple cloning sites which can be used to easily cut and transfer the gene cassette into your desired expression vector.

Preparation and Storage

Formulation	cDNA is provided in 10 mM Tris-Cl, pH 8.5
Shipping	Ships at ambient temperature
Stability	1 year from date of receipt when stored at -20°C to -80°C
Storage	Use a manual defrost freezer and avoid repeated freeze-thaw cycles.



FOR RESEARCH USE ONLY

NOT FOR USE IN HUMANS

> RDC2557 Plasmid DNA Sequence

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301  tacgccagct ggcgaaaggg ggaatgtctg caaggcgatt aagtttggga acgccagggt tttcccagtc acgacgttgt aaaacgacgg ccagtgtaatt
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> RDC2557 Translated Insert Sequence

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201  etegqledpv tgepatwmtf visywgqig qkirkidcf hchvfpyleg eearfrtlqg lqqsgselqe vlgetdrfls qvlgrvqql1 ppwqvqihkm
301  kavyltlncq svnthkcli aevwcaardl ptvqqalqsg sseegvsava hripcqdmpp tliitrnfts sfqgividayg vgyryevnpa pytiitfpfl
401  favmfgdvgh gllmlfala mvltenrpav kaaqneiwt ffggryllll mglfsvytgf iynecfsrat tifpsgwsa amangsgwsd eylsqhsm1t
501  lnpnitgvfl gpytfgidpi wslatnhlsf lnsfkmkmsv ilgvtthmafz vflsifnhvh fggahrlille tlpe1lflig lfylylvliiv ykwvnsvsaas
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701  agspgdeete fvpseifmhq ahtiefclg cisntasyrl lwalslahaq lsevlwamvm riglmgrei gvaavvlvpv faafavltva illvmeg1sa
801  flhalrlhwv eqnkyfysg gyklspftft vdsd

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