

Product datasheet for RC204021L3V

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Inosine triphosphate pyrophosphatase (ITPA) (NM_033453) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type: Lentiviral Particles

Product Name: Inosine triphosphate pyrophosphatase (ITPA) (NM_033453) Human Tagged ORF Clone

Lentiviral Particle

Symbol: Inosine triphosphate pyrophosphatase

Synonyms: C20orf37; DEE35; dJ794l6.3; HLC14-06-P; ITPase; My049; NTPase

Mammalian Cell

Selection:

Puromycin

Vector: pLenti-C-Myc-DDK-P2A-Puro (PS100092)

Tag: Myc-DDK
ACCN: NM_033453

ORF Size: 582 bp

ORF Nucleotide

Sequence:

The ORF insert of this clone is exactly the same as(RC204021).

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.

RefSeq: NM 033453.2

 RefSeq Size:
 1202 bp

 RefSeq ORF:
 585 bp

 Locus ID:
 3704

 UniProt ID:
 Q9BY32

 Cytogenetics:
 20p13

Domains: Ham1p_like



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Protein Families: Druggable Genome

Protein Pathways: Drug metabolism - other enzymes, Metabolic pathways, Purine metabolism, Pyrimidine

metabolism

MW: 21.4 kDa

Gene Summary: This gene encodes an inosine triphosphate pyrophosphohydrolase. The encoded protein

hydrolyzes inosine triphosphate and deoxyinosine triphosphate to the monophosphate nucleotide and diphosphate. This protein, which is a member of the HAM1 NTPase protein family, is found in the cytoplasm and acts as a homodimer. Defects in the encoded protein

can result in inosine triphosphate pyrophosphorylase deficiency which causes an accumulation of ITP in red blood cells. Alternate splicing results in multiple transcript

variants. [provided by RefSeq, Jun 2012]