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Lieferung & Zahlungsart

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Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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ATP6V1C1 Pre-design Chimera RNAi

Catalog # : H00000528-R04

規格 : [10 nmol] [20 nmol]

List All

Specification

Product Description: Homo sapiens ATPase, H⁺ transporting, lysosomal 42kDa, V1 subunit C, isoform 1 (ATP6V1C1), transcript variant 1, mRNA.

Reactivity: Human

Supplied Product: DEPC water

Target Refseq: NM_001695

Target Region: Coding sequence

Storage Instruction: Store at -20°C, do not exceed 4 - 5 freeze-thaw cycles to ensure product integrity.

Note: Position of the Chimera RNAi.
The related RNAi products listed below were designed from different accession number but sharing the same RNAi sequence.



Application Image

RNAi Knockdown

Publication Reference

- [dsCheck: highly sensitive off-target search software for double-stranded RNA-mediated RNA interference.](#)
Naito Y, Yamada T, Matsumiya T, Ui-Tei K, Saigo K, Morishita S. *Nucleic Acids Res.* 2005 Jul 1;33(Web Server issue):W589-91.
- [Functional dissection of siRNA sequence by systematic DNA substitution: modified siRNA with a DNA seed arm is a powerful tool for mammalian gene silencing with significantly reduced off-target effect.](#)
Ui-Tei K, Naito Y, Zenno S, Nishi K, Yamato K, Takahashi F, Juni A, Saigo K. *Nucleic Acids Res.* 2008 Apr;36(7):2136-51. Epub 2008 Feb 11.
- [Guidelines for the selection of highly effective siRNA sequences for mammalian and chick RNA interference.](#)
Ui-Tei K, Naito Y, Takahashi F, Haraguchi T, Ohki-Hamazaki H, Juni A, Ueda R, Saigo K. *Nucleic Acids Res.* 2004 Feb 9;32(3):936-48. Print 2004.
- [siDirect: highly effective, target-specific siRNA design software for mammalian RNA interference.](#)
Naito Y, Yamada T, Ui-Tei K, Morishita S, Saigo K. *Nucleic Acids Res.* 2004 Jul 1;32(Web Server issue):W124-9.

Applications

RNAi Knockdown

Gene Information

Entrez GeneID: [528](#)

Gene Name: ATP6V1C1

Gene Alias: ATP6C,ATP6D,FLJ20057,VATC,Vma5

Gene Description: ATPase, H⁺ transporting, lysosomal 42kDa, V1 subunit C1

Omim ID: [603097](#)

Gene Ontology: [Hyperlink](#)

Gene Summary: This gene encodes a component of vacuolar ATPase (V-ATPase), a multisubunit enzyme that mediates acidification of intracellular compartments of eukaryotic cells. V-ATPase dependent acidification is necessary for such intracellular processes as protein sorting, zymogen activation, receptor-mediated endocytosis, and synaptic vesicle proton gradient generation. V-ATPase is composed of a cytosolic V1 domain and a transmembrane V0 domain. The V1 domain consists of three A and three B subunits, two G subunits plus the C, D, E, F, and H subunits. The V1 domain contains the ATP catalytic site. The V0 domain consists of five different subunits: a, c, c', c'', and d. Additional isoforms of many of the V1 and V0 subunit proteins are encoded by multiple genes or alternatively spliced transcript variants. This gene is one of two genes that encode the V1 domain C subunit proteins and is found ubiquitously. This C subunit is analogous but not homologous to gamma subunit of F-ATPases. Previously, this gene was designated ATP6D. [provided by RefSeq]

Other Designations: ATPase, H⁺ transporting, lysosomal (vacuolar proton pump) 42kD,ATPase, H⁺ transporting, lysosomal 42kD, V1 subunit C, isoform 1,ATPase, H⁺ transporting, lysosomal 42kDa, V1 subunit C, isoform 1,H(+)-transporting two-sector ATPase, subunit C,H⁺ -ATPase C s

Gene Pathway

[Epithelial cell signaling in Helicobacter pylori infection](#) [Metabolic pathways](#)
[Oxidative phosphorylation](#) [Vibrio cholerae infection](#)

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[Tobacco Use Disorder](#)