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Produktinformation

- Forschungsprodukte & Biochemikalien
- Zellkultur & Verbrauchsmaterial
- Diagnostik & molekulare Diagnostik
- Laborgeräte & Service

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See the following pages for more information!

Lieferung & Zahlungsart

siehe unsere Liefer- und Versandbedingungen

Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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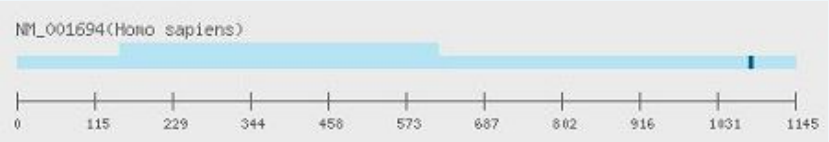
ATP6V0C Pre-design Chimera RNAi

Catalog # : H00000527-R02 **規格 :** [10 nmol] [20 nmol]

List All

Specification

Product Description:	Homo sapiens ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c (ATP6V0C), mRNA.
Reactivity:	Human
Supplied Product:	DEPC water
Target Refseq:	NM_001694
Storage Instruction:	Store at -20°C, do not exceed 4 - 5 freeze-thaw cycles to ensure product integrity.
Note:	Position of the Chimera RNAi.



Publication Reference

1. 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.
2. 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.
3. 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.
4. 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:	527
Gene Name:	ATP6V0C
Gene Alias:	ATP6C,ATP6L,ATPL,VATL,Vma3

Application Image

RNAi Knockdown

Gene Description:	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
Omim ID:	108745
Gene Ontology:	Hyperlink
Gene Summary:	This gene encodes a component of vacuolar ATPase (V-ATPase), a multisubunit enzyme that mediates acidification of eukaryotic intracellular organelles. V-ATPase dependent organelle 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 encoded protein is part of the V0 domain. This gene had the previous symbols of ATP6C and ATP6L. [provided by RefSeq
Other Designations:	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD,ATPase, H+ transporting, lysosomal 16kD, V0 subunit c,ATPase, H+ transporting, lysosomal, 16-KD,ATPase, H+ transporting, lysosomal, V0 subunit c,H(+)-transporting two-sector ATPase, 16 kDa sub

Gene Pathway

Epithelial cell signaling in Helicobacter pylori infection Lysosome Metabolic pathways Oxidative phosphorylation Vibrio cholerae infection

Related Disease

Attention Deficit Disorder with Hyperactivity Autistic Disorder NARP