



# SZABO SCANDIC

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## Produktinformation



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### Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

### SZABO-SCANDIC HandelsgmbH

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## ATP6V1B2 Pre-design Chimera RNAi

Catalog # : H00000526-R02

規格 : [ 10 nmol ] [ 20 nmol ]

List All

### Specification

**Product Description:** Homo sapiens ATPase, H<sup>+</sup> transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2 (ATP6V1B2), mRNA.

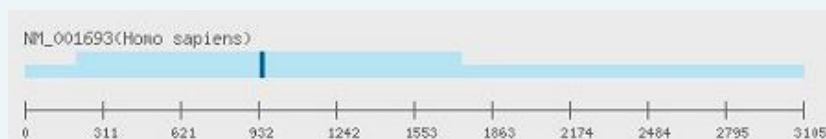
**Reactivity:** Human

**Supplied Product:** DEPC water

**Target Refseq:** NM\_001693

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

**Note:** Position of the Chimera RNAi.



### 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:** [526](#)

**Gene Name:** ATP6V1B2

**Gene Alias:** ATP6B1B2,ATP6B2,HO57,VATB,VPP3,Vma2

**Gene** ATPase, H<sup>+</sup> transporting, lysosomal 56/58kDa, V1 subunit B2  
**Description:**

**Omim ID:** [606939](#)

**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, three B, and two G subunits, as well as a C, D, E, F, and H subunit. The V1 domain contains the ATP catalytic site. The protein encoded by this gene is one of two V1 domain B subunit isoforms and is the only B isoform highly expressed in osteoclasts. [provided by RefSeq]

**Other Designations:** ATPase, H<sup>+</sup> transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2,ATPase, H<sup>+</sup> transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2,H<sup>+</sup> transporting two-sector ATPase,V-ATPase B2 subunit,endomembrane proton pump 58 kDa subu

#### Gene Pathway

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[Oxidative phosphorylation](#) [Vibrio cholerae infection](#)

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