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Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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ATP5I Pre-design Chimera RNAi

Catalog # : H00000521-R01

規格 : [10 nmol] [20 nmol]

List All

Specification

Product Description: Homo sapiens ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit e (ATP5I), nuclear gene encoding mitochondrial protein, mRNA.

Reactivity: Human

Supplied Product: DEPC water

Target Refseq: NM_007100

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.



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: [521](#)

Gene Name: ATP5I

Gene Alias: ATP5K,MGC12532

Gene Description: ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit E

Omim ID: [601519](#)

Gene Ontology: [Hyperlink](#)

Gene Summary: Mitochondrial ATP synthase catalyzes ATP synthesis, utilizing an electrochemical gradient of protons across the inner membrane during oxidative phosphorylation. It is composed of two linked multi-subunit complexes: the soluble catalytic core, F1, and the membrane-spanning component, F0, which comprises the proton channel. The F1 complex consists of 5 different subunits (alpha, beta, gamma, delta, and epsilon) assembled in a ratio of 3 alpha, 3 beta, and a single representative of the other 3. The F0 seems to have nine subunits (a, b, c, d, e, f, g, F6 and 8). This gene encodes the e subunit of the F0 complex. [provided by RefSeq]

Other Designations: ATP synthase e chain, mitochondrial,F1F0-ATP synthase, murine e subunit

Gene Pathway

[Metabolic pathways](#) [Oxidative phosphorylation](#)

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