



IVTScrip™ mRNA-Human ATP5E, (Cap 1, 5-Methyl-CTP & Pseudo-UTP, 30 nt-poly(A))

Cat. No.: GTTS-WK28798MR

This product is for research use only and is not intended for diagnostic use.

PRODUCT INFORMATION

Product overview

This product GTTS-WK28798MR is a type of mRNA having 30 nt poly(A) tail and modified with Cap 1 & 5-Methyl-CTP & Pseudo-UTP. It encodes the ATP5E protein. This product can be used in Oligodendrocyte-related researches.

Specifications

| | |
|-----------------------|---------------------------|
| Modified bases | 5-Methyl-CTP & Pseudo-UTP |
| 5' Cap | Cap 1 |
| Species | Human |
| RefSeq | NM_006886.4 |
| Applications | Gene therapy research |
| Format | Powder |
| Quantity | 100 µg |
| Purification | Chromatography |

SPECIFICATIONS

| | |
|-----------------------|---------------------------|
| Modified bases | 5-Methyl-CTP & Pseudo-UTP |
| 5' Cap | Cap 1 |
| Species | Human |
| RefSeq | NM_006886.4 |
| Applications | Gene therapy research |
| Format | Powder |
| Quantity | 100 µg |
| Purification | Chromatography |

GENE INFORMATION

| | |
|--------------------------|---|
| Alternative Names | ATPE; ATP5E; MC5DN3 |
| Description | <p>This gene encodes a subunit of mitochondrial ATP synthase. Mitochondrial ATP synthase catalyzes ATP synthesis, utilizing an electrochemical gradient of protons across the inner membrane during oxidative phosphorylation. ATP synthase is composed of two linked multi-subunit complexes: the soluble catalytic core, F1, and the membrane-spanning component, Fo, comprising the proton channel. The catalytic portion of mitochondrial ATP synthase consists of 5 different subunits (alpha, beta, gamma, delta, and epsilon) assembled with a stoichiometry of 3 alpha, 3 beta, and a single representative of the other 3. The proton channel consists of three main subunits (a, b, c). This gene encodes the epsilon subunit of the catalytic core. Two pseudogenes of this gene are located on chromosomes 4 and 13. Read-through transcripts that include exons from this gene are expressed from the upstream gene SLMO2.[provided by RefSeq, Mar 2011]</p> |