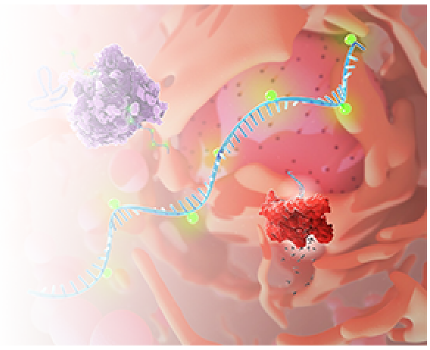

IVTScrip™ mRNA-Human ANG, (Cap 0, Pseudo-UTP, 30 nt-poly(A))

Cat. No.: GTTS-WK16376MR

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

PRODUCT INFORMATION

Product overview

This product GTTS-WK16376MR is a type of mRNA having 30 nt poly(A) tail and modified with Cap 0 & Pseudo-UTP. It ecodes the ANG protein. This product can be used in Ciliated cell-related researches.

Specifications

Modified bases	Pseudo-UTP
5' Cap	Cap 0
Species	Human
RefSeq	NM_001097577.3
Applications	Gene therapy research
Format	Powder
Quantity	100 µg
Purification	Chromatography

SPECIFICATIONS

Modified bases	Pseudo-UTP
5' Cap	Cap 0
Species	Human
RefSeq	NM_001097577.3
Applications	Gene therapy research
Format	Powder
Quantity	100 μg
Purification	Chromatography

GENE INFORMATION

Alternative Names	ALS9; RAA1; HEL168; RNASE4; RNASE5
Description	The protein encoded by this gene is a member of the RNase A superfamily though it has relatively weak ribonucleolytic activity. This protein is a potent mediator of new blood vessel formation and thus, in addition to the name RNase5, is commonly called angiogenin. This protein induces angiogenesis after binding to actin on the surface of endothelial cells. This protein also accumulates at the nucleolus where it stimulates ribosomal transcription. Under stress conditions this protein translocates to the cytosol where it hydrolyzes cellular tRNAs and influences protein synthesis. A signal peptide is cleaved from the precursor protein to produce a mature protein which contains a nuclear localization signal, a cell binding motif, and a catalytic domain. This protein has been shown to be both neurotrophic and neuroprotective and the mature protein has antimicrobial activity against some bacteria and fungi, including S. pneumoniae and C. albicans. Due to its effect on rRNA production and angiogenesis this gene plays important roles in cell growth and tumor progression. Mutations in this gene are associated with progression of amyotrophic lateral sclerosis (ALS). This gene and the neighboring RNase4 gene share promoters and 5 exons though each gene then splices to a distinct 3 exon containing the complete coding region of each gene. Alternative splicing results in multiple transcript variants encoding the same protein. [provided by RefSeq, Jul 2020]