

## Product datasheet for **SR302810**

### Methionyl tRNA synthetase (MARS) Human siRNA Oligo Duplex (Locus ID 4141)

#### Product data:

Product Type:	siRNA Oligo Duplexes
Purity:	HPLC purified
Quality Control:	Tested by ESI-MS
Sequences:	Available with shipment
Stability:	One year from date of shipment when stored at -20°C.
# of transfections:	Approximately 330 transfections/2nmol in 24-well plate under optimized conditions (final conc. 10 nM).
Note:	Single siRNA duplex (10nmol) can be ordered.
RefSeq:	<a href="#">NM_004990</a>
UniProt ID:	<a href="#">P56192</a>
Synonyms:	CMT2U; ILFS2; ILLD; MARS; METRS; MRS; MTRNS; SPG70
Components:	MARS (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 4141) Included - SR30004, Trilencer-27 Universal Scrambled Negative Control siRNA Duplex - 2 nmol Included - SR30005, RNase free siRNA Duplex Resuspension Buffer - 2 ml
Summary:	This gene encodes a member of the class I family of aminoacyl-tRNA synthetases. These enzymes play a critical role in protein biosynthesis by charging tRNAs with their cognate amino acids. The encoded protein is a component of the multi-tRNA synthetase complex and catalyzes the ligation of methionine to tRNA molecules. [provided by RefSeq, Jan 2011]
Performance Guaranteed:	OriGene guarantees that at least two of the three Dicer-Substrate duplexes in the kit will provide at least 70% or more knockdown of the target mRNA when used at 10 nM concentration by quantitative RT-PCR when the TYE-563 fluorescent transfection control duplex (cat# SR30002) indicates that >90% of the cells have been transfected and the HPRT positive control (cat# SR30003) provides 90% knockdown efficiency.

For non-conforming siRNA, requests for replacement product must be made within ninety (90) days from the date of delivery of the siRNA kit. To arrange for a free replacement with newly designed duplexes, please contact Technical Services at [techsupport@origene.com](mailto:techsupport@origene.com). Please provide your data indicating the transfection efficiency and measurement of gene expression knockdown compared to the scrambled siRNA control (quantitative RT-PCR data required).



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