

Product datasheet for SR301359

OriGene Technologies, Inc.

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EGR2 Human siRNA Oligo Duplex (Locus ID 1959)

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: NM 000399, NM 001136177, NM 001136178, NM 001136179, NM 001321037

UniProt ID: P11161

Synonyms: AT591; CHN1; CMT1D; CMT4E; KROX20

Components: EGR2 (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 1959)

Included - SR30004, Trilencer-27 Universal Scrambled Negative Control siRNA Duplex - 2 nmol

Included - SR30005, RNAse free siRNA Duplex Resuspension Buffer - 2 ml

Summary: The protein encoded by this gene is a transcription factor with three tandem C2H2-type zinc

fingers. Defects in this gene are associated with Charcot-Marie-Tooth disease type 1D (CMT1D), Charcot-Marie-Tooth disease type 4E (CMT4E), and with Dejerine-Sottas syndrome

(DSS). Multiple transcript variants encoding two different isoforms have been found for this

gene. [provided by RefSeq, Oct 2008]



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. 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).