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Product datasheet for SR313148

ABHD11 Human siRNA Oligo Duplex (Locus ID 83451)

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_001145363, NM_001145364, NM_001301058, NM_001321382, NM_001321383, NM_031295, NM_148912, NM_148913, NM_148914, NM_148915, NM_148916, NR_026910, NR_026912, NR_135627
UniProt ID:	Q8NFV4
Synonyms:	abhydrolase domain containing 11; PP1226; WBSCR21; Williams Beuren syndrome chromosome region 21
Components:	ABHD11 (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 83451) 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 protein containing an alpha/beta hydrolase fold domain. This gene is deleted in Williams syndrome, a multisystem developmental disorder caused by the deletion of contiguous genes at 7q11.23. [provided by RefSeq, Mar 2016]

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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).