

Product datasheet for **SR319418**

ATP12A Human siRNA Oligo Duplex (Locus ID 479)

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_001185085 , NM_001676
UniProt ID:	P54707
Synonyms:	ATP1AL1; H-K-ATPase; HK
Components:	ATP12A (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 479) 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 belongs to the family of P-type cation transport ATPases. This gene encodes a catalytic subunit of the ouabain-sensitive H ⁺ /K ⁺ -ATPase that catalyzes the hydrolysis of ATP coupled with the exchange of H ⁽⁺⁾ and K ⁽⁺⁾ ions across the plasma membrane. It is also responsible for potassium absorption in various tissues. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jun 2010]



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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).