

## Product datasheet for **SR300510**

### Complement C8A (C8A) Human siRNA Oligo Duplex (Locus ID 731)

#### 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_000562</a>
UniProt ID:	<a href="#">P07357</a>
Components:	C8A (Human) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 731) Included - SR30004, Trilencer-27 Universal Scrambled Negative Control siRNA Duplex - 2 nmol Included - SR30005, RNase free siRNA Duplex Resuspension Buffer - 2 ml
Summary:	C8 is a component of the complement system and contains three polypeptides, alpha, beta and gamma. This gene encodes the alpha subunit of C8. C8 participates in the formation of the membrane attack complex (MAC). The MAC assembles on bacterial membranes to form a pore, permitting disruption of bacterial membrane organization. Mutations in this gene cause complement C8 alpha-gamma deficiency. [provided by RefSeq, Nov 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](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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