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Product datasheet for TR308127

Ikaros (IKZF1) Human shRNA Plasmid Kit (Locus ID 10320)

Product data:

Product Type:	shRNA Plasmids
Product Name:	Ikaros (IKZF1) Human shRNA Plasmid Kit (Locus ID 10320)
Locus ID:	10320
Synonyms:	CVID13; Hs.54452; IK1; IKAROS; LyF-1; LYF1; PPP1R92; PRO0758; ZNFN1A1
Vector:	pRS (TR20003)
E. coli Selection:	Ampicillin
Mammalian Cell Selection:	Puromycin
Format:	Retroviral plasmids
Components:	IKZF1 - Human, 4 unique 29mer shRNA constructs in retroviral untagged vector(Gene ID = 10320). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pRS Vector, TR30012, included for free.
RefSeq:	NM_001220765, NM_001220766, NM_001220767, NM_001220768, NM_001220769, NM_001220770, NM_001220771, NM_001220772, NM_001220773, NM_001220774, NM_001220775, NM_001220776, NM_001291837, NM_001291838, NM_001291839, NM_001291840, NM_001291841, NM_001291842, NM_001291843, NM_001291844, NM_001291845, NM_001291846, NM_001291847, NM_006060, NM_006060.1, NM_006060.2, NM_006060.3, NM_006060.4, NM_006060.5, NM_001220772.1, NM_001220776.1, NM_001220775.1, NM_001220774.1, NM_001220773.1, NM_001220771.1, NM_001220771.2, NM_001220770.1, NM_001220770.2, NM_001220769.1, NM_001220767.1, NM_001220767.2, NM_001220766.1, NM_001220768.1, NM_001220768.2, NM_001220765.1, NM_001220765.2, NM_001291846.1, NM_001291847.1, NM_001291845.1, NM_001291840.1, NM_001291844.1, NM_001291843.1, NM_001291842.1, NM_001291841.1, NM_001291839.1, NM_001291838.1, NM_001291837.1, BC018349, BC064594, BC075820, BM148203, NM_001291837.2, NM_001291838.2, NM_006060.6, NM_001291839.2, NM_001220765.3, NM_001291847.2, NM_001291846.2, NM_001291845.2
UniProt ID:	Q13422

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Summary:

This gene encodes a transcription factor that belongs to the family of zinc-finger DNA-binding proteins associated with chromatin remodeling. The expression of this protein is restricted to the fetal and adult hemo-lymphopoietic system, and it functions as a regulator of lymphocyte differentiation. Several alternatively spliced transcript variants encoding different isoforms have been described for this gene. Most isoforms share a common C-terminal domain, which contains two zinc finger motifs that are required for hetero- or homo-dimerization, and for interactions with other proteins. The isoforms, however, differ in the number of N-terminal zinc finger motifs that bind DNA and in nuclear localization signal presence, resulting in members with and without DNA-binding properties. Only a few isoforms contain the requisite three or more N-terminal zinc motifs that confer high affinity binding to a specific core DNA sequence element in the promoters of target genes. The non-DNA-binding isoforms are largely found in the cytoplasm, and are thought to function as dominant-negative factors. Overexpression of some dominant-negative isoforms have been associated with B-cell malignancies, such as acute lymphoblastic leukemia (ALL). [provided by RefSeq, May 2014]

shRNA Design:

These shRNA constructs were designed against multiple splice variants at this gene locus. To be certain that your variant of interest is targeted, please contact techsupport@origene.com. If you need a special design or shRNA sequence, please utilize our custom shRNA service.

Performance Guaranteed:

OriGene guarantees that the sequences in the shRNA expression cassettes are verified to correspond to the target gene with 100% identity. One of the four constructs at minimum are guaranteed to produce 70% or more gene expression knock-down provided a minimum transfection efficiency of 80% is achieved. Western Blot data is recommended over qPCR to evaluate the silencing effect of the shRNA constructs 72 hrs post transfection. To properly assess knockdown, the gene expression level from the included scramble control vector must be used in comparison with the target-specific shRNA transfected samples.

For non-conforming shRNA, requests for replacement product must be made within ninety (90) days from the date of delivery of the shRNA kit. To arrange for a free replacement with newly designed constructs, 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 shRNA control (Western Blot data preferred).

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