

Product datasheet for **SC330619**

IKZF3 (NM_001257410) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	IKZF3 (NM_001257410) Human Untagged Clone
Tag:	Tag Free
Symbol:	IKZF3
Synonyms:	AIO; AIOLOS; ZNFN1A3
Vector:	pCMV6-Entry (PS100001)
Fully Sequenced ORF:	>SC330619 representing NM_001257410. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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ATGGAAGATATACAAACAAATGCGGAAGTGAAGCACTCAGGAGCAGTCTGTGCCCGCAGAAAGTGCA
GCGGTTTTGAATGACTACAGTTTAACCAAATCTCATGAAATGGAAATGTGGACAGTGGAGAAGGCCCA
GCCAATGAAGATGAAGACATAGGAGGTGAACGCCATTCCAGTGTAACTAGTGTGGGGCATCTTTTACT
CAGAAAGGTAACCTCTCCGCCACATTAAGTGCACACAGGGGAAAAACCTTTTAAGTGTACCTCTGC
AACTATGCATGCCAAGAAGAGATGCGCTCAGGGGCATCTTAGGACACATTCTGTGGAGAAACCCTAC
AAATGTGAGTTTTGTGGAAGGAGTTACAAGCAGAGAAGTTCCTTGAGGAGCACAAGGAGCGCTGCCGT
ACATTTCTTCAGAGCACTGACCCAGGGGACACTGCAAGTGGGAGGCAAGACACATCAAAGCAGAGATG
GGAAGTGAAGAGCTCTCGTACTGGACAGATTAGCAAGCAATGTGGCAAAACGAAAAAGCTCAATGCCT
CAGAAATTCATTGGTGAAGCGCCACTGCTTTGATGTCAACTATAATTCAAGTTACATGTATGAGAAA
GAGAGTGAGCTCATACAGACCCGCATGATGGACCAAGCCATCAATAACGCCATCAGCTATCTTGGCGCC
GAAGCCCTGCGCCCTTGGTCCAGACACCGCCTGCTCCACCTCGGAGATGGTTCCAGTTATCAGCAGC
ATGTATCCCATAGCCCTCACCCGGGCTGAGATGTCAAACGGTGCCCTCAAGAGCTGGAAAGAAAAAGC
ATCCACCTTCAGAGAAGAGCGTGCCTTCTGAGAGAGGCCTCTCTCCCAACAATAGTGGCCACGACTCC
ACGGACACTGACAGCAACCATGAAGAAGCCAGAATCACATCTATCAGCAAAATCACATGGTCTGTCT
CGGGCCCGCAATGGGATGCCACTTCTGAAGGAGGTTCCCGCTCTTACGAACTCCTCAAGCCCCCGCCC
ATCTGCCCAAGAGACTCCGTCAAAGTGATCAACAAGGAAGGGGAGGTGATGGATGTGTATCGGTGTGAC
CACTGCCGCGTCTCTTCTGGACTATGTGATGTTACAGATTACATGGGCTGCCACGGCTTCCGTGAC
CCTTTCGAGTGTAACATGTGTGGATATCGAAGCCATGATCGGTATGAGTTCTCGTCTCACATAGCCAGA
GGAGAACACAGAGCCCTGCTGAAGTGA
  
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Restriction Sites:	SgfI-MluI
ACCN:	NM_001257410
Insert Size:	1269 bp


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OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	<ol style="list-style-type: none"> 1. Centrifuge at 5,000xg for 5min. 2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. 3. Close the tube and incubate for 10 minutes at room temperature. 4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	<u>NM_001257410.1</u>
RefSeq Size:	9425 bp
RefSeq ORF:	1269 bp
Locus ID:	22806
UniProt ID:	<u>Q9UKT9</u>
Cytogenetics:	17q12-q21.1
MW:	48 kDa
Gene Summary:	<p>This gene encodes a member of the Ikaros family of zinc-finger proteins. Three members of this protein family (Ikaros, Aiolos and Helios) are hematopoietic-specific transcription factors involved in the regulation of lymphocyte development. This gene product is a transcription factor that is important in the regulation of B lymphocyte proliferation and differentiation. Both Ikaros and Aiolos can participate in chromatin remodeling. Regulation of gene expression in B lymphocytes by Aiolos is complex as it appears to require the sequential formation of Ikaros homodimers, Ikaros/Aiolos heterodimers, and Aiolos homodimers. Several alternative transcripts encoding different isoforms have been described, as well as some non-protein coding variants. [provided by RefSeq, Apr 2012]</p> <p>Transcript Variant: This variant (9) lacks an alternate in-frame exon compared to variant 1. The resulting isoform (9, also known as Aio-del3) has the same N- and C-termini but is shorter compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.</p>