

Product datasheet for SC332545

IKZF3 (NM 001257409) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: IKZF3 (NM_001257409) Human Untagged Clone

Tag: Tag Free Symbol: IKZF3

Synonyms: AIO; AIOLOS; ZNFN1A3

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF: >SC332545 representing NM_001257409.

Blue=Insert sequence Red=Cloning site Green=Tag(s)

ATGGAAGATATACAAACAAATGCGGAACTGAAAAGCACTCAGGAGCAGTCTGTGCCCGCAGATGATTCA ATGAAAGTGAAAGATGAATACAGTGAAAGAGATGAGAATGTTTTAAAGTCAGAACCCATGGGAAATGCA GAAGAGCCTGAAATCCCTTACAGCTATTCAAGAGAATATAATGAATATGAAAACATTAAGTTGGAGAGA TGCATCAGCTTCAATGTCTTAATGGTTCATAAGCGAAGCCATACTGGTGAACGCCCATTCCAGTGTAAT CAGTGTGGGGCATCTTTTACTCAGAAAGGTAACCTCCTCCGCCACATTAAACTGCACACAGGGGAAAAA CCTTTTAAGTGTCACCTCTGCAACTATGCATGCCAAAGAAGAGATGCGCTCACGGGGCATCTTAGGACA CATTCTGCAAGTGCGGAGGCAAGACACATCAAAGCAGAGATGGGAAGTGAAAGAGCTCTCGTACTGGAC AGATTAGCAAGCAATGTGGCAAAACGAAAAAGCTCAATGCCTCAGAAATTCATTGGTGAGAAGCGCCAC TGCTTTGATGTCAACTATAATTCAAGTTACATGTATGAGAAAGAGAGTGAGCTCATACAGACCCGCATG ATGGACCAAGCCATCAATAACGCCATCAGCTATCTTGGCGCCGAAGCCCTGCGCCCCTTGGTCCAGACA CCGCCTGCTCCCACCTCGGAGATGGTTCCAGTTATCAGCAGCATGTATCCCATAGCCCTCACCCGGGCT GAGATGTCAAACGGTGCCCCTCAAGAGCTGGAAAAGAAAAGCATCCACCTTCCAGAGAAGAGCGTGCCT TCTGAGAGAGCCTCTCTCCCAACAATAGTGGCCACGACTCCACGGACACTGACAGCAACCATGAAGAA CGCCAGAATCACATCTATCAGCAAAATCACATGGTCCTGTCTCGGGCCCGCAATGGGATGCCACTTCTG AAGGAGGTTCCCCGCTCTTACGAACTCCTCAAGCCCCCGCCCATCTGCCCAAGAGACTCCGTCAAAGTG ATCAACAAGGAAGGGAGGTGATGGATGTGTATCGGTGTGACCACTGCCGCGTCCTCTTCCTGGACTAT GTGATGTTCACGATTCACATGGGCTGCCACGGCTTCCGTGACCCTTTCGAGTGTAACATGTGTGGATAT CGAAGCCATGATCGGTATGAGTTCTCGTCTCACATAGCCAGAGGAGAACACAGAGCCCTGCTGAAGTGA

Restriction Sites: Sgfl-Mlul

ACCN: NM_001257409

Insert Size: 1311 bp



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IKZF3 (NM_001257409) Human Untagged Clone - SC332545

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: 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: NM 001257409.1

 RefSeq Size:
 9467 bp

 RefSeq ORF:
 1311 bp

 Locus ID:
 22806

 UniProt ID:
 Q9UKT9

Cytogenetics: 17q12-q21.1

MW: 49.8 kDa

Gene Summary: 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]

Transcript Variant: This variant (8) lacks two alternate in-frame exons compared to variant 1. The resulting isoform (8, also known as Aio-del2,5) 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.