

## Product datasheet for **SC330620**

### **IKZF3 (NM\_001257411) Human Untagged Clone**

#### Product data:

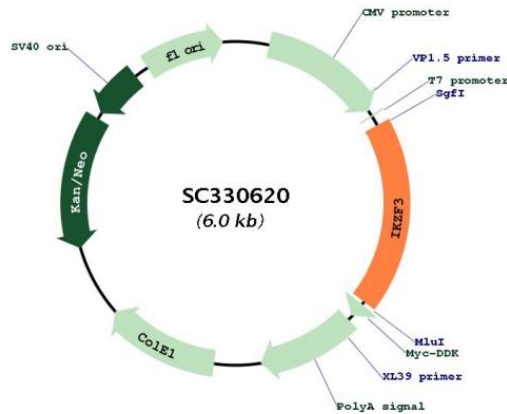
**Product Type:** Expression Plasmids  
**Product Name:** IKZF3 (NM\_001257411) Human Untagged Clone  
**Tag:** Tag Free  
**Symbol:** IKZF3  
**Synonyms:** AIO; AIOLOS; ZNFN1A3  
**Vector:** pCMV6-Entry (PS100001)  
**Fully Sequenced ORF:** >SC330620 representing NM\_001257411.  
Blue=Insert sequence Red=Cloning site Green=Tag(s)

ATGGAAGATATACAAACAAATGCGGAAGTAAAAGCACTCAGGAGCAGTCTGTGCCCGCAGAAAAGTGCA  
GCGGTTTTGAATGACTACAGTTTAAACCAATCTCATGAAATGGAAAATGTGGACAGTGGAGAAGGCCCA  
GCCAATGAAGATGAAGACATAGGAGTGGAGAAACCCTACAATGTGAGTTTTGTGGAAGGAGTTACAAG  
CAGAGAAGTTCCTTGAGGAGCACAAGGAGCGCTGCCGTACATTTCTTCAGAGCACTGACCCAGGGGAC  
ACTGCAAGTGGGAGGCAAGACACATCAAAGCAGAGATGGGAAGTAAAAGAGCTCTCGTACTGGACAGA  
TTAGCAAGCAATGTGGCAAACGAAAAAGCTCAATGCCTCAGAAATTCATTGGTGAGAAGCGCCACTGC  
TTTGATGTCAACTATAATTCAAGTTACATGTATGAGAAAAGAGAGTGAGCTCATAAGACCCGCATGATG  
GACCAAGCCATCAATAACGCCATCAGCTATCTTGCGCGCGAAGCCCTGCGCCCTTGGTCCAGACACCG  
CCTGCTCCACCTCGGAGATGGTTCCAGTTATCAGCAGCATGTATCCCATAGCCCTCACCCGGGCTGAG  
ATGTCAAACGGTGGCCCTCAAGAGCTGGAAAAGAAAAGCATCCACCTCCAGAGAAGAGCGTGCCTTCT  
GAGAGAGGCTCTCTCCAACAATAGTGGCCACGACTCCACGGACACTGACAGCAACCATGAAGAACGC  
CAGAATCACATCTATCAGCAAAATCACATGGTCTGTCTCGGGCCCGCAATGGGATGCCACTTCTGAAG  
GAGGTTCCCGCTCTTACGAACCTCTCAAGCCCCGCCATCTGCCAAGAGACTCCGTCAAAGTGATC  
ACAAGGAAGGGGAGGTGATGGATGTATCGGTGTGACCACTGCCGCGTCTCTCTGGACTATGTG  
ATGTTACGATTCACATGGGCTGCCACGGCTTCGGTGACCCTTTTCGAGTGTAAACATGTGTGGATATCGA  
AGCCATGATCGGTATGAGTTCTCGTCTCATAGCCAGAGGAGAACACAGAGCCCTGCTGAAGTGA

**Restriction Sites:** SgfI-MluI



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**Plasmid Map:**


**ACCN:** NM\_001257411

**Insert Size:** 1101 bp

**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\\_001257411.1](#)

**RefSeq Size:** 9257 bp

RefSeq ORF: 1101 bp

Locus ID: 22806

UniProt ID: [Q9UKT9](#)

Cytogenetics: 17q12-q21.1

MW: 41.6 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 (10) lacks two alternate in-frame exons compared to variant 1. The resulting isoform (10, also known as Aio-del3,4) 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.