

## Product datasheet for **SC328938**

### ZFX (NM\_001178086) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	ZFX (NM_001178086) Human Untagged Clone
Tag:	Tag Free
Symbol:	ZFX
Synonyms:	ZNF926
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)

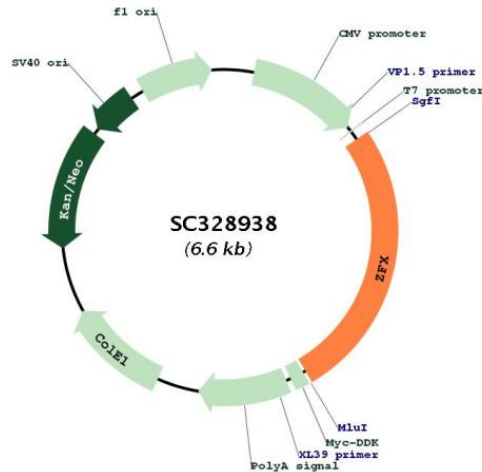


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**Fully Sequenced ORF:** >SC328938 representing NM\_001178086.  
Blue=Insert sequence Red=Cloning site Green=Tag(s)

```
GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTGACTG
GATCCGGTACCGAGGAGATCTGCCGCCCGCATCGCC
ATGACCATGGACACAGAGTCGGAATTGATCCTTGTAAGTGGATGGCACTTGCCCTGAGGTCATCAAG
GTGTACATTTTTAAAGCTGACCCTGGAGAAGATGACTTAGGTGGAAGTGTAGACATTGTGGAGAGTGAG
CCTGAGAATGATCATGGAGTTGAACTGCTTGATCAGAACAGCAGTATTCGTGTTCCAGGGAAAAGATG
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TGTGATAAAGGCTTTACAGGCCTTCAGAACTCAAGAAACACGTGGCTGCCACAAAGGGCAAAAAATG
CACCAGTGTAGACATTGTGACTTTAAGATTGCAGATCCATTTGTTCTAAGTCGCCATATTCTCTCAGTT
CACACAAAGGATCTTCCATTTAGGTGCAAGAGATGTAGAAAGGGATTTAGGCAACAGAGTGAGCTTAAA
AAGCATATGAAGACACACAGTGGCAGGAAAGTGTATCAGTGTGAGTACTGTGAGTATAGCACTACAGAT
GCCTCAGGCTTTAAACGGCACGTTATTTCCATTACACGAAAGACTATCCTCACCAGGTGTGAGTACTGC
AAGAAAGGCTTCCGAAGACCTTCAGAAAAGAACCAGCACATAATGCGACATCATAAAGAAGTTGGCCTG
CCCTAA
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
```

**Restriction Sites:** SgfI-MluI

**Plasmid Map:**


**ACCN:** NM\_001178086

**Insert Size:** 1731 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).

**OTI Annotation:** This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

**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\\_001178086.1](#)

**RefSeq Size:** 6801 bp

**RefSeq ORF:** 1731 bp

**Locus ID:** 7543

**UniProt ID:** [P17010](#)

**Cytogenetics:** Xp22.11

**Protein Families:** Transcription Factors

**MW:** 66.1 kDa

**Gene Summary:** This gene on the X chromosome is structurally similar to a related gene on the Y chromosome. It encodes a member of the krueppel C2H2-type zinc-finger protein family. The full-length protein contains an acidic transcriptional activation domain (AD), a nuclear localization sequence (NLS) and a DNA binding domain (DBD) consisting of 13 C2H2-type zinc fingers. Studies in mouse embryonic and adult hematopoietic stem cells showed that this gene was required as a transcriptional regulator for self-renewal of both stem cell types, but it was dispensable for growth and differentiation of their progeny. Multiple alternatively spliced transcript variants encoding different isoforms have been identified, but the full-length nature of some variants has not been determined. [provided by RefSeq, May 2010]  
Transcript Variant: This variant (4) lacks several exons in the 5' region, resulting in a downstream AUG start codon, as compared to variant 1. The resulting isoform (2) has a shorter N-terminus, as 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.