

Product datasheet for MC226097

Xaf1 (NM_001291153) Mouse Untagged Clone

Product data:

OriGene Technologies, Inc.

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Product Type:	Expression Plasmids
Product Name:	Xaf1 (NM_001291153) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Xaf1
Synonyms:	Fbox39
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC226097 representing NM_001291153 Red=Cloning site Blue=ORF Orange=Stop codon
	TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCC <mark>GCGATCGCC</mark>
	ATGGAGGCTGACTTCCAAGTGTGCAGGAACTGCAAAAGAAATGTGGCCTCTCTCCACTTCATGCTCCACG AGGCCCACTGCCTGCGCTTCATAGTCCTTTGCCCAGAATGTGAAGAGCCCATCCCAGAGTCAAAGATGAA AGAGCACATGGAAGTTGTGCACCAGCAGAAACAATGTTCCGCCCCAAACACTGTGACACGTATTCGGGAT GAAAGTATAATAGTCATTCCTTCAACCCTTGCATTTATGGACTCTGGAAATCGAAGATCCACAGTGAGAT AAGATGTTCGTCCAAAGACAAAAAATAGAAACAGCTCAACAAAGCGAGAGACAAAAAAACAAAATGGCAC TGTGGCTCTGCCTTTGAAGTCTGGGCTCCAGCAGAGGGGCTGATCTTCCCACAGGAGACGAGACGAGACGGCCTAT GACACTCTCCCAGAACTGTTGTCAGTGCCGAATTTTACTTCCCTTGCCCATTCTAAATGAGCACCAGGAGA AGTGCCAGAGGTTAGCTCACCAAAAGAAACTCCAGTGGGGCTGGTGA ACGCCTACGCGGCCGCCCCGAGCAGAAACTCCATCCAGAAGAGGATCTGGCAGCAGCAGCACCAGGAGA AGTGCCAGAGGTTAGCTCACCAAAAGAAACTCCAGTGGGGCTGGTGA ACGCCTACGCGGCCGCCCGAGCAGAAACTCCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACAATAAGGTTTAA
Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001291153
Insert Size:	537 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).



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Service Servic	
OTI Annotation:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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:	 Centrifuge at 5,000xg for 5min. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. Close the tube and incubate for 10 minutes at room temperature. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	<u>NM 001291153.1, NP 001278082.1</u>
RefSeq Size:	2313 bp
RefSeq ORF:	537 bp
Locus ID:	327959
UniProt ID:	<u>Q5NBU8</u>
Cytogenetics:	11 B4
Gene Summary:	Seems to function as a negative regulator of members of the IAP (inhibitor of apoptosis protein) family. Inhibits anti-caspase activity of BIRC4. Induces cleavage and inactivation of BIRC4 independent of caspase activation. Mediates TNF-alpha-induced apoptosis and is involved in apoptosis in trophoblast cells. May inhibit BIRC4 indirectly by activating the mitochondrial apoptosis pathway. After translocation to mitochondria, promotes translocation of BAX to mitochondria and cytochrome c release from mitochondria. Seems to promote the redistribution of BIRC4 from the cytoplasm to the nucleus, probably independent of BIRC4 inactivation which seems to occur in the cytoplasm. The BIRC4-XAF1 complex mediates down-regulation of BIRC5/survivin; the process requires the E3 ligase activity of BIRC4. Seems to be involved in cellular sensitivity to the proapoptotic actions of TRAIL. May be a tumor suppressor by mediating apoptosis resistance of cancer cells (By similarity).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (2) lacks two exons in the central coding region but maintains the reading frame, compared to variant 1. The encoded isoform (2) 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.

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