

#### OriGene Technologies, Inc.

9620 Medical Center Drive, Ste 200 Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com CN: techsupport@origene.cn

# Product datasheet for SC331513

#### MDMX (MDM4) (NM\_001204172) Human Untagged Clone

### **Product data:**

Product Type:	Expression Plasmids
Product Name:	MDMX (MDM4) (NM_001204172) Human Untagged Clone
Tag:	Tag Free
Symbol:	MDMX
Synonyms:	BMFS6; HDMX; MDMX; MRP1
Vector:	pCMV6-Entry (PS100001)
Fully Sequenced ORF:	<pre>&gt;SC331513 representing NM_001204172. Blue=Insert sequence Red=Cloning site Green=Tag(s)</pre>
	ATGACATCATTTTCCACCTCTGCTCAGTGTTCAACATCTGACAGTGCTTGCAGGATCTCTCCTGGACAA ATCAATCAGGAAAATGAAGGAAATGATGTCCCTGATTGTCGAAGAACCATTTCGGCTCCTGTCGTTAGA CCTAAAGATGCGTATATAAAGAAAGAAAACTCCAAACTTTTTGATCCCTGCAACTCAGTGGAATTCTTG GATTTGGCTCACAGTTCTGAAAGCCAAGAGACCATCTCAAGCATGGGAGAACAGTTAGATAACCTTTCT GAACAGAGAACAGATACAGAAAACATGGAGGACTGCCAGAATCTCTTGAAGCCATGTAGCTTATGTGAG AAAAGACCACGAGACGGGAACATTATTCATGGAAGGACGGGCCATCTTGTCACTTGTTTTCACTGTGCC AGAAGACTAAAGAAGGCTGGGGCTTCATGCCCATTTGCAAGAAAGA
<b>Restriction Sites:</b>	Sgfl-Mlul
ACCN:	NM_001204172
Insert Size:	495 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).



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## **MDMX (MDM4) (NM\_001204172) Human Untagged Clone – SC331513**

Reconstitution Method:	<ol> <li>Centrifuge at 5,000xg for 5min.</li> <li>Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>Close the tube and incubate for 10 minutes at room temperature.</li> <li>Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
RefSeq:	<u>NM 001204172.1</u>
RefSeq Size:	9112 bp
RefSeq ORF:	495 bp
Locus ID:	4194
UniProt ID:	<u>015151</u>
Cytogenetics:	1q32.1
Protein Families:	Druggable Genome, Transcription Factors
Protein Pathways:	p53 signaling pathway
MW:	18.2 kDa
Gene Summary:	This gene encodes a nuclear protein that contains a p53 binding domain at the N-terminus and a RING finger domain at the C-terminus, and shows structural similarity to p53-binding protein MDM2. Both proteins bind the p53 tumor suppressor protein and inhibit its activity, and have been shown to be overexpressed in a variety of human cancers. However, unlike MDM2 which degrades p53, this protein inhibits p53 by binding its transcriptional activation domain. This protein also interacts with MDM2 protein via the RING finger domain, and inhibits the latter's degradation. So this protein can reverse MDM2-targeted degradation of p53, while maintaining suppression of p53 transactivation and apoptotic functions. Alternatively spliced transcript variants encoding different isoforms have been noted for this gene. [provided by RefSeq, Feb 2011] Transcript Variant: This variant (3, also known as MDM4-211 or HDMX211) is missing 8 consecutive coding exons, and uses an alternate acceptor splice site at the 3' terminal exon compared to variant 1. However, it maintains the reading frame, and encodes a very short isoform (3) that lacks the N-terminal p53 binding domain, but retains the ring finger domain at the C-terminus. This isoform has been shown to bind and stabilize oncoprotein HDM2, and also indirectly stabilize p53 protein by counteracting its degradation by HDM2. Screening of lung cancer biopsies shows the presence of this isoform in samples that overexpress HDM2 protein, supporting a pathologic role for this protein (PMID:16266988). Sequence Note: This RefSeq record was created from transcript and genomic sequence data because no single transcript was available for the full length of the gene. The extent of this transcript is supported by transcript alignments.

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