

Product datasheet for **MC226003**

Ube2w (NM_001271017) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Ube2w (NM_001271017) Mouse Untagged Clone
Tag: Tag Free
Symbol: Ube2w
Synonyms: 6130401J04Rik
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC226003 representing NM_001271017
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGGATCGCC**

ATGTTGGGCCCCCGGGCGTGACGCGAGCACGGCGGCTCCGCCCCCTGCGTCTCGGGCTCGCTGGCCTT
GGGGGATGGTTTCATCATGGCGTCAATGCAGAAACGACTACAAAAGAAGCTGTTGGCTTTCGACAATGA
CCCACCTCCTGGAATGACTTTAAATGAAAAGAGTGTTTCAGAATCAATCACGCAGTGGATCGTAGACATG
GAAGGTGCACCAGGAACCTTATATGAAGGGGAAAATTTCAACTTTTGTAAATTTAGTAGTCGATACC
CTTTTGACTCTCCTCAGAAGACTGGTCCCCGGCGCTCTCAGTGCAGTCAGTCTGTCTCAGCATTATCAGC
ATGCTTTCCAGCTGCAAAGAAAAGAGACGACCACCAGATAATTCCTTTTATGTGCGAACATGTAACAAGA
ATCCAAAGAAAACAAAATGGTGGTATCATGATGACACTTGTGATGCCGCTGCCCTCCTCCTG**TAG**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001271017
Insert Size: 486 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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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:	<ol style="list-style-type: none">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:	<u>NM_001271017.1</u> , <u>NP_001257946.1</u>
RefSeq Size:	3060 bp
RefSeq ORF:	486 bp
Locus ID:	66799
Cytogenetics:	1 A3
Gene Summary:	<p>Accepts ubiquitin from the E1 complex and catalyzes its covalent attachment to other proteins. Specifically monoubiquitinates the N-terminus of various substrates, including ATXN3, MAPT/TAU, POLR2H/RPB8 and STUB1/CHIP, by recognizing backbone atoms of disordered N-termini (PubMed:21855799, PubMed:21229326). Involved in degradation of misfolded chaperone substrates by mediating monoubiquitination of STUB1/CHIP, leading to recruitment of ATXN3 to monoubiquitinated STUB1/CHIP, and restriction of the length of ubiquitin chain attached to STUB1/CHIP substrates by ATXN3 (PubMed:21855799). After UV irradiation, but not after mitomycin-C (MMC) treatment, acts as a specific E2 ubiquitin-conjugating enzyme for the Fanconi anemia complex by associating with E3 ubiquitin-protein ligase FANCL and catalyzing monoubiquitination of FANCD2, a key step in the DNA damage pathway (PubMed:21229326). In vitro catalyzes 'Lys-11'-linked polyubiquitination. UBE2W-catalyzed ubiquitination occurs also in the presence of inactive RING/U-box type E3s, i.e. lacking the active site cysteine residues to form thioester bonds with ubiquitin, or even in the absence of E3, albeit at a slower rate (By similarity).[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (3) uses an alternate splice site that results in a frameshift in the 3' coding region, compared to variant 1. The encoded isoform (3) has a distinct and shorter C-terminus, 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.</p>