

## Product datasheet for **MC226129**

### Ube2w (NM\_001271016) Mouse Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** Ube2w (NM\_001271016) 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:** >MC226129 representing NM\_001271016  
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**CGATCGCC**

ATGTTGGGCCCCCGGGCGTGACGCGAGCACGGCGGCTCCGCCCTCGCTCTCGGGCTCGCTGGCCTT  
GGGGGATGGTTTCATCATGGCGTCAATGCAGAAACGACTACAAAAGAAGTGTGGCTTTGCAGAAATGA  
CCCACCTCTGGAATGACTTTAAATGAAAAGAGTGTTTCAGAAATCAATCACGCAGTGGATCGTAGACATG  
GAAGGTGCACCAGGAACCTTATATGAAGGGGAAAATTTCAACTTTTGTAAATTTAGTAGTCGATACC  
CTTTTGACTCTCCTCAGAAGACTGGTCCCCGGCGCTCTCAGTGCAGTCAGTCTGTCTCAGCATTATCAGC  
ATGCTTTCCAGCTGCAAAGAAAAGAGACGACCACCAGATAATTCCTTTTATGTGCGAACATGTAACAAGA  
ATCCAAAGAAAACAAAATGGTGGTATCATGGTGGATACAGTGCCCGTGGAGGCCAGAAGAGGGACTCTTA  
CCCCTGGAAGTGGAGTTTAAAGATAGTTGTGTGCTGTGCATGTGAGTTCTATGGTCACC**TGA**

**ACGCGT**ACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
ACAAGGATGACGACGATAAGGTTTAA

**Restriction Sites:** SgfI-MluI  
**ACCN:** NM\_001271016  
**Insert Size:** 552 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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<b>OTI Annotation:</b>	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"><li>1. Centrifuge at 5,000xg for 5min.</li><li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li><li>3. Close the tube and incubate for 10 minutes at room temperature.</li><li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li><li>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.</li></ol>
<b>RefSeq:</b>	<u><a href="#">NM_001271016.1</a></u> , <u><a href="#">NP_001257945.1</a></u>
<b>RefSeq Size:</b>	1551 bp
<b>RefSeq ORF:</b>	552 bp
<b>Locus ID:</b>	66799
<b>Cytogenetics:</b>	1 A3
<b>Gene Summary:</b>	<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 (2) uses an alternate splice site and has alternate 3' exon structure, and it thus differs in the 3' coding region and 3' UTR, compared to variant 1. The encoded isoform (2) has a distinct and longer C-terminus, compared to isoform 1.</p>