

## Product datasheet for **MC227185**

### Wdr45 (NM\_001290795) Mouse Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** Wdr45 (NM\_001290795) Mouse Untagged Clone  
**Tag:** Tag Free  
**Symbol:** Wdr45  
**Synonyms:** C79260; DXlmx38e; JM5; Sfc19; Wdrx1; WIPI-4  
**Mammalian Cell Selection:** Neomycin  
**Vector:** pCMV6-Entry (PS100001)  
**E. coli Selection:** Kanamycin (25 ug/mL)  
**Fully Sequenced ORF:** >MC227185 representing NM\_001290795  
**Red**=Cloning site **Blue**=ORF **Orange**=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**CGGATCGCC**

ATGACTCAGCAGCCACTTCGAGGTGTGACCAGCCTACATTTCAACCAAGACCAAGCTGCTTTTGCTGCG  
CCATGGAGACAGGCGTCCGGATCTACAATGTGGAGCCACTTATGGAGAAGGGGCATCTTGACCACGAGCA  
GGTAGGCAGCGTGGCCCTGGTAGAGATGCTGCACCGATCCAACCTGCTGGCCCTGGTGGCGGTGGGAGC  
AGCCCCAAGTTCTCTGAGATCTCAGTGTGATCTGGGACGATGCCCGAGAAGGCAAGGACTCCAAGGACA  
AACTGGTGTGGAGTTCACCTTCAACCAAGCCAGTGTGGCTGTGCGCATGCGCCATGACAAGATCGTGAT  
TGTGCTGAGGAACCGCATCTATGTGTACTCCTCCCTGACAGTCCAAGAAAGCTGTTTGAGTTTGACT  
CGGGACAACCCCAAGGGCTGTGTGACCTCTGTCCAAGCCTGGAGAAGCAGCTGCTCGTGTTCCTGGAC  
ACAAGTGTGGAAGTCTGCAACTGTGGATCTCGCAAGCACAAAGCCTGGTACTTCGTCGGCGCCATTAC  
TATCAATGCACATCAGAGTGTGGCTGTGTCCCTGAACCAGCCAGGCACTGTAGTGGCGTCAGCC  
TCCCAGAAGGGCACCCCTTATTCGTCTCTTTGATACCCAATCCAAGGAAAAGCTGGTAGAGCTTCAAGAG  
GCACCGACCCTGCCACCCTGTACTGTGACAAGGGCACTGTCCACATCTTCGCTCTTAAAGACACCCGCT  
TAACCGCCGCTCTGCGCTGGCTCGTGTGGCAAAGTGGGACCTATGATTGGGCAATACGTGGACTCTCAG  
TGGAGCCTGGCCAGCTTTACTGTGCCTGTGAGTCAGCCTGCATCTGCGCCTTTGGTCGAAATACTCCA  
AGAATGTCAATTCTGTAATTGCCATCTGTGTAGATGGGACCTTCCACAAATATGTCTTCACTCTGATGG  
AAACTGCAACAGAGAGGCCCTTTGACGTGTACCTTGACATCTGTGATGACGAGGACTTCTAA

**ACGCGT**ACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
ACAAGGATGACGACGATAAGGTTTAA

**Restriction Sites:** SgfI-MluI



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<b>ACCN:</b>	NM_001290795
<b>Insert Size:</b>	1041 bp
<b>OTI Disclaimer:</b>	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).
<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>NM_001290795.1, NP_001277724.1</u>
<b>RefSeq Size:</b>	1559 bp
<b>RefSeq ORF:</b>	1041 bp
<b>Locus ID:</b>	54636
<b>UniProt ID:</b>	<u>Q91VM3</u>
<b>Cytogenetics:</b>	X 3.48 cM
<b>Gene Summary:</b>	<p>Component of the autophagy machinery that controls the major intracellular degradation process by which cytoplasmic materials are packaged into autophagosomes and delivered to lysosomes for degradation. Activated by the STK11/AMPK signaling pathway upon starvation, WDR45 is involved in autophagosome assembly downstream of WIPI2, regulating the size of forming autophagosomes. Probably recruited to membranes through its PtdIns3P activity. [UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (4) uses an alternate in-frame splice site in the 3' coding region, compared to variant 1. The encoded isoform (b) is shorter than isoform a. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p>