

Product datasheet for **MC225811**

Rnf138 (NM_001303005) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Rnf138 (NM_001303005) Mouse Untagged Clone
Tag: Tag Free
Symbol: Rnf138
Synonyms: 2410015A17Rik; 2810480D20Rik; STRIN; Trif; Trif-d
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC225811 representing NM_001303005
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGGATCGCC**

ATGCTGTTCAAAAAGATTATATTTTAACCAATAATTTACAGATTAATTTCTATCGCATGAGACATCATT
ACAAATCTTGTAAGAAGTATCAGGATGAATATGGTGTTCCTTCTGTTCATCCAACTTTAAGATTTCTCA
AGATTCAGTAAGGAGCAGTAATAGGAGTAAACATCTGCATCTGATAACACAGAACTTATCAAGAGGAT
ACAAGTTCCTTCTGGGCATCCTACCTTTAAGTGTCCCTTATGTCAAGAGTCAAATTCACCAGACAACGTT
TATTGGATCACTGTAATAGTAACCACCTATTTTCAGATAGTTCTGTGAATCTTCAGCTAGATGAGGAAAC
CCAATATCAAACCTGCTGTGGAAGAGTCTTTTCAAGTAAACATG**TGA**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI

ACCN: NM_001303005

Insert Size: 396 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).

OTI Annotation: Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.



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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_001303005.1, NP_001289934.1</u>
RefSeq Size:	3070 bp
RefSeq ORF:	396 bp
Locus ID:	56515
UniProt ID:	<u>Q9CQE0</u>
Cytogenetics:	18 A2
Gene Summary:	<p>E3 ubiquitin-protein ligase involved in DNA damage response by promoting DNA resection and homologous recombination. Recruited to sites of double-strand breaks following DNA damage and specifically promotes double-strand break repair via homologous recombination. Two different, non-exclusive, mechanisms have been proposed. According to a report, regulates the choice of double-strand break repair by favoring homologous recombination over non-homologous end joining (NHEJ): acts by mediating ubiquitination of XRCC5/Ku80, leading to remove the Ku complex from DNA breaks, thereby promoting homologous recombination. According to another report, cooperates with UBE2Ds E2 ubiquitin ligases (UBE2D1, UBE2D2, UBE2D3 or UBE2D4) to promote homologous recombination by mediating ubiquitination of RBBP8/CtIP. Together with NLK, involved in the ubiquitination and degradation of TCF/LEF. Also exhibits auto-ubiquitination activity in combination with UBE2K. May act as a negative regulator in the Wnt/beta-catenin-mediated signaling pathway.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (3) uses an alternate splice site in the 5' coding region and lacks an alternate in-frame exon in the 3' coding region, compared to variant 1. These differences cause translation initiation at an alternate downstream start codon and result in an isoform (3) that is shorter and has a distinct N-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>