

Product datasheet for **MC217167**

Rad18 (NM_021385) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Rad18 (NM_021385) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Rad18
Synonyms:	2810024C04Rik; Rad18sc
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin



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Fully Sequenced ORF: >MC217167 representing NM_021385
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGGATCGCC**

ATGGAGTCTGGCCGAGCCGCGATGGCCTCCGGGTTGGCGGTGATGAAGACAATAGATGACTTGCTGC
GCTGTGGGATTTGCTTTGAGTATTTCAACATTGCAGTGATAATCCCCAGTGCTCTCACAACATTGTTCC
ACTCTGTATAAGAAAGTTTTTATCCTATAAACTCAGTGCCCACTTGTTCGCTGGCAGTAACGGAGCCA
GACCTGAGAAATAATCGCCTCTTAGATGAACTGGTAAAAAGCATGAATTTGCACGGACTCACCTGTTGC
AGTTTGTCTTAGAGTACCACCCATATCTCCTGTGTCTCCACCTCAAAGAAGGTTGTTGTTAAAGTGCA
TAATGCTGACGCCGCCAACACCCTGTCAAACAGGCGAACAGGTTAATGGATAAGTTCCTGATTAGAGAA
ACTGGTACTGTGATTTGAGTTGTTGGGAAAAGAAAATGAGAGGAAATTCAGCCCTCAAAAAGAGCTAA
GCACCTCTGCTGAGATTAAGAGACAAGTCTCCTAGGAAAGCCGGTACTGGGGCTCTCGGATGCTAATGG
TCCTGTGACTCCCTCTACATCCACTATGAACTGGATACTAAAGTGTCTTGTCTGTTTGTGGGGTCAAG
ATTCCAGAAAATCATATCAATAAGCATTAGACAGTTGTTTATCAGTGAAGAGAAGAAGGAGAGCCTGC
GAAGTTCTGCTCACAAAAGGAAGCCGTTGCCCAAACTGTATATAACTTGCTCTCTGATCGTGATTTAAA
GAAAAAGCTGAAACAGTATGGCTTATCTGTTCAAGGAAACAAACAGCAGCTTATTTAAAGGCATCAGGAG
TTTGTGCACATGTATAATGCCAGTGGCATGCTTTGCATCCTAAATCAGCTGCTGAAATCGTCCAAGAAA
TTGAAAGCATGGAGAAGACCAGGATGCGCCTTGAAGCAAGTAACTCAATGAAAATGTCATGGTTTTTAC
AAAGAACCAAACAGAGAAGGAAATGAGGAAGTTCACAGTGAATATCGTAAAAAGCACCAGAATGCATTC
CAGCTTCTGGTGGATCAGGCCAAAAAGGATAAAGAAAAGTGGCAGAGTTTCAAAAGCTGCAGCGATGA
GAACAGATGAACCTGCAGAGACTGCCGTCGATGAGAACAGATGAACCTGCAGAGACACTGCCGTCGAT
GAGAACAGATGAACCTGCAGAGACTGCCGTTGATGAGAGCAGATGAACCTGCAGAAAACACTGCCGCTCT
GAGTGTATCGACAAGAAGATAATGTGAGCTTCTCAGATACTGTCTCAGTAAACAAACACTTTTCTCAGC
CCCAGCTGGACTCGCCAGGCCGTCGGAGCCTGAGAGGCCGGATGATTCTTCTAGTTGACTGATATTCT
TTTCTCTCGGACTCAGACTCATGCAATAGAAATGATCAAACAGAGAAGTCAAGCCACAACAGACTCGC
CGCACTAGAGCCAGTGAATGTGTTGAGATTGAACCAAGAAACAAGCGGAATAAGAAT**TAG**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI

ACCN: NM_021385

Insert Size: 1530 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).

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:	NM_021385.2 , NP_067360.2
RefSeq Size:	2560 bp
RefSeq ORF:	1530 bp
Locus ID:	58186
UniProt ID:	Q9QXK2
Cytogenetics:	6 E3
Gene Summary:	<p>E3 ubiquitin-protein ligase involved in postreplication repair of UV-damaged DNA. Postreplication repair functions in gap-filling of a daughter strand on replication of damaged DNA. Associates to the E2 ubiquitin conjugating enzyme UBE2B to form the UBE2B-RAD18 ubiquitin ligase complex involved in mono-ubiquitination of DNA-associated PCNA on 'Lys-164'. Has ssDNA binding activity.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) lacks two alternate in-frame exons compared to variant 1. The resulting isoform (2) has the same N- and C-termini but is shorter compared to isoform 1.</p> <p>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>