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Product datasheet for MC226715

Rad1 (NM_001289448) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Rad1 (NM_001289448) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Rad1
Synonyms:	mRAD1
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
Fully Sequenced ORF:	>MC226715 representing NM_001289448 Red=Cloning site Blue=ORF Orange=Stop codon TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCCGCGATCGCC ATGCCTCTCCTAACCCAGTACAATGAAGAGGAGTACGAACAGTACTGCTTAGTGGCCAGCCTTGACAACG TTAGGAATCTCTCCACTGTCTTGAAAGCCATTCATTTCAGAGAACACGCCACGTGTTTTGCTACCAAAAA CGGAATCAAGGTTACAGTGGAGAATGCAAAGTGTGTGCAAGCAAATGCCTTTATTCAGGCTGACGTGTTT CAGGAATTTGTCATTCAGGAAGAATCTGTTACTTTTCGAATTAACTTAACTATCCTTTTAGACTGTTTAT CTATTTTTGGATCAAGTCCTACACCAGGGACTTTGACTGCGCTTCGGATGTGTTACCAAGGTTATGGTCA CCCACTGATGCTATTTCTAGAAGAAGGAGGAGTGGTGACGGTCTGCAAAATTACCACTCAGGAGCCTGAG GAGACACTGGATTTTGATTTCTGCAGCACCAATGTTATGAATAAAATTATCCTGCAGTCAGAGGGGCTCC GGGAAGCCTTTTCTGAGCTGGACATGACAGGTGATGTCCTACAGATCACTGTGTCTCCTGACAAGCCCTA TTTCAGGTTGTCTACTTTTGGAAATGCAGGAAACTCCCATCTTGACTATCCCAAAGATTCCGACTTGGTG GAAGCCTTTCACTGTGATAAGACCCAGGTCAACAGAATTTCGGATGTAAAGTATTCCTGTAAAACATGGT TGCAGCTACCTGAAGGGGTAGGCTATGATCCTCTCAGCGGTTTGGAGTGGACTCTTTCAGAACGCGATGG AGAGCAGGAGGTGGCTCAGTGGGTAAACGTGGTCCCTGTGCAAGCTTGA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_001289448
Insert Size:	819 bp

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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.
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:	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_001289448.1, NP_001276377.1
RefSeq Size:	4136 bp
RefSeq ORF:	819 bp
Locus ID:	19355
UniProt ID:	Q9QWZ1
Cytogenetics:	15 A1
Gene Summary:	Component of the 9-1-1 cell-cycle checkpoint response complex that plays a major role in DNA repair. The 9-1-1 complex is recruited to DNA lesion upon damage by the RAD17-replication factor C (RFC) clamp loader complex. Acts then as a sliding clamp platform on DNA for several proteins involved in long-patch base excision repair (LP-BER). The 9-1-1 complex stimulates DNA polymerase beta (POLB) activity by increasing its affinity for the 3'-OH end of the primer-template and stabilizes POLB to those sites where LP-BER proceeds; endonuclease FEN1 cleavage activity on substrates with double, nick, or gap flaps of distinct sequences and lengths; and DNA ligase I (LIG1) on long-patch base excision repair substrates. The 9-1-1 complex is necessary for the recruitment of RHNO1 to sites of double-stranded breaks (DSB) occurring during the S phase. Isoform 1 possesses 3'->5' double stranded DNA exonuclease activity (By similarity).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (3) differs in the 3' UTR and 3' coding region compared to variant 1. The encoded isoform (2) 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.