

Product datasheet for **MR217268**

Exosc1 (NM_001164561) Mouse Tagged ORF Clone

Product data:

Product Type: Expression Plasmids
Product Name: Exosc1 (NM_001164561) Mouse Tagged ORF Clone
Tag: Myc-DDK
Symbol: Exosc1
Synonyms: 2610035C18Rik; 2610104C07Rik; 2610312F07Rik; AI447561
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
ORF Nucleotide Sequence: >MR217268 representing NM_001164561
Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**GCGATCGCC**

ATGGCACCACCGGTGAGGTACTGCATCCCCGGCGAACGTCTGTGTAACTTGGAGGAAGGCAGCCCCGGCA
GCGGCACCTACACCCGGCATGGCTACATCTTTTCGTCGCTGGCTGGCTGCCTGATGAAGACCAGCGAGAA
TGCGCGGTTCCCGTGGTGTCACTGATGAGAGAAACAGAGTCCCAGTTGCTTCCAGATGTGGGAGCTGTC
GTCACCTGTAAGGTAGAAATTTACAAGAGTTTTCGGCCAGGTGACATAGTTTTGGCCAAAGTTATCTCCC
TAGGCGATGCACAGTCCAATTACCTGCTGACTACTGCTGAAAACGAGCTGGGCGTTGTGGTGGCCACAG
TGAGTCAGGTGTTCAAGTGGTCCCATCAGCTGGTGTGAGATGCAGTGCCCAAGACCCACACTAAAGAA
TTCCGAAAAGTGGCCCGAGTACAGCCCGAGTTCCTACAGACC

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Protein Sequence: >MR217268 representing NM_001164561
Red=Cloning site Green=Tags(s)

MAPPVRYCIPGERLCNLEEGSPGSGTYTRHGYIFSSLAGCLMKTSENGAVPVVSVMRETESQLLPDVGAV
VTCKVEIYKSFPRPGDIVLAKVISLGAQSNYLLTTAENELGVVVAHSESGVMVPISWCEMQCPKTHKE
FRKVARVQPEFLQT

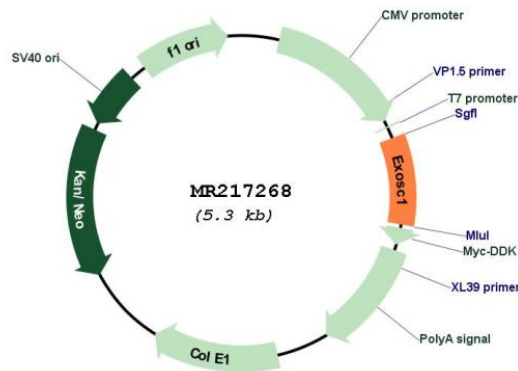
TRTRPLEQKLISEEDLAANDILDYKDDDDKV

Restriction Sites: SgfI-MluI



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Cloning Scheme:

Plasmid Map:


ACCN: NM_001164561

ORF Size: 462 bp

OTI Disclaimer: The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. [More info](#)

OTI Annotation: This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.

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_001164561.1, NP_001158033.1</u>
RefSeq Size:	1499 bp
RefSeq ORF:	465 bp
Locus ID:	66583
UniProt ID:	<u>Q9DAA6</u>
Cytogenetics:	19 C3
MW:	17.2 kDa
Gene Summary:	<p>Non-catalytic component of the RNA exosome complex which has 3'->5' exoribonuclease activity and participates in a multitude of cellular RNA processing and degradation events. In the nucleus, the RNA exosome complex is involved in proper maturation of stable RNA species such as rRNA, snRNA and snoRNA, in the elimination of RNA processing by-products and non-coding 'pervasive' transcripts, such as antisense RNA species and promoter-upstream transcripts (PROMPTs), and of mRNAs with processing defects, thereby limiting or excluding their export to the cytoplasm. The RNA exosome may be involved in Ig class switch recombination (CSR) and/or Ig variable region somatic hypermutation (SHM) by targeting AICDA deamination activity to transcribed dsDNA substrates. In the cytoplasm, the RNA exosome complex is involved in general mRNA turnover and specifically degrades inherently unstable mRNAs containing AU-rich elements (AREs) within their 3' untranslated regions, and in RNA surveillance pathways, preventing translation of aberrant mRNAs. It seems to be involved in degradation of histone mRNA. The catalytic inactive RNA exosome core complex of 9 subunits (Exo-9) is proposed to play a pivotal role in the binding and presentation of RNA for ribonucleolysis, and to serve as a scaffold for the association with catalytic subunits and accessory proteins or complexes. EXOSC1 as peripheral part of the Exo-9 complex stabilizes the hexameric ring of RNase PH-domain subunits through contacts with EXOSC6 and EXOSC8 (By similarity).[UniProtKB/Swiss-Prot Function]</p>