

Product datasheet for **MC201853**

Exosc1 (NM_025644) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Exosc1 (NM_025644) Mouse Untagged Clone
Tag: Tag Free
Symbol: Exosc1
Synonyms: 2610035C18Rik; 2610104C07Rik; 2610312F07Rik; AI447561
Mammalian Cell Selection: Neomycin
Vector: PCMV6-Kan/Neo (PCMV6KN)
E. coli Selection: Kanamycin (25 ug/mL)

Fully Sequenced ORF: >BC024423 sequence for NM_025644
ATGGTGGCAAGCATGGCACC GCCGGTGAGGACTGCATCCCCGGCGAACGCTGTGTAACCTGGAGGAAG
GCAGCCCCGGCAGCGGCACCTACACCCGGCATGGCTACATCTTTTCGTCGCTGGCTGCCTGATGAA
GACCAGCGAGAATGGCGCGGTTCCCGTGGTGTCAGTGATGAGAGAAACAGAGTCCCAGTTGCTTCCAGAT
GTGGGAGCTGTCGTACCTGTAAGGTCTCTAGCATCAACTCACGTTTGGCAAAGTACACATCCTGTATG
TGGGATCCACACCACTCAAAAATGCTTTTCGAGGAACTATCCGCAAAGAAGATATCCGAGCAACTGAAAA
AGACAAGGTAGAAATTTACAAGAGTTTTTCGGCCAGGTGACATAGTTTTGGCCAAAGTTATCTCCCTAGGC
GATGCACAGTCCAATTACCTGCTGACTACTGCTGAAAACGAGCTGGGCGTTGTGGTGGCCCCACAGTGAGT
CAGGTGTTTCAGATGGTTCATCAGCTGGTGTGAGATGCAGTGCCCAAGACCCACACTAAAGAATCCG
AAAAGTGGCCCGAGTACAGCCCGAGTTCCTACAGACCTAAGCCCACTACCCCAAAGAGGACTTCAGCAC
TTCAGCTACTTCTAAAAGTACACATATAAAAAAACCATCAAGATGCAATGGTCTTTATTAAGGTACCTGC
GGTCAGCTGGCAACCATCTCTTGAAACAATGTGCCGAAATGTATTCATGCTGTAATGACACCCAAGGCC
CCTGCCGCTGCTGAGACAGGGAGATTGTTAGTGCCCAAGTTTGAGGCCAGCTGGGCTACATATTAAGAC
TCTTTCAACCAAAAAGACAAAAA

Restriction Sites: RsrII-NotI

ACCN: NM_025644

Insert Size: 588 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).



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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: [BC024423](#), [AAH24423](#)

RefSeq Size: 872 bp

RefSeq ORF: 588 bp

Locus ID: 66583

UniProt ID: [Q9DAA6](#)

Cytogenetics: 19 C3

Gene Summary: 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]

Transcript Variant: This variant (1) represents the predominant transcript and encodes the longest isoform (1). It contains an in-frame AUG four codons upstream from the currently annotated translation start site; however, Kozak signal strength and conservation data support the use of the annotated downstream AUG.