

Product datasheet for **MC210974**

Exosc8 (NM_027148) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Exosc8 (NM_027148) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Exosc8
Synonyms:	2310032N20Rik; CIP3; mKIAA4013
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
Fully Sequenced ORF:	>MC210974 representing NM_027148 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**GCGATCGCC**

ATGGCGGCTGGTTCAAACCTGTGGAGCCGCTGGAGTATTACAGGAGATTTCTGAAGGAAAACCTGCCGTC
CTGATGGAAGAGAACTTGGTGAATTCAGAGCCACAACCTGTCAACATAGGTTCAATCAGTACAGCGGATGG
CTCTGCTCTCGTGAAGCTGGGGAATACCACGGTCATTTGTGGCGTTAAAGCAGAATTTGCAGCACCACCA
GTAGATGCCCCCGATAGAGGATATGTCGTCCTAATGTGGATCTACCACCGCTGTGTTCTTCGAGGTTCC
GGACAGGACCTCCTGGGGAAGAGGCTCAAGTAACCAGCCAGTTTCATTGCAGATGTCGTTGACAACTCACA
GGTGATTAAGAAAGAGGATTTATGCATTTCTCCAGGCAAGCTTGCTTGGGTTCTATACTGTGACCTCATT
TGTCTAGACTACGATGGGAACATTTTGGATGCCTGCACATTTGCTTTGTTAGCAGCTTTAAAGAATGTAC
AGTTGCCTGAAGTTACTATAAACGAAGAGACTGCTTTAGCCGAAGTCAATTTAAAGAAGAAAAGTTATTT
GAATGTTAGAACAACCCAGTTGCTACTTCCTTTGCTGTGTTGATGACACTCTACTGATAGTCGATCCT
ACCGCGGAGGAGGACACCTGTCCACAGGAACCCTAACCGTAGTCACGGACGAGGACGGCAAGCTGTGCT
GTCTTCAAGCCAGGTGGGAGTGGGCTGACTGGAGCTAACTTCAGGACTGCATGAGTCGAGCGGTAAC
GAGACACAAAGAAGTGAGCAAGCTACTGGATGAAGTAATTCAGAGCATGAGACACAAATGA

ACGCGTACGCGGCCGCTCGAGCAGAAAACCTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	Sgfl-MluI
ACCN:	NM_027148
Insert Size:	831 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).
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_027148.3 , NP_081424.3
RefSeq Size:	1270 bp
RefSeq ORF:	831 bp
Locus ID:	69639
UniProt ID:	Q9D753
Cytogenetics:	3 C
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. EXOSC8 binds to ARE-containing RNAs (By similarity). [UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) uses an alternate in-frame splice junction at the 5' end of an exon compared to variant 1. The resulting isoform (2) has the same N- and C-termini but is shorter compared to isoform 1.</p>