

Product datasheet for MC217822

Exosc7 (BC052656) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Exosc7 (BC052656) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Exosc7
Synonyms:	2610002K22Rik; AV212732; mKIAA0116
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>BC052656 Red=Cloning site Blue=ORF Green=Tags(s)

TTTGTAAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGC**C

ATGGCGTCGGTGGCGCTAAGCGAGGCCGAGAAGGTCTACATCGTTCATGGAGTGCAGGAAGACCTTCGGG
TGGATGGCCGTGGCTGTGAGGACTACCGATGTGTTGAAGTAGAGACTGATGTGGTGTCTAACACCAGTGG
GTCTGCCAGAGTCAAGCTGGGTACACAGACATCTTGGTGGGAGTGAAAGCAGAAATGGGGACACCGAAG
CTGGAGAAACCGAATGAAGGCTACCTGGAGTCTTTGTTGACTGTTTCAGCCAATGCTACCCAGAATTTCG
AAGGGCGAGGAGGTGATGACCTTGGCACAGAGATTGCTAACCCCTCTACCGGATATTTAAACAACAAGAG
CAGCGTAGACCTGAGGTCCCTCTGCATCAGTCCGAGAGCACTGCTGGGTTCTATATGTGGATGTGCTG
CTGCTGGAATGTGGTGGGAATTTGTTTGTGCTATTTCCATTGCTGTAAAAGCTGCTCTCTTCGACACAA
GGATACCAAGGGTTCGTGTTCTGGAGGATGAAGAGGGGGCAAAGGACATTGAGCTGTCTGACGATCCTTA
TGACTGCATCCGACTGAGTGTAGAGAATGTCCCTGCATTGTCACCCTGTGCAAGATTGGCTGCCGGCAT
GTGGTAGATGCCACACTCCAAGAGGAGGCTGTCCCTGGCCAGCTTGTGGTGTGAGTACCCAGCAAGG
GAGTAGTGACATGCATGAGGAAAGTGGGAAAGGAAGCCTGGATCCTGAGAGCATCTTCGAGATGATGGA
GAGCAGCAAGCGAGTGGCAAGGTGCTGCACGTGTCCTTGACAGACCTTCTGCACAAGGAAGAAAGCCTG
GGCCCCAAGAGGCCGAGAGTCGGGTTCTGGGGTGA

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCTGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	SgfI-MluI
ACCN:	BC052656
Insert Size:	876 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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	BC052656 , AAH52656
RefSeq Size:	1030 bp
RefSeq ORF:	875 bp
Locus ID:	66446
Cytogenetics:	9 F4
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 (By similarity).[UniProtKB/Swiss-Prot Function]</p>