

Product datasheet for **RG210665**

EXOSC5 (NM_020158) Human Tagged ORF Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	EXOSC5 (NM_020158) Human Tagged ORF Clone
Tag:	TurboGFP
Symbol:	EXOSC5
Synonyms:	hRrp46p; p12B; RRP41B; RRP46; Rrp46p
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-AC-GFP (PS100010)
E. coli Selection:	Ampicillin (100 ug/mL)
ORF Nucleotide Sequence:	>RG210665 representing NM_020158 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGCC**

ATGGAGGAGGAGATGCATACTGACGCCAAAATCCGTGCTGAAAATGGAACAGGGTCCAGCCCTCGGGGTC
CTGGCTGCAGCCTCCGGCACTTTGCCTGCGAACAGAACCTGTGTGCGGGCCAGATGGCTCTGCTTCCTT
CCTGCAAGGTGACACCTCTGTCTGGCGGGTGTGTACGGGCCGGCCGAGGTGAAGTGCAGAAAGAGATT
TTCAACAAGGCCACACTCGAAGTATCCTGAGGCCGAAGATTGGGCTGCCTGGTGTGCAGAGAAGAGCC
GGGAGCGGCTGATCAGGAACACGTGCGAGGCGGTGGTGTGGGCACGTTGCACCCCGCACCTCCATCAC
CGTGGTGCTGCAGGTTGTCAGCGATGCCGGCTCTCTCCTGGCCTGTTGTCTGAATGCCGCCTGCATGGCA
TTGGTGGATGCAGGTGTGCCATGCGGGCTCTTCTGTGGGGTGCCTGCGCCCTGGACTCTGATGGGA
CCCTCGTGTGGATCCTACATCCAAGCAAGAAAAGGAGGCCCGGGCAGTCTGACCTTTGCCCTGGACAG
CGTGGAACGGAAGCTGTGATGTCCAGCACCAAGGGGCTCTACTCAGACACTGAGCTCCAGCAGTGCCTG
GCTGCGGCCAGGCCGCTTCGCAACACGTCTCCGTTTCTACCGGAATCGTGCAGAGGCGTTACTCCA
AGAGC

ACGCGTACGCGGCCGCTCGAG - GFP Tag - GTTTAA



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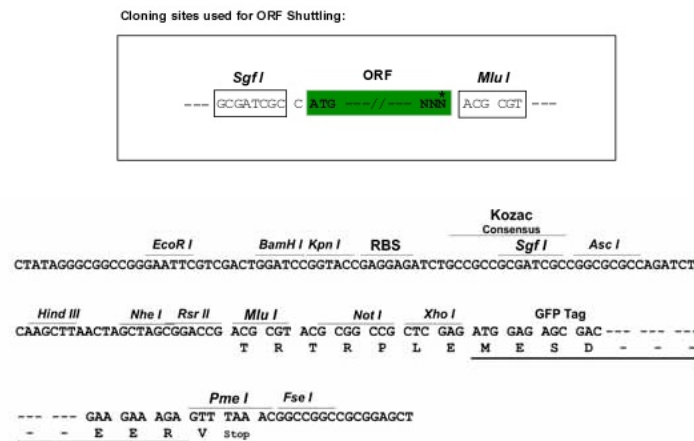
Protein Sequence: >RG210665 representing NM_020158
Red=Cloning site Green=Tags(s)

MEEEMHTDAKIRAENGTGSSPRGPGCSLRHFACQNLRSRPDGSASFQGDTSVLAVGYGPAEVKVSKEI
 FNKATLEVILRPKIGLPGVAEKSRRERLIRNTCEAVVLGTLHPRTSITVVLQVVS DAGSLLACCLNAACMA
 LVDAGVPMRALFCGVACALDSDGTLVLDPTSKQEKEARAVLTFALDSVERKLLMSSTKGLYSDTELQOCL
 AAAQAASQHVFRFYRESLQRRYSKS

TRTRPLE - GFP Tag - V

Restriction Sites: SgfI-MluI

Cloning Scheme:



ACCN: NM_020158

ORF Size: 705 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:

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_020158.3](#), [NP_064543.3](#)

RefSeq Size: 1006 bp

RefSeq ORF: 708 bp

Locus ID: 56915

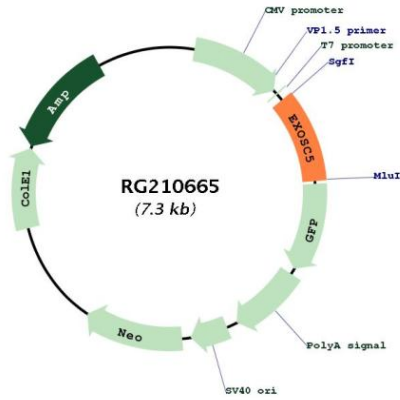
UniProt ID: [Q9NQ4](#)

Cytogenetics: 19q13.2

Protein Pathways: RNA degradation

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.[UniProtKB/Swiss-Prot Function]

Product images:



Circular map for RG210665