

## Product datasheet for **SC101005**

### EXOSC7 (NM\_015004) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	EXOSC7 (NM_015004) Human Untagged Clone
Tag:	Tag Free
Symbol:	EXOSC7
Synonyms:	EAP1; hRrp42p; p8; RRP42; Rrp42p
Mammalian Cell Selection:	None
Vector:	<u><a href="#">pCMV6-XL6</a></u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF within SC101005 sequence for NM_015004 edited (data generated by NextGen Sequencing)

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ATGGCGTCCGTGACGCTGAGCGAGGCGGAGAAGGTGTACATCGTGCATGGCGTCCAGGAA
GACCTCCGTGTGGATGGCCGTGGCTGTGAGGACTACCGATGTGTGCGAAGTGGAACTGAT
GTGGTGTCCAACACTAGTGGGTCCGCCAGGGTCAAGCTGGGTCACACAGACATCTTGGTG
GGAGTGAAAGCAGAAATGGGGACGCCGAAGCTGGAGAAACCAAATGAAGGCTACTTGGAG
TTCTTTGTTGATTGTTTCAGCCAGTGCTACCCCTGAATTTGAAGGTAGAGGAGGTGATGAC
CTTGGCACCAGATCGCTAACACCCTCTATCGGATATTTAAACAATAAAGCAGTGTGCGAC
TTAAAGACCCTCTGCATTAGTCCCTCGGGAGCACTGCTGGGTTCTCTATGTGGATGTGCTG
CTTCTGGAATGTGGTGGAAATTTGTTTGATGCCATTTCCATTGCTGTAAGGCTGCTCTC
TTCAATACAAGGATACCAAGGGTTCGAGTTTTGGAGGATGAAGAGGGGTCGAAGGACATT
GAATTGTCAGATGACCCTTATGACTGCATACGACTAAGTGTGGAGAATGTCCCCTGCATT
GTCACCTCTGTGCAAGATTGGCTATCGGCATGTGGTGGATGCTACTCTTCAGGAGGAGGCC
TGCTCGCTGGCCAGCTTGTGGTGTGCGGTGACCAGCAAGGGAGTTGTGACGTGCATGAGG
AAAGTGGGGAAGGGCAGCCTGGACCCAGAGAGCATCTTCGAGATGATGGAGACTGGCAAG
CGTGTGGGCAAGGTAAGTGCATGCCTCCTTGCAGAGTGTGTGTCACAAGGAAGAAAGCCTG
GGCCCAAGAGACAGAAAGTTGGATTCTGGGATGA

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Clone variation with respect to NM\_015004.3  
252 c=>t



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<b>5' Read Nucleotide Sequence:</b>	<p>&gt;OriGene 5' read for NM_015004 unedited</p> <pre>CCTTCCGCCGCCCGTTGCCGCTTATGGGCGTAGGCGTGTACGGTGGGAGGTCTATATAAG CAGAGCTCATTTAGGTGACACTATAGAATAACAAGTACTTGTCTTTTTGCAGCGGCCGC GAATTCGGCACGAGGGGGGACGTCGGCAGCATGGCGTCCGTGACGCTGAGCGAGGCGGA GAAGGTGTACATCGTGCATGGCGTCCAGGAAGACCTCCGTGTGGATGGCCGTGGCTGTGA GGACTACCGATGTGTGCGAAGTGGAACTGATGTGGTGTCCAACACTAGTGGTCCGCCAG GGTCAAGCTGGGTCACACAGACATCTTGGTGGGAGTGAAGCAGAAATGGGGACGCCGAA GCTGGAGAAACCAATGAAGGCTACTTGGAGTTCTTTGTTGATTGTTAGCCAGTGCTAC CCCTGAATTTGAAGGTAGAGGAGGTGATGACCTTGGCACCGAGATCGCTAACACCCTCTA TCGGATATTTAACAATAAAAGCAGTGTGCGACTTAAAGACCCTCTGCATTAGTCTCGGGA GCACTGCTGGGTCTCTATGTGGATGTGCTGCTTCTGGAATGTGGTGGAAATTTGTTTGA TGCCATTTCCATTGCTGTAAAGGCTGCTCTTTCATACAAGGATACCAAGGGTTCGAGTT TTGGAGGATGAAGAGGGTGAAGGACATTGAATTGTCAGATGACCTTATGACTGCATA CGACTAAGTGTGGAGAATGTCCCTGCATTGTCCTCTGTGCAAGATTGGGCTATCGCAT GTGGTGGATGCTACTCTTTCAGAGGAGCCCTGCTCGCTGGCCAGCTTGTGGTGTCCGTG ACCAGCAAGGGAGATGTGACCTGCATGANGAAAGTGGGAAAGGCAGCCTGGACCCGAGA GCATTTTCNATATAATGAGACTGCAAGCTGT</pre>
<b>3' Read Nucleotide Sequence:</b>	<p>&gt;OriGene 3' read for NM_015004 unedited</p> <pre>GTCGCTACCCNAATCAGAGTTGAGTTTTAAATCTTTTTTTTTTTTTTTTTTTTTTTTCC AGACCAAAAAATAGCCTTTAATTTTACATGTACAAATGCTGCTGTAATTCGTAACAGCG AAAAAATATATACGAACCGGTTTAAAAGGAAAAGTAAAAACAATCCACAGTTGAGCA GTTGATGTGCAAAATCATCCAGGAATCCAATTTCTGTCTTTGGGCCCCAGGCTTCTT CCTTGTGCACAACACTCTGCAAGGAGGCATGCAGTACCTTGCCACACGCTTGCCAGTCT CCATCATCTCGAAGATGCTCTCTGGGTCCAGGCTGCCCTTCCCCACTTTCCTCATGCACG TCACAACCTCCCTTGTGGTCACCGACACCAGCAAGCTGGCCAGCGAGCAGGCCTCCTCT GAAGAGTAGCATCCACCACATGCCGATAGCCAATCTTGACAGAGTGACAATGCAGGGGA CATTCTCCACACTTAGTCGTATGCAGTCATAAGGGTCACTGACAATTCATGTCCTTCC ACCCCTTTCATCCTCCAAAACCTCGAACCTTGGTATCCTTGTATTGAAGAGAGCAGCCT TTACAGCAATGGAAATGGCATCAAACAAATTTCCACCACATTCCAGAAGCAGCACATCCA CATAGAGAACCCAGCAGTGTCCCGAGGACTAATGCAGAGGGGTCTTAAGTCGACTGTC TTTTATTGTTAAATATCCGATANGAGGGTGGTAGCGATCTNCGTGCCAAGGTCATACCT CCTCTACCTTCAAATTCAGGGGTAGCACTGGCTGANNNCATCACAAAGACTCCNAGTAGC CCTTCATTGGTTTCTTCAGCTTCGGGGTCCCCATTTGGCTTTATTCCACCAAGATGTCT GGGTGACCAAGTTTGCNTGGCGAACCCCTATGGTTGAAACCAATCAGTTTCACCTCGA ACATGGGTAGCCTCCACGCCACGCCTTCN</pre>
<b>Restriction Sites:</b>	NotI-NotI
<b>ACCN:</b>	NM_015004
<b>Insert Size:</b>	1200 bp
<b>OTI Disclaimer:</b>	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).
<b>Components:</b>	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).

<b>Reconstitution Method:</b>	<ol style="list-style-type: none"><li>1. Centrifuge at 5,000xg for 5min.</li><li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li><li>3. Close the tube and incubate for 10 minutes at room temperature.</li><li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li><li>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.</li></ol>
<b>RefSeq:</b>	<a href="#">NM_015004.2</a> , <a href="#">NP_055819.1</a>
<b>RefSeq Size:</b>	1036 bp
<b>RefSeq ORF:</b>	876 bp
<b>Locus ID:</b>	23016
<b>UniProt ID:</b>	<a href="#">Q15024</a>
<b>Cytogenetics:</b>	3p21.31
<b>Domains:</b>	RNase_PH_C
<b>Protein Families:</b>	Stem cell - Pluripotency
<b>Protein Pathways:</b>	RNA degradation
<b>Gene Summary:</b>	<p>Non-catalytic component of the RNA exosome complex which has 3'-&gt;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]</p> <p>Transcript Variant: This variant (1) encodes the protein.</p>