

Product datasheet for PH301419

EXOSC7 (NM_015004) Human Mass Spec Standard

Product data:

Product Type:	Mass Spec Standards
Description:	EXOSC7 MS Standard C13 and N15-labeled recombinant protein (NP_055819)
Species:	Human
Expression Host:	HEK293
Expression cDNA Clone or AA Sequence:	RC201419
Predicted MW:	31.8 kDa
Protein Sequence:	>RC201419 protein sequence Red =Cloning site Green =Tags(s) MASVTLSAEKVVYIVHGVQEDLRVDGRGCEDYRCVEVETDVVSNTSGSARVKLGHTDILVGVKAEMGTPK LEKPNEGYLEFFVDCSASATPEFEGRGDDLGTIANTLYRIFNNKSSVDLKTLCISPREHCWLYVDVL LLECGNLFDAISIAVKAALFNTRIPRVRLVEDEEGSKDIELSDDPYDCIRLSVENVPCIVTLCKIGYRH VVDATLQEEACSLASLLVSVTSKGVVTCMRKVGKGLDPESIFEMMETGKRVGKVLHASLQSVLHKESL GPKRQKVGFLG TRTRPLEQKLISEEDLAANDILDYKDDDDKV
Tag:	C-Myc/DDK
Purity:	> 80% as determined by SDS-PAGE and Coomassie blue staining
Concentration:	>0.05 µg/µL as determined by microplate BCA method
Labeling Method:	Labeled with [U- ¹³ C ₆ , ¹⁵ N ₄]-L-Arginine and [U- ¹³ C ₆ , ¹⁵ N ₂]-L-Lysine
Buffer:	25 mM Tris-HCl, 100 mM glycine, pH 7.3
Storage:	Store at -80°C. Avoid repeated freeze-thaw cycles.
Stability:	Stable for 3 months from receipt of products under proper storage and handling conditions.
RefSeq:	<u>NP_055819</u>
RefSeq Size:	1059
RefSeq ORF:	873
Synonyms:	EAP1; hRrp42p; p8; RRP42; Rrp42p
Locus ID:	23016



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UniProt ID: [Q15024](#), [A0A024R2T3](#), [B2RDZ9](#)

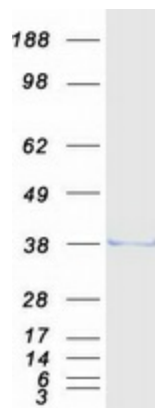
Cytogenetics: 3p21.31

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]

Protein Families: Stem cell - Pluripotency

Protein Pathways: RNA degradation

Product images:



Coomassie blue staining of purified EXOSC7 protein (Cat# [TP301419]). The protein was produced from HEK293T cells transfected with EXOSC7 cDNA clone (Cat# [RC201419]) using MegaTran 2.0 (Cat# [TT210002]).