

OriGene Technologies, Inc.

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Product datasheet for RC216215L3V

MRPL55 (NM_181463) Human Tagged ORF Clone Lentiviral Particle

Product data:

Droduct Turoe	Lentiviral Particles
Product Type:	
Product Name:	MRPL55 (NM_181463) Human Tagged ORF Clone Lentiviral Particle
Symbol:	MRPL55
Synonyms:	AAVG5835; L55nt; MRP-L55; PRO19675
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-Myc-DDK-P2A-Puro (PS100092)
Tag:	Myc-DDK
ACCN:	NM_181463
ORF Size:	384 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC216215).
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. <u>More info</u>
OTI Annotation:	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
RefSeq:	<u>NM 181463.2</u>
RefSeq Size:	774 bp
RefSeq ORF:	387 bp
Locus ID:	128308
UniProt ID:	<u>Q7Z7F7</u>
Cytogenetics:	1q42.13
MW:	15.1 kDa



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Gene Summary:Mammalian mitochondrial ribosomal proteins are encoded by nuclear genes and help in
protein synthesis within the mitochondrion. Mitochondrial ribosomes (mitoribosomes)
consist of a small 28S subunit and a large 39S subunit. They have an estimated 75% protein
to rRNA composition compared to prokaryotic ribosomes, where this ratio is reversed.
Another difference between mammalian mitoribosomes and prokaryotic ribosomes is that
the latter contain a 5S rRNA. Among different species, the proteins comprising the
mitoribosome differ greatly in sequence, and sometimes in biochemical properties, which
prevents easy recognition by sequence homology. This gene encodes a 39S subunit protein.
Multiple transcript variants encoding two different isoforms were identified through
sequence analysis. [provided by RefSeq, Jul 2008]

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