OriGene Technologies, Inc.
9620 Medical Center Drive, Ste 200
Rockville, MD 20850, US
Phone: +1-888-267-4436
https://www.origene.com
techsupport@origene.com
EU: info-de@origene.com
CN: techsupport@origene.cn

Product datasheet for RC218652L4V

SFRS5 (SRSF5) (NM_006925) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Product Name:	SFRS5 (SRSF5) (NM_006925) Human Tagged ORF Clone Lentiviral Particle
Symbol:	SFRS5
Synonyms:	HRS; SFRS5; SRP40
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-mGFP-P2A-Puro (PS100093)
Tag:	mGFP
ACCN:	NM_006925
ORF Size:	816 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC218652).
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.
RefSeq:	NM_006925.3
RefSeq Size:	1517 bp
RefSeq ORF:	819 bp
Locus ID:	6430
UniProt ID:	Q13243
Cytogenetics:	14q24.1
Protein Pathways:	Spliceosome
MW:	31.3 kDa

View online »

Gene Summary: The protein encoded by this gene is a member of the serine/arginine (SR)-rich family of pre-mRNA splicing factors, which constitute part of the spliceosome. Each of these factors contains an RNA recognition motif (RRM) for binding RNA and an RS domain for binding other proteins. The RS domain is rich in serine and arginine residues and facilitates interaction between different SR splicing factors. In addition to being critical for mRNA splicing, the SR proteins have also been shown to be involved in mRNA export from the nucleus and in translation. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Feb 2016]