

Product datasheet for **SC336650**

C18orf54 (NM_001288981) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	C18orf54 (NM_001288981) Human Untagged Clone
Tag:	Tag Free
Symbol:	C18orf54
Synonyms:	LAS2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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Fully Sequenced ORF: >SC336650 representing NM_001288981.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

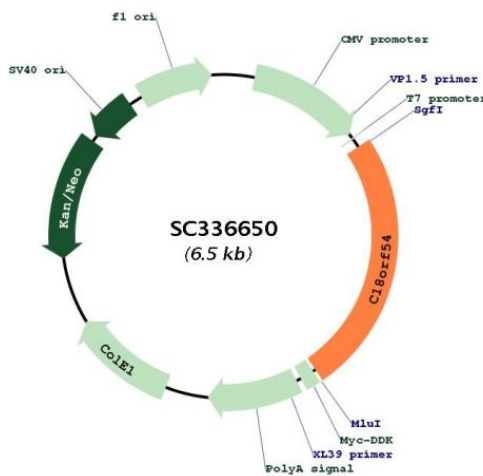
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Restriction Sites:

SgfI-MluI

Plasmid Map:



ACCN:	NM_001288981
Insert Size:	1602 bp
OTI Disclaimer:	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).
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:	<ol style="list-style-type: none">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_001288981.1
RefSeq Size:	5525 bp
RefSeq ORF:	1602 bp
Locus ID:	162681
UniProt ID:	Q8IYD9
Cytogenetics:	18q21.2
Protein Families:	Secreted Protein
MW:	60.3 kDa
Gene Summary:	Might play a role in cell proliferation.[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (2) differs in the 5' UTR, compared to variant 1. Both variants 1 and 2 encode the same isoform (a). Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.