

Product datasheet for **SC336731**

IRX4 (NM_001278635) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	IRX4 (NM_001278635) Human Untagged Clone
Tag:	Tag Free
Symbol:	IRX4
Synonyms:	IRXA3
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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Fully Sequenced ORF: >SC336731 representing NM_001278635.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

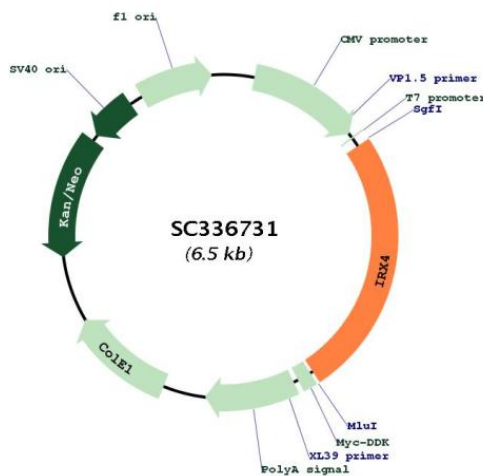
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Restriction Sites:

Sgfl-MluI

Plasmid Map:



ACCN:	NM_001278635
Insert Size:	1638 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_001278635.1
RefSeq Size:	2411 bp
RefSeq ORF:	1638 bp
Locus ID:	50805
UniProt ID:	P78413
Cytogenetics:	5p15.33
MW:	57 kDa
Gene Summary:	<p>Likely to be an important mediator of ventricular differentiation during cardiac development. [UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (4) represents the longest transcript. Both variants 2 and 4 encode the same protein. 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.</p>