

Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001271631
Insert Size:	1266 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).
OTI Annotation:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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:	<u>NM_001271631.1</u> , <u>NP_001258560.1</u>
RefSeq Size:	5724 bp
RefSeq ORF:	1266 bp
Locus ID:	12393
Cytogenetics:	17 21.33 cM
Gene Summary:	<p>This gene encodes a member of the runt domain-containing family of transcription factors. This protein is essential for osteoblastic differentiation and skeletal morphogenesis and acts as a scaffold for nucleic acids and regulatory factors involved in skeletal gene expression. The protein can bind DNA both as a monomer or, with more affinity, as a subunit of a heterodimeric complex. Transcript variants that encode different protein isoforms result from the use of alternate promoters as well as alternate splicing. [provided by RefSeq, Sep 2015]</p> <p>Transcript Variant: This variant (6) represents use of a proximal promoter. It lacks two alternate exons including the 5' UTR and a portion of the 5' coding region, initiates translation in an alternate 5' segment, and lacks two internal in-frame coding exons, compared to variant 1. The encoded isoform (4) has a distinct N-terminus and is shorter than isoform 1. 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>