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Product datasheet for SC330526

ZNF195 (NM_001256823) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	ZNF195 (NM_001256823) Human Untagged Clone
Tag:	Tag Free
Symbol:	ZNF195
Synonyms:	HRF1; ZNFP104
Vector:	pCMV6-Entry (PS100001)
Fully Sequenced ORF:	>SC330526 representing NM_001256823. Blue=Insert sequence Red=Cloning site Green=Tag(s) ATGGCTGGTGCTCAGACTCTGTTGACGTTCAGGGATGTGGCCATAGAATTCTCCCTGGAGGAGTGGAAA TGCCTGGACCTCGCTCAGCAGAATTTGTACAGGGATGTGATGTTGGAGAACTACAGAAACTTGTTCTCC GTTGGTCTCACTGTCTGTAAGCCAGGCCTGATCACCTGCCTGGAGCAACGAAAAGAGCCCTGGAATGTG AAGAGACAGGAGGCAGCAGACGGACATCCAGGTATTTTCTTTGTGGTTACCATGGAAATTATATAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_001256823
Insert Size:	273 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:	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_001256823.1

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RefSeq Size:	3203 bp
RefSeq ORF:	273 bp
Locus ID:	7748
UniProt ID:	O14628
Cytogenetics:	11p15.4
Protein Families:	Transcription Factors
MW:	10.4 kDa
Gene Summary:	This gene encodes a protein belonging to the Krueppel C2H2-type zinc-finger protein family. These family members are transcription factors that are implicated in a variety of cellular processes. This gene is located near the centromeric border of chromosome 11p15.5, next to an imprinted domain that is associated with maternal-specific loss of heterozygosity in Wilms' tumors. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Feb 2012] Transcript Variant: This variant (8) differs in its 5' UTR, uses an alternate start codon, and lacks two alternate exons but includes an additional exon that causes a frameshift in the 3' coding region, compared to variant 1. The encoded isoform (7) has distinct N- and C-termini 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.