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Product datasheet for SC206662

C9orf75 (TPRN) (NM_173691) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Symbol:	C9orf75
Synonyms:	C9orf75; DFNB79; FLJ90254; MGC131933; RP11-350O14.7
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_173691
Insert Size:	525 bp
Insert Sequence:	>SC206662 3'UTR clone of NM_173691 The sequence shown below is from the reference sequence of NM_173691. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC TTCCGCAGCGAGCCAGCCCTGTATTTCTGAGCCCAGCACTGCCAGGACCAAGGCTGAGCCCAGCTGTGG GAGTCCCGGAAGCTGGGCAGTAGCCAGGGACTACTGCACCCGCTTCTGCCTTGTTTGGCCTCACTGTAT CCCACCCACCCCTCCTGGCCCTGGAAGCAGCTAGGGTGCCTCCTGCCATCGGGGCCAGGTCTGGGTCTC ACTCCCCGGCCCTGATTTGGGAGGGTCCAAGGGGGAAGTGGGGTGGGGAACTGCCTGTGGGTGAGTGCC AGGGGCCTGCTGGGTGGTGGCCATCTGCGACCCGGCAGGGGGCTGTGCAGATTCTGCACCTGGCCATTC CCTGTCCTGTCTCCTCAGCCTGCCTCACAGTGGCCATGGGGTGTCGGGGTGAAGGGCTGTCCCAGCTAC TTGTCCTCTGCAGGACCCTAAGCCCCTGCCCGCAGCCCACATGCCCTCTGTGATGAGTGGCGTCTTTCC TGCCTCTGATGATGGACTCAATAAACAGCACTGGACAAGGCT ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG
Restriction Sites:	SgfI-MluI
OTI Disclaimer:	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).

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Components:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	NM_173691.3
Summary:	This locus encodes a sensory epithelial protein. It was defined by linkage analysis in three Pakistani families to lie between D9S1818 (centromeric) and D9SH6 (telomeric). Mutations at this locus have been associated with autosomal recessive deafness. [provided by RefSeq, Oct 2010]
Locus ID:	286262
MW:	18.9