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Product datasheet for SC335941

KRT78 (NM_001300814) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	KRT78 (NM_001300814) Human Untagged Clone
Tag:	Tag Free
Symbol:	KRT78
Synonyms:	CK-78; K5B; K78; Kb40
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC335941 representing NM_001300814. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGGAAGGTCATGAGGCTTCCCCTGCCCAGGTTGGGCAGGGGGACAGGGGAAAGGTGCGGTTCCTGGAG CAGCAGAACAAGGTCCTGGAGACGAAGTGGCATCTGCTGCAGCAACAGGGGTTGAGTGGCAGCCAGCAG GGCCTGGAGCCTGTCTTTGAGGCCTGCCTGGATCAGCTCAGGAAGCAGCTGGAGCAGCTCCAGGGAGAA CGAGGGGCTCTGGATGCTGAGTTGAAGGCCTGCCGGGACCAGGAGGAGGAGTATAAGTCCAAGTATGAG GAGGAGGCCCACAGGCGTGCCACACTTGAGAACGACTTTGTGGTCCTCAAGAAGGATGTGGATGGGGTT TTCCTGAGCAAGATGGAGTTGGAGGGCAAGCTGGAGGCTCTGAGAGAGTACCTCTACTTCTTGAAGCAT CTGAATGAAGAAGAGCTGGGCCAGCTCCAGACCCAGGCCAGCGACACGTCTGTGGTGCTGTCCATGGAC AACAACCGCTACCTGGACTTCAGCAGCATCATCACTGAGGTCCGCGCCCGGTACGAGGAGATCGCCCGG AGCAGCAAGGCTGAGGCTGAGGCCTTGTACCAGACCAAGTACCAGGAACTTCAGGTGTCTGCCCAGCTT CATGGGGACAGGATGCAGGAAACGAAAGTCCAGATCTCTCAGCTACACCAAGAGATTCAGAGGCTGCAG AGTCAGACTGAGAACCTCAAGAAGCAGAACGCCAGCCTGCAGGCCGCCATCACTGATGCTGAGCAGCGT GGGGAGCTGGCCCTCAAGGACGCTCAGGCCAAGGTGGACGAGCTGGAGGCTGCTCTGAGGATGGCCAAG CAGAACCTGGCCCGGCTGCTGTGCGAGTACCAGGAGCTGACGAGCACGAAGCTTTCCCTGGATGTGGAG ATTGCCACTTACCGCAGGCTGCTGGAGGGCGAGGAGTGCAGGATGTCTGGGGAGTGCACCAGCCAGGTC ACTATCTCCTCGGTGGGAGGCAGCGCTGTCATGTCTGGAGGAGTTGGTGGAGGCTTGGGGAGCACTTGT GGACTCGGTAGTGGGAAAGGCAGCCCTGGGTCCTGCTGCACCAGCATTGTGACTGGAGGCTCCAACATC ATTCTGGGCTCTGGGAAGGACCCTGTTTTGGATTCCTGCTCTGTGTCTGGCTCCAGCGCTGGCTCCAGC TGCCACACCATCCTGAAGAAGACAGTTGAGTCGAGTCTGAAGACATCCATCACCTACTGA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	SgfI-MluI

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ACCN:	NM_001300814
Insert Size:	1233 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_001300814.1
RefSeq Size:	2572 bp
RefSeq ORF:	1233 bp
Locus ID:	196374
UniProt ID:	Q8N1N4
Cytogenetics:	12q13.13
MW:	45 kDa
Gene Summary:	This gene is a member of the type II keratin gene family and encodes a protein with an intermediate filament domain. Keratins are the major structural proteins in epithelial cells, forming a cytoplasmic network of 10 to 12 nm wide intermediate filaments and creating a scaffold that gives cells the ability to withstand mechanical and non-mechanical stresses. The genes of the type II keratin family are located as a gene cluster at 12p13.13. Four pseudogenes of this gene family have been identified. [provided by RefSeq, Jul 2008] Transcript Variant: This variant (2) differs in the 5' UTR, lacks a portion of the 5' coding region, and initiates translation at an alternate start codon compared to variant 1. The encoded isoform (2) 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.