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Product datasheet for SC331222

ASCC1 (NM_001198798) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	ASCC1 (NM_001198798) Human Untagged Clone
Tag:	Tag Free
Symbol:	ASCC1
Synonyms:	ASC1p50; CGI-18; p50; SMABF2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC331222 representing NM_001198798. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGGAAGTTCTGCGTCCACAGCTTATAAGAATTGATGGCCGGAATTACAGGAAGAATCCAGTCCAAGAA CAGACCTATCAACATGAAGAAGATGAAGAGGACTTCTATCAAGGCTCCATGGAGTGTGCTGATGAGCCC TGTGATGCCTACGAGGTGGAGCAGACCCCACAAGGATTCCGGTCTACTTTGAGGGCCCCCAGCTTGCTC TATAAGCATATAGTTGGAAAGAGAGGGGACACTAGGAAGAAAATAGAAATGGAGACCAAAACTTCTATT AGCATTCCTAAACCTGGACAAGACGGGGAAATTGTAATCACTGGCCAGCATCGAAATGGTGTAATTTCA GCCCGAACACGGATTGATGTTCTTTTGGACACTTTTCGAAGAAAGCAGCCCTTCACTCACTTCCTTGCC TTTTTCCTCAATGAAGTTGAGGTTCAGGAAGGATTCCTGAGATTCCAGGAGGAAGTACTGGCGAAGTGC TCCATGGATCATGGGGTTGACAGCAGCATTTTCCAGAATCCTAAAAAGCTTCATCTAACTATTGGGATG TTGGTGCTTTTGAGTGAGGAAGAGATCCAGCAGACATGTGAGATGCTACAGCAGTGTAAAGAGGAATTC ATTAATGATATTTCTGGGGGTAAACCCCTAGAAGTGGAGATGGCAGGGATAGAATACATGAATGATGAT CCTGGCATGGTGGATGTTCTTTACGCCAAAGTCCATATGAAAGATGGCTCCAACAGGCTACAAGAATTA GTTGATCGAGTGCTGGAACGTTTTCAGGCATCTGGACTAATAGTGAAAGAGTGGAATAGTGTGAAACTG CATGCTACAGTTATGAATACACTATTCAGGAAAGACCCCAATGCTGAAGGCAGGTACAATCTCTACACA GCGGAAGGCAAATATATCTTCAAGGAAAGAGAATCATTTGATGGCCGAAATATTTTAAAGTTGTTTGAG AACTTCTACTTTGGCTCCCTAAAGCTGAATTCAATTCACATCTCTCAGAGGTTCACCGTAGACAGCTTT GGAAACTACGCTTCCTGTGGACAAATTGACTTCTCCTGA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	SgfI-MluI
ACCN:	NM_001198798

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Insert Size:	1074 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_001198798.2
RefSeq Size:	2683 bp
RefSeq ORF:	1074 bp
Locus ID:	51008
UniProt ID:	Q8N9N2
Cytogenetics:	10q22.1
MW:	41.2 kDa
Gene Summary:	This gene encodes a subunit of the activating signal cointegrator 1 (ASC-1) complex. The ASC-1 complex is a transcriptional coactivator that plays an important role in gene transactivation by multiple transcription factors including activating protein 1 (AP-1), nuclear factor kappa-B (NF-kB) and serum response factor (SRF). The encoded protein contains an N-terminal KH-type RNA-binding motif which is required for AP-1 transactivation by the ASC-1 complex. Mutations in this gene are associated with Barrett esophagus and esophageal adenocarcinoma. Alternatively spliced transcripts encoding multiple isoforms have been observed for this gene. [provided by RefSeq, Dec 2011] Transcript Variant: This variant (4) differs in the 5' UTR and lacks three exons in the coding region, which results in a translational frameshift, compared to variant 1. Variants 2 and 4 encode the same isoform (b) which is shorter and has a distinct C-terminus, compared to isoform a. 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.