

Product datasheet for **SC332128**

ARNTL2 (NM_001248005) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: ARNTL2 (NM_001248005) Human Untagged Clone
Tag: Tag Free
Symbol: ARNTL2
Synonyms: bHLHe6; BMAL2; CLIF; MOP9; PASD9
Vector: pCMV6-Entry (PS100001)
Fully Sequenced ORF: >SC332128 representing NM_001248005.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

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ATGGCGCGGAAGAGGAGGCTGCGGCGGGAGGTGAGGTTGCCGGTGGCGAGGCGACGGCCCCAGGTAAA
GTGTTGAGAGAGGAGAACCAGTGCATTGCTCCTGTGGTTCCAGCCGCGTGAGTCCAGGGACAAGACCA
ACAGCTATGGGGTCTTTCAGCTCACACATGACAGAGTTTCCACGAAAACGCAAAGGAAGTATTGAGAC
CCATCCCAAGAAGCTCATAGCCAACTGAAAAGCGGAGGAGAGATAAAATGAATAACCTGATTGAAGAA
CTGTCTGCAATGATCCCTCAGTGAACCCCATGGCGCGTAACTGGACAACTTACAGTTTTAAGAATG
GCTGTTCAACACTTGAGATCTTTAAAAGGCTTGACAAATCTTATGTGGGAAGTAATTATAGACCATCA
TTTCTTCAGGATAATGAGCTCAGACATTTAATCCTTAAGACTGCAGAAGGCTTCTTATTTGTGGTTGGA
TGTGAAAGAGGAAAAATTCTCTTCGTTTCTAAGTCAGTCTCCAAAATACTTAATTATGATCAGGCTAGT
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TCTTTTGTATTTACCAAGAGAAAAAGCTAATAGATGCCAAAAGTGGTTTGAAGTTCACAGTAATCTC
CACGCTGGAAGGACACGTGTGTATTCTGGCTCAAGACGATCTTTTTCTGTCCGATAAAGAGTTGTAAA
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TATGTAGATCAAAGGCAACAGCGATTTTAGGATATCTGCCTCAGGAACTTTTGGAACTTCTTGTAT
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TTTAGTTTACAAATCCTTGGACAAAAGAACTGGAATATATTGTATCTGTCAACACTTTAGTTTTGGGA
CATAGTGAGCCTGGAGAAGCATATTTTACCTTGTAGCTCTCAATCATCAGAAGAAATCCTCTAGACAG
TCCTGTATGAGTGTACCTGGAATGTCTACTGGAACAGTACTTGGTCTGGTAGTATTGGAACAGATATT
GCAAATGAAATCTGGATTTACAGAGGTTACAGTCTTCTTACATACCTTGATGATTCGAGTCCAACAGGT
TTAATGAAAGATACTCATACTGTAACCTGCAGGAGTGTGATGGTGCACAGTTGGATTTTCGATGCCCTAT
GTGACAATGATGACACAGCCATGGCTGCATTTATGA
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Restriction Sites: SgfI-MluI
ACCN: NM_001248005



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Insert Size:	1623 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:	<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:	NM_001248005.1
RefSeq Size:	7191 bp
RefSeq ORF:	1623 bp
Locus ID:	56938
UniProt ID:	Q8WYA1
Cytogenetics:	12p11.23
Protein Families:	Druggable Genome, Transcription Factors
MW:	60.4 kDa
Gene Summary:	<p>This gene encodes a basic helix-loop-helix transcription factor belonging to the PAS (PER, ARNT, SIM) superfamily. The PAS proteins play important roles in adaptation to low atmospheric and cellular oxygen levels, exposure to certain environmental pollutants, and diurnal oscillations in light and temperature. This protein forms a transcriptionally active heterodimer with the circadian CLOCK protein, the structurally related MOP4, and hypoxia-inducible factors, such as HIF1alpha. Consistent with its role as a biologically relevant partner of circadian and hypoxia factors, this protein is coexpressed in regions of the brain such as the thalamus, hypothalamus, and amygdala. Alternatively spliced transcript variants encoding different isoforms have been described for this gene. [provided by RefSeq, Oct 2011]</p> <p>Transcript Variant: This variant (5) uses an alternate in-frame donor splice site, lacks two consecutive in-frame coding exons, and another exon in the 3' region that causes a frame-shift, compared to variant 1. This results in a shorter isoform (3) with a distinct C-terminus compared to 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>