

## Product datasheet for **SC318828**

### ALP (PDLIM3) (NM\_001114107) Human Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** ALP (PDLIM3) (NM\_001114107) Human Untagged Clone  
**Tag:** Tag Free  
**Symbol:** PDLIM3  
**Synonyms:** ALP  
**Vector:** pCMV6 series

**Fully Sequenced ORF:** >NCBI ORF sequence for NM\_001114107, the custom clone sequence may differ by one or more nucleotides

```
ATGCCCCAGACGGTGATCCTCCCGGGCCCTGCGCCCTGGGGCTTCAGGCTCTCAGGGGGC
ATAGACTTCAACCAGCCTTTGGTCATCACCAGGATTACACCAGGAAGCAAGGCGGCAGCT
GCCAACCTGTGCTCCTGGAGATGTCATCCTGGCTATTGACGGCTTTGGGACAGAGTCCATG
ACTCATGCTGATGCGCAGGACAGGATTAAGCAGCAGCTCACCAGCTGTGTCTCAAATTT
GACAGGGGAGAACTCACTTATGGTCTCCACAAGTATCTGAAGATGGGAAAGCCCATCCT
TTCAAATCAACTAGAATCAGAACCACAGGAATCAAACCCATTGGTACCGCGCACAAAC
AGAAGGGCCCAGCCTTTTGTTCAGCTGCAAACATTGATGACAAAAGACAGGTAGTGAGC
GCTTCCTATAACTCGCCAATTGGGCTCTATTCAACTAGCAATATACAAGATGCGCTTCAC
GGACAGCTGCGGGGTCTCATTCTAGCTCACCTCAAACGAGCCACAGCCTCGGTGCC
CCCGAGTCGGACGTGTACCGGATGCTCCACGACAATCGGAATGAGCCACACAGCCTCGC
CAGTCGGGCTCCTTCAGAGTGCTCCAGGGAATGGTGGACGATGGCTCTGATGACCGTCCG
GCTGGAACGCGGAGTGTGAGAGCTCCGGTGACGAAAGTCCATGGCGGTTTCAGGCGGGCA
CAGAGGATGCCGCTCTGTGACAAATGTGGGAGTGGCATAAGTCGGTGTGTGGTGAAGGCG
CGGGATAAGTACCGGCACCCTGAGTGCTTCGTGTGTGCCGACTGCAACCTCAACCTCAAG
CAAAGGGCTACTTTCATAGAAGGGGAGCTGTACTGCGAAACCCACGCAAGAGCCCGC
ACAAAGCCCCAGAGGGCTATGACACGGTCACTCTGTATCCCAAAGCT
```

**Restriction Sites:** Please inquire  
**ACCN:** NM\_001114107  
**Insert Size:** 2709 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).



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<b>OTI Annotation:</b>	This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"><li>1. Centrifuge at 5,000xg for 5min.</li><li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li><li>3. Close the tube and incubate for 10 minutes at room temperature.</li><li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li><li>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.</li></ol>
<b>RefSeq:</b>	<a href="#">NM_001114107.1</a> , <a href="#">NP_001107579.1</a>
<b>RefSeq Size:</b>	2709 bp
<b>RefSeq ORF:</b>	2709 bp
<b>Locus ID:</b>	27295
<b>UniProt ID:</b>	<a href="#">Q53GG5</a>
<b>Cytogenetics:</b>	4q35.1
<b>Gene Summary:</b>	<p>The protein encoded by this gene contains a PDZ domain and a LIM domain, indicating that it may be involved in cytoskeletal assembly. In support of this, the encoded protein has been shown to bind the spectrin-like repeats of alpha-actinin-2 and to colocalize with alpha-actinin-2 at the Z lines of skeletal muscle. Alternatively spliced transcript variants encoding multiple isoforms have been observed for this gene. Aberrant alternative splicing of this gene may play a role in myotonic dystrophy. [provided by RefSeq, Apr 2012]</p> <p>Transcript Variant: This variant (2) lacks two consecutive exons in the coding region and contains an alternate coding exon, but maintains the reading frame, compared to variant 1. The encoded isoform (b) is shorter than 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.</p>