

Product datasheet for **MC216151**

Pdlim7 (NM_001114088) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Pdlim7 (NM_001114088) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Pdlim7
Synonyms:	LMP
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin



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Fully Sequenced ORF: >MC216151 representing NM_001114088
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGGATCGCC**

ATGGATTCCTCAAGGTGGTCTGGAAGGGCCAGCCCCTTGGGGCTTCCGCTGCAAGGGGCAAGGACT
 TCAATGTGCCCTCTCTATCTCTCGGCTCACGCCGAGGCAAAGCTGCACAGGCCGGTGTGGCTGTGGG
 AGACTGGTACTGAATATTGACGGTGAGAACCGGGCAGCCTCACGCACATCGAAGCCCAGAACAGATC
 CGCGCCTGTGGGAGCGCCTCAGCCTGGGTCTTAGCAGAGCCAGCCTGTTAGAGCAAACCACAGAAGG
 CCCTGACCCCTCCCGCCAGCCCGGAGGTACTTTTGCACCAAGCGCCTCCCTCAACAAGACGGCCCG
 GCCCTTCGGGGCACCCACCTACTGACAGCACCTGCGGCAGAATGGACAGTTGCTCAGACAGCCGGTC
 CCCGATGCCAGCAAGCAGCGGCTGATGGAGGATACCGAAGACTGGCGGCCGCGCCGGGGACAGGCCAGT
 CCCGCTCCTTCGCATCCTTGCCACCTCACGGGCACAGAGTTTCAAGACCCGGATGAGGAATTCAT
 GAAGAAGTCAAGCCAGGTGCCCAGGACAGAAGCCCGAGCCCGAGCCTCAACTATACCCAGGAATCCTGG
 CCTGGCCCCACCTCCAGCCCAAGCCGCCCCACCTGGGGCTGTGGATCCTGCATTTGCTGAGCGCT
 ATGCCCCAGACAAAACAGCACAGTGTGACCCGGCACAGCCAGCCAGCCACCCACGCCTCTGCAGAA
 CCGCACCTCCATAGTGCAGGCCGAGCTGGAGGGGACAGGAGGGGGCAGCAACAACGGCAAGACTCCT
 GTATGCCACCAAGTCCACAAGATCATCCGCGCCGCTACCTGGTAGCACTGGGCCACGCATACCATCCCG
 AGGAGTTTGTGTGCAGCCAGTGTGGAAGGTCTGGAAGAGGGTGGCTTCTTCGAGGAGAAGGGAGCTAT
 CTTTTGCCCTCCTGCTATGATGTGCGCTATGCACCAACTGTGCCAAATGCAAGAAGAAGTCACTGGA
 GAGATCATGCATGCTCTGAAGATGACCTGGCACGTCCATTGCTTACCTGTGCTGCCTGCAAAACGCCAA
 TTCGCAACAGAGCCTTTTACATGGAAGAAGGGCCCTACTGCGAGCGAGACTATGAGAAGATGTTTGG
 CACAAAATGTCGAGGCTGTGACTTCAAGATTGATGCTGGAGACCCTTCCCTGGAAGCGCTGGGCTTCAGC
 TGGCATGACACATGCTTTGTTTGCGAATATGTGAGATCAACTTGAAGGAAAGACCTTCTACTCCAAGA
 AGGACAAGCCCTCTGCAAGAGCCACGCCTTCTCACGT**TGA**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI

ACCN: NM_001114088

Insert Size: 1374 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_001114088.2](#), [NP_001107560.1](#)

RefSeq Size: 2626 bp

RefSeq ORF: 1374 bp

Locus ID: 67399

UniProt ID: [Q3TJD7](#)

Cytogenetics: 13 B1

Gene Summary: May function as a scaffold on which the coordinated assembly of proteins can occur. May play a role as an adapter that, via its PDZ domain, localizes LIM-binding proteins to actin filaments of both skeletal muscle and nonmuscle tissues. Involved in both of the two fundamental mechanisms of bone formation, direct bone formation (e.g. embryonic flat bones mandible and cranium), and endochondral bone formation (e.g. embryonic long bone development). Plays a role during fracture repair. Involved in BMP6 signaling pathway (By similarity).[UniProtKB/Swiss-Prot Function]
Transcript Variant: This variant (a) represents the longest transcript and encodes the longest 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.