

Product datasheet for SC331729

OriGene Technologies, Inc.

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HNRPDL (HNRNPDL) (NM_001207000) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: HNRPDL (HNRNPDL) (NM_001207000) Human Untagged Clone

Tag: Tag Free
Symbol: HNRPDL

Synonyms: HNRNP; HNRPDL; JKTBP; JKTBP2; laAUF1; LGMD1G; LGMDD3

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF: >SC331729 representing NM_001207000.

Blue=Insert sequence Red=Cloning site Green=Tag(s)

ATGGAGGTCCCGCCCAGGCTTTCCCATGTGCCGCCGCCATTGTTCCCCTCCGCTCCCGCTACTTTAGCC CCCAGCTCCGCCCGGCAGGGGGCGCCGGGCCCAGCCCCACGTCACCGCCCAGCAGCCCTCCCGATTG GCGGGCGGGCGCTATAAAGGGAGGCGCAGGCGGCCCCGGATCTCTTCCGCCGCCATTTTAAATCC AGCTCCATACAACGCTCCGCCGCCGCTGCTGCCGCGACCCGGACTGCGCGCCAGCACCCCCCTGCCGAC AGCTCCGTCACTATGGAGGATATGAACGAGTACAGCAATATAGAGGGAATTCGCAGAGGGATCCAAGATC AACGCGAGCAAGAATCAGCAGGATGACGGTAAAATGTTTATTGGAGGCTTGAGCTGGGATACAAGCAAA AAAGATCTGACAGAGTACTTGTCTCGATTTGGGGAAGTTGTAGACTGCACAATTAAAACAGATCCAGTC ACTGGGAGATCAAGAGGATTTGGATTTGTGCTTTTCAAAGATGCTGCTAGTGTTGATAAGGTTTTGGAA CTGAAAGAACACAAACTGGATGGCAAATTGATAGATCCCAAAAGGGCCAAAGCTTTAAAAGGGAAAGAA CCTCCCAAAAAGGTTTTTGTGGGTGGATTGAGCCCGGATACTTCTGAAGAACAAATTAAAGAATATTTT GGAGCCTTTGGAGAGATTGAAAATATTGAACTTCCCATGGATACAAAAACAAATGAAAGAAGAGGATTT TGTTTTATCACATATACTGATGAAGAGCCAGTAAAAAAATTGTTAGAAAGCAGATACCATCAAATTGGT TCTGGGAAGTGTGAAATCAAAGTTGCACAACCCAAAGAGGTATATAGGCAGCAACAGCAACAACAAAAA GGTGGAAGAGGTGCTGCAGCTGGTCGACGAGGTGGTACGAGGGGTCGTGGCCGAGGCCAACAGAGCACT TATGGCAAGGCATCTCGAGGGGGTGGCAATCACCAAAACAATTACCAGCCATAC<mark>TAA</mark>

Restriction Sites: Sgfl-Mlul

ACCN: NM 001207000

Insert Size: 1092 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: <u>NM 001207000.1</u>

 RefSeq Size:
 3986 bp

 RefSeq ORF:
 1092 bp

 Locus ID:
 9987

 UniProt ID:
 014979

 Cytogenetics:
 4q21.22

 MW:
 40 kDa

Gene Summary:

This gene belongs to the subfamily of ubiquitously expressed heterogeneous nuclear ribonucleoproteins (hnRNPs). The hnRNPs are RNA binding proteins and they complex with heterogeneous nuclear RNA (hnRNA). These proteins are associated with pre-mRNAs in the nucleus and appear to influence pre-mRNA processing and other aspects of mRNA metabolism and transport. While all of the hnRNPs are present in the nucleus, some seem to shuttle between the nucleus and the cytoplasm. The hnRNP proteins have distinct nucleic acid binding properties. The protein encoded by this gene has two RRM domains that bind to RNAs. Three alternatively spliced transcript variants have been described for this gene. One of the variants is probably not translated because the transcript is a candidate for nonsense-mediated mRNA decay. The protein isoforms encoded by this gene are similar to its family member HNRPD. [provided by RefSeq, May 2011]

Transcript Variant: This variant (4) lacks an alternate in-frame exon compared to variant 3. The resulting isoform (b) has the same N- and C-termini but is shorter 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.