EMPOWER YOUR RESEARCH

## Product datasheet for SC335634

## Dematin (DMTN) (NM_001302817) Human Untagged Clone

## Product data:

## Product Type:

Expression Plasmids
Dematin (DMTN) (NM_001302817) Human Untagged Clone
Tag Free
DMTN
DMT; EPB49
Neomycin
pCMV6-Entry (PS100001)
Kanamycin ( $25 \mathrm{ug} / \mathrm{mL}$ )
>SC335634 representing NM_001302817.
Blue=Insert sequence Red=Cloning site Green=Tag(s)
GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGGAACGGCTGCAGAAGGCCAAGATGGACAATCAGGTGCTGGGCTACAAGGACCTGGCTGCCATCCCC AAGGACAAGGCCATCCTGGACATCGAGCGGCCCGACCTCATGATCTACGAGCCTCACTTCACTTATTCC CTCCTGGAACACGTGGAGCTGCCTCGCAGCCGCGAGGTGTGGGCGGACAGCCGGTCGCCTGGAATCATC TCTCAGGCCTCGGCCCCCAGAACCACTGGAACCCCCCGGACCAGCCTGCCCCATTTCCACCACCCTGAG ACCTCCCGCCCAGATTCCAACATCTACAAGAAGCCTCCCATCTATAAGCAGAGAGAGTCCGTGGGAGGC AGCCCTCAGACCAAGCACCTCATCGAGGATCTCATCATCGAGTCATCCAAGTTTCCTGCAGCCCAGCCC CCAGACCCCAACCAGCCAGCCAAAATCGAAACCGACTACTGGCCATGCCCCCCGTCTCTGGCTGTTGTG GAGACAGAATGGAGGAAGCGGAAGGCGTCTCGGAGGGGAGCAGAGGAAGAGGAGGAGGAGGAAGATGAC GACTCTGGAGAGGAGATGAAGGCTCTCAGGGAGCGTCAGAGAGAGGAACTCAGTAAGGTTACTTCCAAC TTGGGAAAGATGATCTTGAAAGAAGAGATGGAAAAGTCATTGCCGATCCGAAGGAAAACCCGCTCTCTG CCTGACCGGACACCCTTCCATACCTCCTTGCACCAGGGAACGTCTAAATCTTCCTCTCTCCCCGCCTAT GGCAGGACCACCCTGAGCCGGCTACAGTCCACAGAGTTCAGCCCATCAGGGAGTGAGACTGGAAGCCCA GGCCTGCAGAACGGAGAGGGCCAGAGGGGGAGGATGGACCGGGGGAACTCCCTGCCCTGTGTGCTGGAG CAGAAGATCTATCCCTATGAAATGCTAGTGGTGACCAACAAGGGGCGAACCAAGCTGCCACCGGGGGTG GATCGGATGCGGCTTGAGAGGCATCTGTCTGCCGAGGACTTCTCAAGGGTATTTGCCATGTCCCCTGAA GAGTTTGGCAAGCTGGCTCTGTGGAAGCGGAATGAGCTCAAGAAGAAGGCCTCTCTCTTCTGA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:

Product Name:

## Tag:

Symbol:
Synonyms:
Mammalian Cell
Selection:
Vector:
E. coli Selection:

Fully Sequenced ORF:
群

Sgfl-Mlul

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## Plasmid Map:



## ACCN:

Insert Size:

## OTI Disclaimer:

Components:
NM_001302817
1098 bp
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).
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 $5,000 \times g$ for 5 min .
2. Carefully open the tube and add 100 ul 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 $-20^{\circ} \mathrm{C}$. The DNA is stable for at least one year from date of shipping when stored at $-20^{\circ} \mathrm{C}$.

| RefSeq: | NM 001302817.2 |
| :--- | :--- |
| RefSeq Size: | 2539 bp |
| RefSeq ORF: | 1098 bp |
| Locus ID: | 2039 |
| UniProt ID: | $\underline{Q 08495}$ |
| Cytogenetics: | $8 p 21.3$ |
| MW: | 41.6 kDa |

Gene Summary:

The protein encoded by this gene is an actin binding and bundling protein that plays a structural role in erythrocytes, by stabilizing and attaching the spectrin/actin cytoskeleton to the erythrocyte membrane in a phosphorylation-dependent manner. This protein contains a core domain in the N -terminus, and a headpiece domain in the C -terminus that binds F -actin. When purified from erythrocytes, this protein exists as a trimer composed of two 48 kDa polypeptides and a 52 kDa polypeptide. The different subunits arise from alternative splicing in the $3^{\prime}$ coding region, where the headpiece domain is located. Disruption of this gene has been correlated with the autosomal dominant Marie Unna hereditary hypotrichosis disease, while loss of heterozygosity of this gene is thought to play a role in prostate cancer progression. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Nov 2014]
Transcript Variant: This variant (8) lacks two alternate in-frame exons in the 5' coding region, compared to variant 1 . Variants 8 and 18 encode the same isoform (4), which is shorter than isoform 1.

