

Product datasheet for SC335430

HIP55 (DBNL) (NM_001284315) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	HIP55 (DBNL) (NM_001284315) Human Untagged Clone
Tag:	Tag Free
Symbol:	DBNL
Synonyms:	ABP1; HIP-55; HIP55; SH3P7
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC335430 representing NM_001284315. Blue=Insert sequence Red=Cloning site Green=Tag(s)

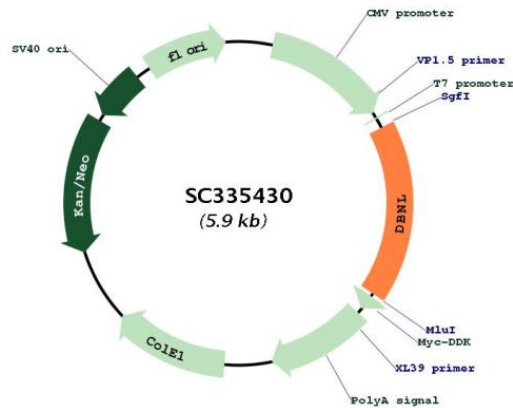
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GCTCGTTTGTAGTGAACCGTCAGAATTTTGTAAACGACTACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGAAGGCAACAGCAATGACATCCGCTGGCTGGCACAGGGGGGGCCCATGTGACCATCAACGCACGG
GCCGAGGAGGATGTGGAGCCTGAGTGCATCATGGAGAAGGTGGCCAAGGCTTCAGGTGCCAACTACAGC
TTTCACAAGGAGAGTGGCCGCTTCCAGGACGTGGGACCCAGGCCCCAGTGGGCTCTGTGTACCAGAAG
ACCAATGCCGTGTCTGAGATTAAGGGTTGGTAAAGACAGCTTCTGGGCCAAAGCAGAGAAGGAGGAG
GAGAACCCTCGGCTGGAGAAAAGCGGGCCGAGGAGGCACAGCGGCAGCTGGAGCAGGAGCGCCGG
GAGCGTGAGCTGCGTGAGGCTGCACGCCGGGAGCAGCGCTATCAGGAGCAGGGTGGCGAGGCCAGCCCC
CAGAGCAGGACGTGGGAGCAGCAGAAGAAGTGGTTTCAAGGAACCGAAATGAGCAGGAGTCTGCCGTG
CACCCGAGGGAGATTTTCAAGCAGAAGGAGAGGGCCATGTCCACCACCTCCATCTCCAGTCTCAGCCT
GGCAAGCTGAGGAGCCCCCTTCTGCAGAAGCAGCTCACCCAACCAGAGACCCACTTTGGCAGAGAGCCA
GCTGCTGCCATCTCAAGGCCAGGGCAGATCTCCCTGCTGAGGAGCCGGCGCCAGCACTCTCCATGT
CTGGTGCAGGCAGAAGAGGAGGCTGTGTATGAGGAACCTCAGAGCAGGAGACCTTCTACGAGCAGCCC
CCACTGGTGCAGCAGCAAGGTGCTGGCTCTGAGCACATTGACCACCACATTCAGGGCCAGGGGCTCAGT
GGGCAAGGGCTCTGTGCCGTGCCCTGTACGACTACCAGGCAGCCGACGACACAGAGATCTCCTTTGAC
CCCGAAGACCTCATCACGGGCATCGAGGTGATCGACGAAGGCTGGTGGCGTGGCTATGGGCCGATGGC
CATTTTGGCATGTTCCCTGCCAACTACGTGGAGCTCATTGAGTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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Restriction Sites: SgfI-MluI



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Plasmid Map:



ACCN: NM_001284315

Insert Size: 1011 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_001284315.1](#)

RefSeq Size: 2025 bp

RefSeq ORF: 1011 bp

Locus ID: 28988

UniProt ID: [Q9UJU6](#)

Cytogenetics: 7p13

MW: 38 kDa

Gene Summary:

Adapter protein that binds F-actin and DNM1, and thereby plays a role in receptor-mediated endocytosis. Plays a role in the reorganization of the actin cytoskeleton, formation of cell projections, such as neurites, in neuron morphogenesis and synapse formation via its interaction with WASL and COBL. Does not bind G-actin and promote actin polymerization by itself. Required for the formation of organized podosome rosettes (By similarity). May act as a common effector of antigen receptor-signaling pathways in leukocytes. Acts as a key component of the immunological synapse that regulates T-cell activation by bridging TCRs and the actin cytoskeleton to gene activation and endocytic processes.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (5) lacks two exons and initiates translation at a downstream start codon compared to variant 1. The encoded isoform (e) has a shorter N-terminus compared to isoform c. 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.