

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of DCUN1D1

<u>Enzyme description:-</u>	Halo-DCUN1D1
<u>Clone number:-</u>	DU24743
<u>Source:-</u>	Recombinant
<u>Tag:-</u>	N-terminal Halo, cleaved from GST
<u>Purification method:-</u>	GSH-agarose, cleaved with RV-3C
<u>Expression system:-</u>	<i>E.coli</i>
<u>Calculated molecular mass:-</u>	
Monoisotopic	65081 Da
Average Mass	65121 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	4.93
<u>Purity:-</u>	90%
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	

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Clone Data Sheet

Protein name DCUN1D1

<u>Protein</u>	Halo-DCUN1D1 1-259 (full length)
<u>Synonyms</u>	DCUN1L1, RP42, SCCRO
<u>Clone Number</u>	DU24743
<u>Species</u>	Human
<u>Accession Number</u>	Protein Q96GG9
<u>Tags</u>	N-terminal Halo-
Aminoacid sequence of the purified protein	<p>GPLGSM AE IGTGF PFDPHYVEVLGERMHYVDVGP RDGTPVLF LHG NPTSS YVWRNIIPHVAPTHRCIAPDLIGMKS DKPDLGYFFDDHVRFM DAFIEAL GLEEVVLVIHDWGSALGFHWAKRNPERVKGI AFMEFIRPIPTWDEWPEFA RETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVVRPLTEVEMDHYREPFLN PVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKLLFWGTPGV LIPPAEAARLAKSLPNCKAVDIGPGLNLLQEDNPD LIGSEIARWLSTLEI SGENLYFOGGSMNKLKSSQKDKVRQFMIF <u>TQSSEKTAVSCLSONDWKLDV</u> ATDNFFQNP ELY IRESVKGSLDRKKLEQLYNRYKDPDENKIGIDGIQQF CDDLALDPASISVLI IAWKFRAATQCEFSKQEFMDGMTELGCDSIEKLKA QIPKMEQELKEPGRFKDFYQFTFNFAKNPGQKGLDLEMAIAYWNLVNLGR FKFLDLWNKFLLEHHKRSIPKDTWNLLLD FSTMIADDSNYDEEGAWPVL IDDFVEFAR PQIAGTKSTTV</p>
Native sequence	in bold
Protease cleavage	TEV-protease site underlined
Cloning sites	BamH1 NotI
<u>DNA sequence of insert</u>	<p>GGATCCATGAACAAGTTGAAATCATCGCAGAAGGATAAAGTTCGTCAGTT TATGATCTTCACACAATCTAGTGAAAAACAGCAGTAAGTTGTCTTTCTC AAAATGACTGGAAGTTAGATGTTGCAACAGATAATTTTTTCCAAAATCCT GAACTTTATATACGAGAGAGTGTA AAAAGGATCATTGGACAGGAAGAAGTT AGAACAGCTGTACAATAGATACAAAGACCCTCAAGATGAGAATAAAAATTG GAATAGATGGCATAACAGCAGTTCTGTGATGACCTGGCACTCGATCCAGCC AGCATTAGTGTGTTGATTATTGCATGGAAGTTCAGAGCAGCAACACAGTG CGAGTTCTCCAAACAGGAGTTCATGGATGGCATGACAGAATTAGGATGTG ACAGCATAGAAAACTAAAGGCCCAGATAACCAAGATGGAACAAGAATTG AAAGAACCAGGACGATTTAAGGATTTTTTACCAGTTTACTTTTAATTTTGC AAAGAATCCAGGACAAAAAGGATTAGATCTAGAAATGGCCATTGCCTACT GGAAC TTAGTGCTTAATGGAAGATTTAAAT TCTTAGACTTATGGAATAAA TTTTTGTTGGAACATCATAAACGATCAATACCAAAAAGACACTTGGAATCT TCTTTTAGACTTCAGTACGATGATTGCAGATGACATGTCTAATTATGATG AGAAGGAGCATGGCCTGTTCTTATTGATGACTTTGTGGAATTTGCACGC CCTCAAATTGCTGGGACAAAAAGTACAACAGTGTAGGCGGCCGC</p>