Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of DCUN1D1

Enzyme description:-	GST-DCUN1D1
Clone number:-	DU20629
Source:-	Recombinant
Tag:-	N-terminal GST
Purification method:-	GSH-Sepharose
Expression level:-	5mg/L

Calculated molecular mass:-

Monoisotopic	57055 Da
Average Mass	57091 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:-	5.58
Purity:-	90%

Enzyme storage buffer:-

50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT

Storage temperature:-	-80ºC

Assay:-

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Clone Data Sheet

Protein name DCUN1D1

Protein	GST-DCUN1D1 1-259 (full length)
Synonyms	DCUN1L1, RP42, SCCRO
Clone Number	DU20629
Species	Human
Accession Number	Protein Q96GG9
Tags	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFQGPLGSGS**MNKLKSSQKDKVRQFMI** **FTQSSEKTAVSCLSQNDWKLDVATDNFFQNPELYIRESVKGSLDRKKLEQ** **LYNRYKDPQDENKIGIDGIQQFCDDLALDPASISVLIIAWKFRAATQCEF** **SKQEFMDGMTELGCDSIEKLKAQIPKMEQELKEPGRFKDFYQFTFNFAKN** **PGQKGLDLEMAIAYWNLVLNGRFKFLDLWNKFLLEHHKRSIPKDTWNLLL** **DFSTMIADDMSNYDEEGAWPVLIDDFVEFARPQIAGTKSTTV**
Native sequence	in bold
Protease cleavage	Prescission site underlined
Cloning sites	BamH1 Not1

DNA sequence of insert

GGATCCATGAACAAGTTGAAATCATCGCAGAAGGATAAAGTTCGTCAGTTT
ATGATCTTCACACAATCTAGTGAAAAAACAGCAGTAAGTTGTCTTTCTCAA
AATGACTGGAAGTTAGATGTTGCAACAGATAATTTTTTCCAAAATCCTGAA
CTTTATATACGAGAGAGTGTAAAAGGATCATTGGACAGGAAGAAGTTAGAA
CAGCTGTACAATAGATACAAAGACCCTCAAGATGAGAATAAAATTGGAATA
GATGGCATACAGCAGTTCTGTGATGACCTGGCACTCGATCCAGCCAGCATT
AGTGTGTTGATTATTGCATGGAAGTTCAGAGCAGCAACACAGTGCGAGTTC
TCCAAACAGGAGTTCATGGATGGCATGACAGAATTAGGATGTGACAGCATA
GAAAAACTAAAGGCCCAGATACCCAAGATGGAACAAGAATTGAAAGAACCA
GGACGATTTAAGGATTTTTACCAGTTTACTTTTAATTTTGCAAAGAATCCA
GGACAAAAAGGATTAGATCTAGAAATGGCCATTGCCTACTGGAACTTAGTG
CTTAATGGAAGATTTAAATTCTTAGACTTATGGAATAAATTTTTGTTGGAA
CATCATAAACGATCAATACCAAAAGACACTTGGAATCTTCTTTTAGACTTC
AGTACGATGATTGCAGATGACATGTCTAATTATGATGAAGAAGGAGCATGG
CCTGTTCTTATTGATGACTTTGTGGAATTTGCACGCCCTCAAATTGCTGGG
ACAAAAAGTACAACAGTGTAGGCGGCCGC