Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of DCUN1D2

Enzyme description:- GST-DCUN1D2

Clone number:- DU20630

Source:- Recombinant

Tag:- N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 5mg/L

Calculated molecular mass:-

Monoisotopic	57634 Da
Average Mass	57670 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.44

Purity:- 90%

Enzyme storage buffer:-

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

Storage temperature:- -80ºC

Assay:-

Division of Signal Transduction Therapy

Clone Data Sheet

Protein name DCUN1D2

Protein	GST-DCUN1D2 1- 259 (full length)
Synonyms	DCUNDL2
Clone Number	DU20630
Species	Human
Accession Number	Protein
Tags	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFQGPLGSPNSRVD**MHKLKSSQKDKVR** **QFMACTQAGERTAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDKK** **KLERLYGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVLVIAWKFRAAT** **QCEFSRKEFLDGMTELGCDSMEKLKALLPRLEQELKDTAKFKDFYQFTFT** **FAKNPGQKGLDLEMAVAYWKLVLSGRFKFLDLWNTFLMEHHKRSIPRDTW** **NLLLDFGNMIADDMSNYDEEGAWPVLIDDFVEYARPVVTGGKRSLF**
Native sequence	in bold
Protease cleavage	Prescission site underlined
Cloning sites	Sal1 Not1

DNA sequence of insert

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GTCGACATGCATAAGCTTAAATCGTCTCAGAAGGACAAGGTCCGCCAGTTT
ATGGCGTGCACTCAGGCTGGCGAGAGAACTGCTATCTACTGCTTAACGCAG
AATGAGTGGAGACTAGACGAGGCCACGGACAGCTTCTTCCAAAACCCAGAC
TCGCTCCACAGGGAGTCCATGCGGAACGCTGTGGACAAGAAGAAGCTGGAG
CGGCTGTACGGCAGGTACAAAGATCCACAAGATGAAAACAAAATTGGAGTC
GATGGGATTCAACAGTTTTGTGATGATCTGAGCCTGGATCCTGCCAGTATC
AGTGTATTGGTCATAGCGTGGAAGTTCAGGGCAGCAACTCAGTGTGAATTT
AGCAGAAAGGAATTTCTAGATGGCATGACAGAACTTGGGTGTGACAGCATG
GAGAAGCTAAAGGCTCTTCTGCCAAGACTGGAGCAGGAGCTGAAGGACACA
GCCAAGTTTAAAGATTTTTATCAGTTTACCTTCACCTTCGCTAAGAACCCA
GGGCAGAAAGGTTTAGACTTAGAAATGGCTGTTGCGTATTGGAAATTAGTG
TTATCTGGAAGGTTTAAATTTTTAGATCTCTGGAACACATTCTTAATGGAA
CATCACAAAAGATCAATTCCAAGGGACACCTGGAACCTCCTGCTGGACTTT
GGAAACATGATTGCGGATGATATGTCTAACTACGATGAAGAAGGAGCTTGG
CCCGTTCTTATAGATGATTTTGTAGAATATGCACGGCCAGTAGTCACAGGT
GGAAAACGCAGCCTTTTCTAGGCGGCCGC
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