Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of RNF8

Enzyme description:- GST-RNF8

Clone number:- DU19751

Source:- Recombinant

Tag:- N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 0.5mg/L

Calculated molecular mass:-

Monoisotopic 83500 Da
Average Mass 83632 Da
[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.70

Purity:- 80 %

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 RNF8

Protein	GST-RNF8 1 - 485 (full length)
Synonyms	
Clone Number	DU19751
Species	Human
Accession Number	Protein: O76064
Tags	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFQGPLGSPEFPGRLERPL**MGEPGFFV** **TGDRAGGRSWCLRRVGMSAGWLLLEDGCEVTVGRGFGVTYQLVSKICPLM** **ISRNHCVLKQNPEGQWTIMDNKSLNGVWLNRARLEPLRVYSIHQGDYIQL** **GVPLENKENAEYEYEVTEEDWETIYPCLSPKNDQMIEKNKELRTKRKFSL** **DELAGPGAEGPSNLKSKINKVSCESGQPVKSQGKGEVASTPSDNLDPKLT** **ALEPSKTTGAPIYPGFPKVTEVHHEQKASNSSASQRSLQMFKVTMSRILR** **LKIQMQEKHEAVMNVKKQTQKGNSKKVVQMEQELQDLQSQLCAEQAQQQA** **RVEQLEKTFQEEEQHLQGLEIAQGEKDLKQQLAQALQEHWALMEELNRSK** **KDFEAIIQAKNKELEQTKEEKEKMQAQKEEVLSHMNDVLENELQCIICSE** **YFIEAVTLNCAHSFCSYCINEWMKRKIECPICRKDIKSKTYSLVLDNCIN** **KMVNNLSSEVKERRIVLIRERKAKRLF**
Native sequence	in bold
Protease cleavage	Prescission site underlined
Cloning sites	Not1

DNA sequence of insert	GCGGCCGCTCATGGGGGAGCCCGGCTTCTTCGTCACAGGAGACCGCGCCGG TGGCCGGAGCTGGTGCCTGCGGCGGGTGGGGATGAGCGCCGGGTGGCTGCT GCTGGAAGATGGGTGCGAGGTGACTGTAGGACGAGGATTTGGTGTCACATA CCAACTGGTATCAAAAATCTGCCCCCTGATGATTTCTCGAAACCACTGTGT TTTGAAGCAGAATCCTGAGGGCCAATGGACAATTATGGACAACAAGAGTCT AAATGGTGTTTGGCTGAACAGAGCGCGTCTGGAACCTTTAAGGGTCTATTC CATTCATCAGGGAGACTACATCCAACTTGGAGTGCCTCTGGAAAATAAGGA GAATGCGGAGTATGAATATGAAGTTACTGAAGAAGACTGGGAGACAATATA TCCTTGTCTTTCCCCAAAGAATGACCAAATGATAGAAAAAAATAAGGAATT GAGAACTAAAAGGAAATTCAGTTTGGATGAATTAGCAGGTCCTGGAGCTGA AGGCCCCTCAAATTTGAAATCCAAAATAAATAAAGTGTCTTGTGAATCTGG TCAGCCAGTGAAATCACAGGGGAAAGGTGAAGTGGCCAGTACACCCTCTGA CAATTTGGATCCTAAGTTGACTGCCCTTGAGCCAAGTAAGACCACAGGGGC TCCCATTTACCCTGGCTTCCCCAAAGTCACAGAGGTTCATCATGAGCAGAA AGCCTCAAACTCTTCAGCATCTCAGAGAAGCTTACAGATGTTTAAGGTGAC CATGTCCAGGATTCTGAGGCTCAAAATACAGATGCAGGAAAAACATGAAGC CGTTATGAATGTGAAAAAGCAGACCCAAAAGGGGAACTCAAAGAAAGTTGT GCAAATGGAGCAGGAACTTCAGGACTTACAGTCCCAGCTGTGTGCAGAGCA GGCTCAGCAGCAGGCAAGAGTGGAGCAACTAGAGAAGACTTTCCAGGAAGA GGAACAGCATCTTCAGGGTTTGGAGATAGCCCAAGGAGAAAAGGACCTGAA GCAACAGCTGGCCCAGGCTCTGCAGGAGCATTGGGCTCTAATGGAAGAGCT AAATCGCAGCAAGAAGGACTTTGAAGCAATCATTCAAGCCAAGAACAAAGA ATTAGAGCAGACCAAGGAAGAGAAGGAGAAGATGCAAGCACAGAAGGAAGA AGTTCTTAGCCACATGAATGATGTGCTAGAGAATGAGCTCCAATGTATTAT TTGTTCAGAATACTTCATTGAGGCTGTCACCTTGAACTGTGCCCACAGTTT CTGCTCCTACTGTATCAATGAATGGATGAAGCGGAAGATAGAATGCCCCAT TTGTCGGAAGGACATTAAGTCCAAAACATACTCTTTGGTTCTGGACAATTG CATTAATAAGATGGTAAATAATCTGAGCTCAGAAGTGAAAGAACGACGAAT TGTTCTCATTAGGGAACGAAAAGCAAAGAGATTGTTCTGAGCGGCCGC