

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of RNF146

<u>Enzyme description:-</u>	GST-RNF146 2 - 359
<u>Clone number:-</u>	DU39064
<u>Source:-</u>	Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH-Sepharose
<u>Expression level:-</u>	1 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	66656 Da
Average Mass	66696 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	5.65
<u>Purity:-</u>	30%
<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 RNF146

<u>Protein</u>	GST-RNF146 2 - 359
<u>Synonyms</u>	
<u>Clone Number</u>	DU39064
<u>Species</u>	human
<u>Accession Number</u>	Protein: Q9NTX7
<u>Tags</u>	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFOGPLGSPNSRVDS SGR MAGCGEIDHSINMLPTNRKANESCSNTAPSLTVPECAICLOTCVHPVSLPCKHVFCYLCVKGASWLGKRCALCRQEIPEDFLDKPTLLSPEELKAASRGNGEYAWYYEGRNGWQYDERTSRELEDAFSKGGKNTLEMLIAGFLYVADLENMVQYRNEHGRRRKIKRDIIDI PKKGVAGLRLCDANTVNLARESSADGADSVSAQSGASVQPLVSSVRPLTSVDGQLTSPATPSPDASTSLEDSFAHLQLSGDN TAERSHRGEGEEDHESPSSGRVPAPDTSIEETESDASSDSEDVSAVVAQHSLTQQRLLVSNANQTVPDRSDRSRGTDRSVAGGGTVSVSVRSRRPDGQCTVTEV
Native sequence	in bold
Protease cleavage	Prescission site underlined
Cloning sites	NotI
<u>DNA sequence of insert</u>	GCGGCCGCATGGCTGGCTGTGGTGAAATTGATCATTCAATAAACATGCTTCCTACAAACAGGAAAGCGAACGAGTCCTGTTCTAATACTGCACCTTCTTTAACCGTCCCTGAATGTGCCATTTGTCTGCAAACATGTGTTTCATCCAGTCA GTCTGCCCTGTAAGCACGTTTTCTGCTATCTATGTGTA AAAAGGAGCTTCA TGGCTTGAAAAGCGGTGTGCTCTTTGTGCGACAAGAAATTC CCGAGGATTT CCTTGACAAGCCAACCTTGTGTGCACCAGAAGAACTCAAGGCAGCAAGTA GAGGAAATGGTGAATATGCATGGTATTATGAAGGAAGAAATGGGTGGTGG CAGTACGATGAGCGCACTAGTAGAGAGCTGGAAGATGCTTTTTCCAAAGG TAAAAAGAACACTGAAATGTTAATTGCTGGCTTTCTGTATGTGCTGATC TTGAAAACATGGTTCAATATAGGAGAAATGAACATGGACGTCGCAGGAAG ATTAAGCGAGATATAATAGATATACCAAAGAAGGGAGTAGCTGGACTTAG GCTAGACTGTGATGCTAATACCGTAAACCTAGCAAGAGAGAGCTCTGCTG ACGGAGCGGACAGTGTATCAGCACAGAGTGGAGCTTCTGTTTCAGCCCCTA GTGTCTTCTGTAAGGCCCTAACATCAGTAGATGGTCAGTTAACAAAGCCC TGCAACACCATCCCCTGATGCAAGCACTTCTCTGGAAGACTCTTTTGGCTC ATTTACAACCTCAGTGGAGACAACACAGCTGAAAGGAGTCATAGGGGAGAA GGAGAAGAAGATCATGAATCACCATCTTCAGGCAGGGTACCAGCACCAGA CACCTCCATTGAAGAACTGAATCAGATGCCAGTAGTGATAGTGAGGATG TATCTGCAGTTGTTGCACAGCACTCCTTGACCCAACAGAGACTTTTTGGTT TCTAATGCAAACCAGACAGTACCCGATCGATCAGATCGATCGGGAAC TGA TCGATCAGTAGCAGGGGTGGAACAGTGAGTGTGAGTGTGAGATCTAGAA GCCTGATGGACAGTGCACAGTA ACTGAAGTTTAAGCGGCCGC

