Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of RNF146

Enzyme description:-	His-RNF146 2 - 359
Clone number:-	DU39063
Source:-	Recombinant
Tag:-	N-terminal His_6
Purification method:-	Ni^{++}-Sepharose
Expression level:-	4 mg/L

Calculated molecular mass:-

Monoisotopic	43682 Da
Average Mass	43707 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:-	6.09
Purity:-	50%

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 RNF146

Protein	His-RNF146 2 - 359
Synonyms	
Clone Number	DU39063
Species	human
Accession Number	Protein: Q9NTX7
Tags	N-terminal His$_6$
Aminoacid sequence of the expressed protein	MGSSHHHHHHSSGLVPRGSH**MASMTGGQQMGRGSEFELRRQACGRMAGCG** **EIDHSINMLPTNRKANESCSNTAPSLTVPECAICLQTCVHPVSLPCKHVF** **CYLCVKGASWLGKRCALCRQEIPEDFLDKPTLLSPEELKAASRGNGEYAW** **YYEGRNGWWQYDERTSRELEDAFSKGKKNTEMLIAGFLYVADLENMVQYR** **RNEHGRRRKIKRDIIDIPKKGVAGLRLDCDANTVNLARESSADGADSVSA** **QSGASVQPLVSSVRPLTSVDGQLTSPATPSPDASTSLEDSFAHLQLSGDN** **TAERSHRGEGEEDHESPSSGRVPAPDTSIEETESDASSDSEDVSAVVAQH** **SLTQQRLLVSNANQTVPDRSDRSGTDRSVAGGGTVSVSVRSRRPDGQCTV** **TEV**
Native sequence	in bold
Protease cleavage	Thrombin site underlined
Cloning sites	Not1
DNA sequence of insert	GCGGCCGCATGGCTGGCTGTGGTGAAATTGATCATTCAATAAACATGCTT CCTACAAACAGGAAAGCGAACGAGTCCTGTTCTAATACTGCACCTTCTTT AACCGTCCCTGAATGTGCCATTTGTCTGCAAACATGTGTTCATCCAGTCA GTCTGCCCTGTAAGCACGTTTTCTGCTATCTATGTGTAAAAGGAGCTTCA TGGCTTGGAAAGCGGTGTGCTCTTTGTCGACAAGAAATTCCCGAGGATTT CCTTGACAAGCCAACCTTGTTGTCACCAGAAGAACTCAAGGCAGCAAGTA GAGGAAATGGTGAATATGCATGGTATTATGAAGGAAGAAATGGGTGGTGG CAGTACGATGAGCGCACTAGTAGAGAGCTGGAAGATGCTTTTTCCAAAGG TAAAAAGAACACTGAAATGTTAATTGCTGGCTTTCTGTATGTCGCTGATC TTGAAAACATGGTTCAATATAGGAGAAATGAACATGGACGTCGCAGGAAG ATTAAGCGAGATATAATAGATATACCAAAGAAGGGAGTAGCTGGACTTAG GCTAGACTGTGATGCTAATACCGTAAACCTAGCAAGAGAGAGCTCTGCTG ACGGAGCGGACAGTGTATCAGCACAGAGTGGAGCTTCTGTTCAGCCCCTA GTGTCTTCTGTAAGGCCCCTAACATCAGTAGATGGTCAGTTAACAAGCCC TGCAACACCATCCCCTGATGCAAGCACTTCTCTGGAAGACTCTTTTGCTC ATTTACAACTCAGTGGAGACAACACAGCTGAAAGGAGTCATAGGGGAGAA GGAGAAGAAGATCATGAATCACCATCTTCAGGCAGGGTACCAGCACCAGA CACCTCCATTGAAGAAACTGAATCAGATGCCAGTAGTGATAGTGAGGATG TATCTGCAGTTGTTGCACAGCACTCCTTGACCCAACAGAGACTTTTGGTT TCTAATGCAAACCAGACAGTACCCGATCGATCAGATCGATCGGGAACTGA TCGATCAGTAGCAGGGGGTGGAACAGTGAGTGTCAGTGTCAGATCTAGAA GGCCTGATGGACAGTGCACAGTAACTGAAGTTTAAGCGGCCGC