

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of RNF220

<u>Enzyme description:-</u>	GST-RNF220
<u>Clone number:-</u>	DU33242
<u>Source:-</u>	Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH-Sepharose
<u>Expression level:-</u>	0.2 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	89532 Da
Average Mass	89586 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	5.61
<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 RNF220

<u>Protein</u>	GST-RNF220 1 - 566 (full length)
<u>Synonyms</u>	
<u>Clone Number</u>	DU33242
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q5VTB9 DNA: NM_018150.2
<u>Tags</u>	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPHYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFOGPLGSMDLHRAAFKMENSSYLPNP LASPALMVLASTAEASRDASIPCQQPRPFGVPSVVDKDVHIPFTNGSYTFASMYHRQGGVPGTFANRDFPPSLLHLHPQFAPPNLDCTPISMLNHSGVGAFRPFASTEDRESYQSAFTPAKRLKNCHDTEPHLRFSDADGKEYDFGTQLPSSSPGSLKVDDTGKKIFAVSGLISDREASSSPEDRNDRCKKAAALFDSQAPICPICQVLLRPSELQEHMEQEQLEQLAQLPSSKNSLLKDAMAPGTPKSLLSASIKREGESPTASPHSSATDDLHHS DRYQTFLRVRANRQTRLNARI GKMKRRKQDEGQREGSCMAEDDAVDIEHENNNRFEEYEWCGQKRIRATTLLEGGFRGSGFIMCSGKENPDSADLDVDGDDTLEYGKPQYTEADVIPCTGEEPGEAKEREALRGAVLNGGPPSTRITPEFSKWADEMPSTSNGESEKQEAMQKTCKNSDIEKITEDSAVTTFEALKARVRELERQLSRGDYKCLICMDSYSMPLTSIQCWHVHCEECWLRTLGAKKLCPCNTITAPGDLRRIYL
Native sequence	in bold
Protease cleavage	Prescission site underlined
Cloning sites	BamH1 / NotI

**DNA sequence of
insert**

GGATCCATGGACTTACACCGGGCAGCCTTCAAGATGGAGAACTCATCCTAC
CTTCCCAACCCTCTGGCATCCCAGCACTGATGGTCCTGGCATCCACGGCT
GAGGCCAGCCGTGATGCTTCCATCCCTTGTGTCAGCAGCCACGACCCTTTGGT
GTACCTGTCTCAGTTGACAAGGACGTGCATATTCCTTTCACCAACGGTTCC
TATACCTTTGCCTCTATGTACCATCGGCAAGGTGGGGTGCCAGGCACTTTT
GCCAATCGTGATTTCCCCCTTCTCTACTACACCTCCACCCTCAATTTGCT
CCCCAAATCTAGATTGCACCCCAATCAGTATGCTGAATCATAGTGGTGTG
GGGGCTTTCCGGCCCTTTGCCTCCACCGAGGACCGGGAGAGCTATCAGTCA
GCCTTTACGCCGGCCAAGCGACTTAAGAAGTCCATGACACAGAGTCTCCC
CACTTGCCTTCTCAGATGCAGATGGCAAGGAATATGACTTTGGGACACAG
CTGCCATCTAGCTCCCCGGTTCATAAAGGTTGATGACACTGGGAAGAAG
ATTTTGTCTGTCTCTGGCCTCATTTCTGATCGGGAAGCCTCATCTAGCCCA
GAGGATCGGAATGACAGATGTAAGAAGAAAGCAGCGGCATTTGTTGACAGC
CAGGCCCAATTTGCCCATCTGCCAGGTCTGCTGAGGCCAGTGAGCTG
CAGGAGCATATGGAGCAGGAAGTGGAGCAGCTAGCCCAACTGCCCTCGAGC
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ACGTCCATCCAGTGTGGCACGTGCACTGCGAGGAGTGTGGCTGCGGACC
CTGGGTGCCAAGAAGCTCTGCCCTCAGTGCAACACGATCACAGCGCCCGGA
GACCTGCGGAGGATCTACTTGTGAGCGGCCGC