

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of RNF25

Enzyme description:- GST-RNF25 1-459 (full length)

Clone number:- DU43457

Source:- BL21 recombinant

Tag:- N-terminal GST-tag

Purification method:- GSH-Sepharose

Expression level:- 1 mg/L

Calculated molecular mass:-

Monoisotopic 78661 Da

Average Mass 78709 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.22

Purity:- 50%

Enzyme storage buffer:-

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

Storage temperature:- -80°C

Assay:-

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Clone Data Sheet

GST-RNF25

<u>Protein</u>	GST-RNF25 (1-459)
<u>Synonyms</u>	ring finger protein 25, E3 ubiquitin-protein ligase RNF25
<u>Clone Number</u>	DU43457
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q96BH1, DNA: NM_022453
<u>Tags</u>	N-terminal GST-tag
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEF PNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRY GVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLY DALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQA TFGGGDHPPKSDLEVL <u>FQGPLGSPNSRVDMAASASAAAGEEDWVLPSEVEVL</u> ESIYLDELQVIKNGRTPWEIYITLHPATAEDQDSQYVCFTLVLQVPAEYP HEVPQISIRNPRGLSDEQIHTILQVLGHVAKAGLGTAMLYELIEKGKEILTD NNIPHGQCVICLYGFQEKFAFTKTPCYHYFHCHCLARYIQHMEQELKAQGE QEQRQHATTKQKAVGVQCPVCREPLVYDLASLKAPEPQQPMELYQPSAES LRQQEERKRLYQRQQERGGI IDLEAERNRYFISLQOPPAPAEPESAVDVSKG SQPPSTLAAELSTSPAVQSTLPPPLPVATQHICEKIPGTRSNQORLGETQKA MLDPPKPSRGPWRQPERRHPKGGEGCHAPKGTRDTQELPPPEGPLKEPMDLKP EPHSQGVGPPQEKGPQSWQGGPPRRTRDCVRWERSKGRTPGSSYPRLPRGQ GAYRPGTRRESLGLSKDGS
Native sequence	in bold
Protease cleavage	Prescission site underlined
Cloning sites	SalI NotI

**DNA sequence of
insert**

GTCGACATGGCGGCGTCTGCGTCTGCAGCTGCAGGGGAGGAGGACTGGGTCCCT
TCCCTCTGAAGTTGAAGTATTGGAGTCCATCTATCTAGATGAACTACAGGTGA
TTAAAGGAAATGGCAGAACTTCACCATGGGAGATCTACATCACTTTGCATCCT
GCCACTGCAGAGGACCAGGATTCACAGTATGTCTGCTTCACTCTGGTGCTTCA
GGTCCCAGCAGAGTATCCCCATGAGGTGCCACAGATCTCTATCCGAAATCCCC
GAGGACTTTCAGATGAACAGATCCACACGATCTTACAGGTGCTGGGCCACGTG
GCCAAGGCTGGGCTGGGCACTGCCATGCTGTATGAACTCATTTGAGAAAGGGAA
GGAAATTCTCACAGATAACAACATCCCTCATGGCCAGTGTGTCATCTGCCTCT
ATGGTTTCCAGGAGAAGGAGGCCTTTACCAAAACACCCTGTTACCACTACTTC
CACTGCCACTGCCTTGCTCGGTACATCCAGCACATGGAGCAAGAGCTGAAGGC
ACAAGGACAGGAGCAGGAACAGGAACGGCAGCATGCTACAACCAACAGAAGG
CAGTCGGTGTGCAGTGTCCAGTGTGCAGAGAGCCCCTCGTGTATGATCTTGCC
TCACTGAAAGCAGCCCCTGAACCCCAACAGCCCATGGAGCTGTACCAGCCCAG
TGCAGAGAGCTTGCGCCAGCAAGAAGAACGCAAGCGGCTCTACCAGAGGCAGC
AGGAGCGGGGGGAATCATTGACCTTGAGGCTGAGCGAAACCGATACTTCATC
AGCCTTCAGCAGCCTCCTGCCCCGCGGAACCTGAGTCAGCTGTAGATGTCTC
CAAAGGATCCCAACCACCAGCACCTTGCCAGCAGAACTATCCACCTCACCAG
CCGTCCAATCCACTTTGCCACCTCCTCTGCCTGTGGCGACCCAGCACATATGT
GAGAAGATTCCAGGGACCAGGTCAAATCAGCAAAGGTTGGGCGAAACCCAGAA
AGCTATGCTAGATCCCCCAAGCCAGTCGAGGTCCCTGGCGACAGCCCGAAC
GGAGGCACCCAAAGGGAGGGGAGTGCCACGCCCTAAAGGTACCCGTGACACC
CAGGAACTGCCACCTCCTGAGGGGCCCTCAAGGAGCCCATGGACCTAAAGCC
AGAACCCCATAGCCAAGGAGTTGAAGGTCTCCACAAGAGAAGGGGCCTGGCA
GCTGGCAGGGGCCCCACCCCGCAGGACTCGGGACTGTGTTGCTGGGAGCGC
TCTAAAGGCCGGACACCCGGTCTTCCTACCTCGCCTGCCTCGGGGCCAGGG
AGCATACCGGCTGGTACTCGGAGGGAGTCCCTGGGCCTGGAATCTAAGGATG
GTTCCCTAGGCGG