

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of USP13 [318 – 863]

Enzyme description:- USP13 [318 – 863]

Clone number:- DU10952

Source:- BL21 Recombinant

Tag:- GST

Purification method:- GSH-Sepharose

Expression level:- 0.5 mg/L

Calculated molecular mass:-

Monoisotopic 88475 Da

Average Mass 88529 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.36

Purity:- 90%

Enzyme storage buffer:-

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

Storage temperature:- -80°C

Assay:-

Ub-Rho110-Gly cleavage assay monitored by Ex/Em 485/535 nm

Assay buffer:-

40 mM Tris pH 7.5, 100 mM NaCl, 5 mM DTT, 0.01% Triton X-100, 0.005% Ovalbumin, 0.5 µM Ub-Rho110-Gly

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Clone Data Sheet

GST-USP13 [318-863]

<u>Protein</u>	GST-USP13 [318-863]
<u>Synonyms</u>	IsoT3
<u>Clone Number</u>	DU10952
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q92995 DNA: NM_003940
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEF PNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRY GVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLY DALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLOGWQA TFGGGDHPPKSDLEVLFOGPLGSEVI QESGTKLKPMYGPYTG LK NLGN SCY LSSVMQAI FSIPEF QRAYVGNLPRIFDYSPLDPTQDFNTQMTKLGHLLSGQ YSKPPVKSELIEQVMKEEHKPOQNGISPRMFKAFVSKSHPEFSSNRQDAQE FFLHLVNLVERNRI SENPSDVFRFLVEERI QCCQTRKVR YTERVDYLMQLP VAMEAATNKDELIAYELTRREAEANRRPLPELVRAKIPFSACLOAFSEPENV DDFWSSAL QAKSAGVKTSRFASFPEYLVVQIKKFTFGLDWVPKKFDV SIDMP DLLDINHLRARGL QPGEELPDISPPIVIPDDSKDR LMNQLIDPSDIDESSV MQLAEMGF PLEACRKAVYFTGNMGAEVAFNWIIVHMEEPDFAEPLTMPGYGG AASAGASVFGASGLDN QPPEEIVAIITSMGFQRNQAIQALRATNN LERALD WIFSHPEFEEDSDFVIEMENNANANI I SEAKPEGPRVKDGS GT YELFAFISH MGTSTMSGHY ICHIKKEGRWVIYNDHKVCASERPPKDLGYMYFYRRIPS
<u>Native sequence</u>	in bold residues 318-end of USP13
<u>Protease cleavage</u>	Precision site underlined
<u>Cloning sites</u>	BamH1 / Xho1

**DNA sequence of
insert**

GGATCCGAAGTGATCCAGGAGTCGGGCACGAAACTGAAGCCAATGTATGGTC
CTGGCTACACGGGTCTGAAGAACCTGGGCAACAGCTGCTATCTCAGCTCTGT
CATGCAGGCCATCTTCAGCATCCCAGAATTCCAGAGAGCGTATGTAGGAAAC
CTTCCCAGAATATTTGACTACTCGCCTTAGATCCAACACAAGATTTCAACA
CACAGATGACTAAGTTAGGACATGGCCTTCTCTCAGGCCAGTATTCAAAGCC
TCCGGTGAATCTGAACTCATTGAACAGGTGATGAAGGAGGAGCACAAGCCA
CAGCAGAACGGGATCTCTCCGCGCATGTTTAAGGCCTTTGTAAGCAAGAGCC
ACCCGGAATTCTCCTCTAACAGGCAGCAAGATGCCAGGAATTCTTCTTGCA
CCTGGTGAATCTAGTAGAGAGGAACCGCATCGGCTCAGAAAACCCAAGCGAT
GTTTTTCGTTTTTTGGTGAAGAACGCATTCAGTGCTGTCAGACCCGGAAAG
TCCGCTACACGGAGAGGGTGGATTACCTGATGCAGTTACCTGTGGCCATGGA
GGCGGCAACCAACAAGGATGAACTGATCGCTTATGAACTAACGAGAAGGGAA
GCAGAAGCAAACAGAAGACCCCTTCTGAGTTGGTACGTGCCAAGATACCAT
TTAGTGCCCTGCCTTCAGGCCTTCTCTGAACCAGAAAAATGTTGATGATTTCTG
GAGCAGTGCCCTACAAGCAAAGTCTGCGGGTGTGAAAACATCTCGCTTTGCT
TCATTCCCTGAATACTTGGTAGTGCAGATAAAGAAGTTCACTTTTGGTCTTG
ACTGGGTTCCCAAAAAATTTGATGTTTCTATTGATATGCCAGACCTACTTGA
TATCAACCATCTCCGAGCCAGGGGGTTACAGCCAGGAGAGGAAGAACTTCCA
GACATCAGCCCCCATAGTCATTCTGATGACTCAAAAGATCGCCTGATGA
ACCAATTGATAGACCCATCAGACATCGATGAGTCATCAGTGATGCAGCTGGC
CGAGATGGGTTTCCCGCTGGAAGCATGTCGCAAGGCTGTGTACTTCACTGGA
AATATGGGCGCCGAGGTGGCCTTCAACTGGATCATTGTTACATGGAAGAGC
CAGATTTTGCTGAGCCGCTGACCATGCCTGGTTATGGAGGGGCAGCTTCTGC
TGGAGCCTCTGTTTTTTGGTGCCTTCTGGACTGGATAACCAACCTCCAGAGGAA
ATCGTAGCTATCATCACCTCCATGGGATTTTCAGCGAAATCAGGCTATTCAGG
CACTACGAGCAACGAATAATAACCTGGAAAGAGCACTGGATTGGATCTTTAG
CCACCCTGAGTTTGAAGAAGACAGTGATTTTGTGATTGAGATGGAGAATAAT
GCCAATGCAAACATTATTTCTGAGGCCAAGCCCAGGACCTAGAGTCAAGG
ATGGATCTGGAACATATGAGCTATTTGCATTCATCAGTCACATGGGAACATC
CACAATGAGTGGTCATTACATTTGCCATATCAAAAAGGAAGGAAGATGGGTG
ATTTACAATGACCACAAAGTTTGTGCCTCAGAAAGGCCCCCTAAAGACCTGG
GCTACATGTACTTTTTACCGCAGGATACCAAGCTAAGCGGCCGC