

Division of Signal Transduction Therapy

Standard Operation Procedure

GST-USP36 [81-461]

Enzyme description:- GST-USP36 [81-461]

Clone number:- DU4944

Source:- BL21 Recombinant

Tag:- N-terminal GST tag

Purification method:- GSH sepharose

Expression level:- 1 mg/L

Calculated molecular mass:-

Monoisotopic 69345 Da

Average Mass 69387 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 9.19

Purity:- 80%

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-USP36 [81-461]

<u>Protein</u>	GST-USP36 [81-461]
<u>Synonyms</u>	
<u>Clone Number</u>	DU4944
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q9P275 DNA: AAH27992.1
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMATIRYIADKHNMLGGCPKERAETISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFOGPLGSARRQGEHTYESCGDGVPA PQKVLFPTERLSLRWERVFRVGAGLHNLGNTCFLNATIQCLTYTPPLANY LLSKEHARSCHQGSFCMLCVMQNHIVQAFANSGNAIKPVSFIRDLKKIAR HFRFGNQEDAHEFLRYTIDAMQKACLNCAKLDRQTQATTLVHQIFGGYL RSRVKCSVCKSVSDTYDPYLDVALEIRQAANIVRALELFVKADVLSGENA YMACAKCKKKVPASKRFTIHRTSNVLTLSLKRFANFSGGKITKDVGYPEFL NIRPYMSQNNGDPMYGLYAVLVHSGYSCHAGHYCYVKASNGQWYQMND SLVHSSNVKVVLNQAYVLFYLRIPGSKKSPEGLISRTGSSSLPGRPSVI PDHSKKNIGNGI
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	Precision site underlined
<u>Cloning sites</u>	BamH1 / NotI

**DNA sequence of
insert**

GGGATCCGCCAGGAGACAGGGCAGTGAGCACACGTATGAGAGCTGTGGTG
ACGGAGTCCCAGCCCCGCAGAAAGTGCTTTTCCCCACGGAGCGACTGTCT
CTGAGGTGGGAGCGGGTCTTCCGCGTGGGCGCAGGACTCCACAACCTTGG
CAACACCTGCTTTCTCAATGCCACCATCCAGTGCTTGACCTACACACCAC
CTCTAGCCAACTACCTGCTCTCCAAGGAGCATGCTCGCAGCTGCCACCAG
GGAAGCTTCTGCATGCTGTGTGTCATGCAGAACCACATTGTCCAGGCCTT
CGCCAACAGCGGCAACGCCATCAAGCCCGTCTCCTTCATCCGAGACCTGA
AAAAGATCGCCCCGACACTTCCGCTTTGGGAACCAGGAGGACGCGCATGAG
TTCCTGCGGTACACCATCGACGCCATGCAGAAAGCCTGCCTGAATGGCTG
TGCCAAGTTGGATCGTCAAACGCAGGCTACTACCTTGGTCCATCAAATTT
TTGGAGGGTATCTCAGATCACGCGTGAAGTGCTCCGTGTGCAAGAGCGTC
TCGGACACCTACGACCCCTACTTGGACGTCGCGCTGGAGATCCGGCAAGC
TGCGAATATTGTGCGTGCTCTGGAACTTTTTGTGAAAGCAGATGTCCTGA
GTGGAGAGAATGCCTACATGTGTGCTAAATGCAAGAAGAAGGTTCCAGCC
AGCAAGCGCTTCACCATCCACAGAACATCCAACGTCTTAACCCTTTCCCT
CAAGCGTTTTTGCCAACTTCAGCGGGGGGAAGATCACCAAGGATGTAGGCT
ATCCGGAATTCCCAACATACGTCCGTATATGTCCCAGAATAATGGTGAT
CCTGTCATGTATGGACTCTATGCTGTCCTGGTGCCTCGGGCTACAGCTG
CCATGCCGGGCCTATTACTGCTACGTGAAGGCAAGCAATGGACAGTGGT
ACCAGATGAATGATTCCTTGGTCCATTCCAGCAACGTCAAGGTGGTTCTG
AACCAGCAGGCCTACGTGCTGTTCTATCTGCGAATTCCAGGCTCTAAGAA
AAGTCCCGAGGGCCTCATCTCCAGGACAGGCTCCTCCTCCCTTCCCGGCC
GCCCGAGTGTGATTCCAGATCACTCCAAGAAGAACATCGGCAATGGGATT
TGAGCGGCCCGC