

## *Division of Signal Transduction Therapy*

### **Standard Operation Procedure**

#### **GST-USP45**

**Enzyme description:-** GST-USP45 (1-814 = full length)

**Clone number:-** DU15681

**Source:-** BL21 Recombinant

**Tag:-** N-terminal GST tag

**Purification method:-** GSH sepharose

**Expression level:-** 0.25 mg/L

**Calculated molecular mass:-**

Monoisotopic 118141 Da

Average Mass 118554 Da

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 8.00

**Purity:-** 50%

**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-USP45**

**Protein** GST-USP45 (1-814 = full length)

**Synonyms**

**Clone Number** DU15681

**Species** Human

**Accession Number** Protein: Q70EL2 DNA: NM\_001080481.1

**Tags** N-terminal GST tag

**Amino acid sequence of expressed protein** MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPPYYIDGDVKLTQSMAIIRYIADKHNLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFOGPLGSMRVKDPTKALPEKAKRSKRPTVPHDEDSSDDIAVGLTCQHVSHAISVNHVKRAIAENLWSVCSECLKERFYDGGQLVLTSDIWLCLKCGFQCGKNSSEQHSLKHKFKSSRTEPHCI IINLSTWIIWCYECDEKLSTHCNKKVLAQIVDFLQKHASKTQTSAFSRIMKLC EEK CETDEIQGGKCRNLSVRGITNLGNTCFNAVMQNLAQTYTLTDLMEIKESSTKLKIFPSSDSQLDPLVVELSRPGPLTSALFLFLHSMKETEKGPLSPKVLFNQLCQKAPRFKDFQQQDSQELLHYLLDAVRTEETKRIQASILKAFNNPTTKTADDETRKKVKAYGKEGVKMNFI DRIFIGELTSTVMCEECANISTVKDPFIDISLPIIEERVSKPLLWGRMNKYRSLRETDHRYSGNVTIENIHQPRAAKKHSSSKDKSQLIHDRKCI RKLSSGETVTYQKNENLEMNGDSL MFASLMNSESRLNESPTDDSEKEASHSESNDADSEPSSESASKQTGLFRSSSGSGVQPDGPLYPLSAGKLLYTKETDSGDKEMAEAI SELRLSSTVTGDQDFDRENQPLNISNNLCFLEGKHLRSYSPQNAFQTL SQSYITTSKECSIQSCLYQFTSMELLMGNKLLCENCTKNKQKYO EETSFAEKKVEGVYTNA RKQLLISAVPAVLILHLKRFHQAGLSLRKVN RVDFPLMLDLAPFCSATCKNASVGDKVLYGLYGIVEHSGSMREGHYTAYVKVRTPSRKLSEHNTKKKNVPGLKAADNESAGQVHVSDTYLQVVPESRALS AQAYLLFYERVL

**Native sequence** in bold

**Protease cleavage** Precision site underlined

**Cloning sites** BamHI / NotI

**DNA sequence of insert**

AGATCTATGCGGGTGAAAGATCCAACCTAAAGCTTTACCTGAGAAAGCCAA  
AAGAAGTAAAAGGCCTACTGTACCTCATGATGAAGACTCTTCAGATGATA  
TTGCTGTAGGTTAACTTGCCAACATGTAAGTCATGCTATCAGCGTGAAT  
CATGTAAAGAGAGCAATAGCTGAGAATCTGTGGTCAGTTTGCTCAGAATG  
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CATGAAACTTTGTGAAGAAAAATGTGAAACAGATGAAATACAGAAGGGAG  
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TGATCTGATGAATGAGATCAAAGAAAGTAGTACAAAACCAAGATTTTTT  
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AGCGGCCGC