

*Division of Signal Transduction Therapy*

**Standard Operation Procedure**

**GST-AMSH LP [264 - 436]**

**Enzyme description:-** GST-AMSH LP [264 - 436]

**Clone number:-** DU15780

**Source:-** BL21 Recombinant

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

**Purification method:-** GSH sepharose

**Expression level:-** 20 mg/L

**Calculated molecular mass:-**

Monoisotopic 47237 Da

Average Mass 47266 Da

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 6.59

**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-AMSH LP [264 – 436]**

**Protein** GST-AMSH LP [264 - 436]

**Synonyms**

**Clone Number** DU15780

**Species** Human

**Accession Number** Protein: Q96FJ0 DNA: BC010846

**Tags** N-terminal GST tag

**Amino acid sequence of expressed protein** MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNLGGCPKERAIEISMLEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFOGPLGSPGIPGSTRAAA**EGLRCVVL****PEDLCHKFLQLAESNTVIRGIETCGILCGKLTHNEFTITHVIVPKQSAGPD****YCDMENVEELFNVQDQHDLLTLGWIHTHTPTQTAFLSSVDLHTHC SYQLML****PEAIAIVCSPKHKDTGIFRLTNAGMLEVSACKKKGFHPHTKEPRLFSICK****HVLVKDIKIVL DLR**

**Native sequence** in bold

**Protease cleavage** Precision site underlined

**Cloning sites** NotI

**DNA sequence of insert** GCGGCCGCGGAAGGACTGCGATGTGTAGTTTTGCCAGAAGATCTTTGCCACAAATTTCTGCAACTGGCAGAATCTAATACAGTGAGAGGAATAGAAACCTGTGGAATACTCTGTGGAAAAGTACACATAATGAATTTACTATTACCCATGTAATTGTGCCAAAGCAGTCTGCGGGACCAGACTATTGTGACATGGAGAA TGTAGAGGAATTATTCAATGTTTCAGGATCAACATGATCTCCTCACTCTAGGATGGATCCATACACATCCCACTCAAAGTGCATTTTTATCCAGCGTTGATCTTCACACTCACTGTTCCCTATCAACTCATGTTGCCAGAGGCCATTGCCAT TGTTTGCTCACCAAAGCATAAAGACACTGGCATCTTCAGGCTCACCAATGCTGGCATGCTTGAGGTTTCTGCTTGTAAGGCTTTCATCCACACACCAAGGAGCCCAGGCTGTTTCAGTATATGCAAACATGTGTTGGTAAAAGACATAAAATAAATTGTGTTGGATCTGAGGTGAGCGGCCG