

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-AMSH [256-424]

Enzyme description:- GST-AMSH [256-424]

Clone number:- DU15719

Source:- BL21 Recombinant

Tag:- N-terminal GST tag

Purification method:- GSH sepharose

Expression level:- 0.5 mg/L

Calculated molecular mass:-

Monoisotopic 47025 Da

Average Mass 47055 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.28

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

Division of Signal Transduction Therapy

Clone Data Sheet

GST-AMSH [256-424]

<u>Protein</u>	GST-AMSH [256-424]
<u>Synonyms</u>	STAM binding protein
<u>Clone Number</u>	DU15719
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q95630 DNA: BC065574.1
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPHYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFOGPLGSPGIPGSTRAAADGLRHVVV PGR LC PQ FL Q LASANTARGVET CG IL CG KLMRNEFT I THVLI PK QSAGSD YC NTENE EEL FL IQ D Q GL I TLGW I HT HPT Q T AF L SSVDL H TH CS Y Q M ML P ES V AI V CS P K F Q E T G F F KL T D H GLE E I S SR Q K G F H PS K DP L FC S CS H VT V DRA V T I T D LR
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	Precision site underlined
<u>Cloning sites</u>	NotI
<u>DNA sequence of insert</u>	GCGGCCGCGGATGGATTGCGCCATGTGGTGGTGCCTGGGCGGCTGTGCCACAGTTTCTCCAGTTAGCCAGTGCCAACACTGCCCGGGAGTGGAGACATGTGGAATTCTCTGTGGAAACTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCAAGCAAAGTCTGGGTCTGATTACTGCAACACAGAGAACGAAGAAGAACTTTTCCTCATAACAGGATCAGCAGGGCCTCATCACACTGGCTGGATTACATACTCACCCACACAGACCGGTTTTCTCTCCAGTGTTCGACTACACACTCACTGCTCTTACCAGATGATGTTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCAGGAACTGGATTCTTTAACTAACTGACCATGGACTAGAGGAGATTTCTTCTGTGCGCCAGAAAGGATTCATCCACACAGCAAGGATCCACCTCTGTTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGGCCG