

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of SAP90 [1 – 723]**

**Protein description:-** SAP90 [1 – 723]

**Clone number:-** DU 390

**Source:-** Recombinant

**Expression system:-** *E.coli*

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Expression level:-** 1 mg/L

**Calculated molecular mass:-** 107, 255 daltons

**Purity:-** 80 %

**Enzyme storage buffer:-**

50 mM Tris-HCl pH 7.5, 50 % glycerol, 150 mM NaCl, 0.1 mM EGTA,  
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 0.2 mM PMSF, 1 mM Benzamidine.

**Storage temperature:-** –20 °C

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**CLONE DATA SHEET**

**SAP90 [1 – 723]**

**Protein** SAP90 [1 – 723]

**Clone number** DU 390

**Species** Rat

**Accession no** M96853

**Tags** N-terminal GST

**Bacterially expressed protein**

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFEL  
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLE  
GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLN  
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPIQIDKY  
LKSSKYIAWPLQGWQATFGGGDHPKSDLVPRGSMDCLCIVTTKKYRY  
QDEDTPPLEHSPAHLPNQANSPPVIVNTDTLEAPGYELQVNGTEGEME  
YEEITLERGNSGLGFSIAGGTDNPHIGDDPSIFITKIIPGGAAAQDGR  
LRVNSILFVNEVDVREVTHSAAVEALKEAGSIVRLYVMRRKPPAEKV  
MEIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAHKDGRLL  
QIGDKILAVNSVGLQEDVMHEDAVAALKNTYDVVYLKVAKPSNAYLSDS  
YAPPDITTSYSQHLNEISHSSYLGTDYPTAMTPTSPRRYSPVAKDLL  
GEEDIPREPRRIVIHGSGTGLGFNIVGGEDGEGIFISFILAGGPADLS  
GELRKGQDQILSVNGVDLRNASHEQAAIALKNAGQVTIIAQYKPEEYS  
RFEAKIHDLREQLMNSSLGSGTASLRSNPKRGFYIRALFDYDKTKDCG  
FLSQALSFRFGDVLHVIDAGDEEWWQARRVHSDSETDDIGFIPSKRRV  
ERREWSRLKAKDWGSSSGSQGREDSVLSYETVTQMEVHYARPIIILGP  
TKDRANDDLLSEFPDKFGSCVPHTTRPKREYEIDGRDYHFVSSREKME  
KDIQAHKFI EAGQYNSHLYGTSVQSVREVAEQGKHCILDVSANAVRRL  
QAAHLHPAIAIFIRPRSLENVLEINKRITEEQARKAFDRATKLEQEFTE  
CFSAIVEGDSFEEIYHKVKRVIEDLSGPYIWVPARERRIHRD

**Native sequence** Amino acids M1 – R723 (L724 end) of rat SAP90.  
Residue M227 of the fusion protein is equivalent to M1 of the native protein. The GST tag is located at residues 1 – 220.

The following sequence is present after the SAP90 sequence, RIHRD, residues 950 – 954.

**Protease cleavage** Thrombin (LVPRGS) residues 221 - 226

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### Cloning sites

### Nucleotide

### sequence of insert

### *Bam*H1 and *Eco*RI of pGEX-4T

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ggatccATGGACTGTCTCTGTATAGTGACAACCAAGAAATACCGCTAC
CAAGATGAAGACACGCCCCCTCTGGAACACAGCCCGGCCACCTCCCC
AACCAGGCCAATTCTCCCCCTGTGATTGTCAACACGGACACCCTAGAA
GCCCCAGGATATGAGTTGCAGGTGAATGGAACAGAGGGGGAGATGGAG
TATGAGGAGATCACATTGGAAGGGGTAACCTCAGGTCTGGGCTTCAGC
ATCGCAGGTGGCACTGACAACCCGCACATCGGTGACGACCCGTCCATT
TTTATCACCAAGATCATTCCCTGGTGGGGCTGCAGCCCAGGATGGCCGC
CTCAGGGTCAATGACAGCATCCTGTTTTGTAAATGAAGTGGATGTTCCG
GAGGTGACCCATTCAGCTGCGGTGGAGGCCCTCAAAGAGGCAGGTTCC
ATCGTTTCGCCTCTATGTCATGCGCCGAAACCCCCAGCCGAAAAGGTC
ATGGAGATCAAACCTCATCAAAGGGCCTAAAGGACTTGGCTTCAGCATT
GCGGGGGCGTTGGGAACCAGCACATCCCTGGAGATAACAGCATCTAT
GTAACGAAGATCATCGAAGGAGGTGCTGCCACAAGGATGGCAGGTTG
CAGATTGGAGACAAGATCCTGGCGGTCAACAGTGTGGGGCTGGAGGAC
GTCATGCACGAGGATGCCGTGGCAGCCCTGAAGAACACATATGACGTT
GTGTACCTAAAGGTGGCCAAGCCCAGCAATGCCTACCTGAGTGACAGC
TATGCTCCCCCAGACATCACAACCTCGTATTCTCAGCACCTGGACAAT
GAGATCAGTCATAGCAGCTACTTGGGCACTGACTACCCACAGCCATG
ACCCCCACTTCCCCTCGGCGTACTCCCCTGTGGCCAAGGACCTGCTG
GGGGAGGAAGACATTCCCCGGGAACCAAGGCGGATCGTGATCCATCGG
GGCTCCACCGGCCTGGGCTTCAACATCGTGGGCGGCGAGGATGGTGAA
GGCATCTTCATCTCCTTCATCCTTGCTGGGGGTCCAGCCGACCTCAGT
GGGAGCTACGGAAGGGGGACCAGATCCTGTGCGTCAATGGTGTGAC
CTCCGCAATGCCAGTCACGAACAGGCTGCCATTGCCCTGAAGAATGCG
GGTCAGACGGTCACGATCATCGCTCAGTATAAACAGAAGAGTATAGT
CGATTCGAGGCCAAGATCCATGATCTTCGGGAACAGCTCATGAATAGT
AGCCTAGGCTCAGGGACTGCATCCTTGCGAAGCAACCCCAAGAGGGGC
TTCTACATTAGGGCCCTGTTTTGATTACGACAAGACCAAGGACTGCGGT
TTCTTGAGCCAGGCCCTGAGCTTCCGCTTCGGGGATGTGCTTCATGTC
ATTGACGCTGGTGACGAAGAGTGGTGGCAAGCACGGCGGGTCCACTCC
GACAGTGAGACCGACGACATTGGCTTCATTCACAGCAAACGGCGGGTC
GAGCGACGAGAGTGGTCAAGGTTAAAGGCCAAGGACTGGGGCTCCAGC
TCTGGATCACAGGTCGAGAAGACTCGGTTCTGAGCTATGAGACGGTG
ACCCAGATGGAAGTGCATATGCTCGTCCCATCATCATCCTTGACCC
ACCAAAGACCGTGCCAACGATGATCTTCTCTCCGAGTTCCCCGACAAG
TTTGGATCCTGTGTCCCTCATAACGACACGTCCTAAGCGGGAATATGAG
ATAGACGGCCGGATTACCACTTTGTCTCCTCCCGGGAGAAAATGGAG
AAGGACATCCAGGCACACAAGTTCATTGAGGCTGGCCAGTACAACAGC
CACCTCTATGGGACCAGCGTCCAGTCTGTGCGAGAGGTAGCAGAGCAG
GGGAAGCACTGCATCCTCGATGTCCTCGGCCAATGCCGTGCGGCGGGTC
CAGGCGGCCACCTGCACCCCATCGCCATCTTCATCCGTCCCCGCTCC
CTGGAGAATGTGCTAGAGATCAATAAGCGGATCACAGAGGAGCAAGCC
CGGAAAGCCTTCGACAGAGCCACGAAGCTGGAGCAGGAGTTCACAGAG
TGCTTCTCAGCCATCGTAGAGGGCGACAGCTTTGAAGAGATCTATCAC
AAAGTGAAACGTGTCATTGAAGACCTCTCAGGCCCTACATCTGGGTC
CCAGCCCGAGAGAGACGAATTC
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