



## *Division of Signal Transduction Therapy*

### **Clone Data Sheet**

#### **MPSK1 [1 - 305]**

<b><u>Protein</u></b>	MPSK1 [1 - 305]
<b><u>Clone number</u></b>	DU 11629
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	CR407675
<b><u>Tags</u></b>	N-terminal GST
<b><u>Bacterially expressed protein</u></b>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYE EHL YERDEGDKWRNKKFEL GLEFPNLPYYIDGDVKLTQSMAI IRYIADKHNMLGGCPKERA EISMLE GAVLDIRYGVSRIAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLN GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAI PQIDKY LKSSKYIAWPLQGWQATFGGGDHPKSDLEVL FQGPLGSMGHALCVCS <b>RGTVI IDNKRYLF IQKLGE GGF SYVDLVEGL HDGHFYALKRI LCHEQQ</b> <b>DREEAQRE ADMHRLF NHPN IRLVAYCLR ERGAKHEAWLL PFFKRGT</b> <b>LWNEIERLKD KGNFLTEDQ ILLWLLGICR GLEAIHAKGYAHRDLKPTN</b> <b>ILLGDEGQPVLMDLGS MNQACIHVEGSRQAL TLQDWA AQRCTI SYRAP</b> <b>ELFSVQSHCVI DERTDVW SLGCVLYAMMFGE GPYDMVFQK GDSVALAV</b> <b>QNQLSIPQSPRHSSALW QLLNSMMTVDPHQ RPHIPLLLS QLEALOPPA</b> <b>PGQHTTQI</b></p>
<b><u>Native sequence</u></b>	<p>Amino acids M1 – I305 of human MPSK1.</p> <p>Residue M232 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.</p>
<b><u>Protease cleavage</u></b>	Prescission site ( <u>LEVLFQGP</u> ) at residues 221 - 228
<b><u>Cloning sites</u></b>	<i>Bam</i> H1 and <i>Not</i> 1 sites of pGEX-6P-2

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**Nucleotide  
sequence of insert**

ggatccATGGGCCACGCGCTGTGTGTCTGCTCTCGGGGAAC TGTCATC  
ATTGACAATAAGCGCTACCTCTTCATCCAGAAACTGGGGGAGGGTGGG  
TTCAGCTATGTGGACCTAGTGGAAGGGTTACATGATGGACACTTCTAC  
GCCCTGAAGCGAATCCTGTGTACGAGCAGCAGGACCGGGAGGAGGCC  
CAGCGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTT  
CGCCTCGTGGCTTACTGTCTGAGGGAAACGGGGTGCTAAGCATGAGGCC  
TGGCTGCTGCTACCATTCTTCAAGAGAGGTACGCTGTGGAATGAGATA  
GAAAGGCTGAAGGACAAAGGCAACTTCTGACCGAGGATCAAATCCTT  
TGGCTGCTGCTGGGGATCTGCAGAGGCCCTTGAGGCCATTCATGCCAAG  
GGTTATGCCACAGAGACTTGAAGCCCACCAATATATTGCTTGGAGAT  
GAGGGGCAGCCAGTTTTAATGGACTTGGGTTCCATGAATCAAGCATGC  
ATCCATGTGGAGGGCTCCCGCCAGGCTCTGACCCTGCAGGACTGGGCA  
GCCAGCGGTGCACCATCTCCTACCGAGCCCCAGAGCTCTTCTCTGTG  
CAGAGTCACTGTGTCATCGATGAGCGGACTGATGTCTGGTCCCTAGGC  
TGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTG  
TTCCAAAAGGGTGACAGTGTGGCCCTTGCTGTGCAGAACCAACTCAGC  
ATCCACAAAGCCCCAGGCATTCTTCAGCATTGTGGCAGCTCCTGAAC  
TCGATGATGACCGTGGACCCGCATCAGCGTCCTCACATTCCTCTCCTC  
CTCAGTCAGCTGGAGGCGCTGCAGCCCCAGCTCCTGGCCAACATACT  
ACCCAAATctgagcggccgc