

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of active MST3 [1 - 431]

<u>Enzyme description:-</u>	MST3 [1 - 431]
<u>Clone number:-</u>	DU 30889
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	Baculovirus expression vector system
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	Glutathione Sepharose

Calculated molecular mass:-

Monoisotopic	75,696.68 daltons
Average Mass	75,744.71 daltons
[cysteines reduced, methionines have not been oxidised]	

Theoretical pI:- 5.47

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270 mM sucrose, 150 mM NaCl, 0.1mM EGTA, 0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF.

Storage temperature:- -70 °C

Assay buffer:-

50 mM Tris-HCl pH 7.5, 0.1 % 2-mercaptoethanol, 0.1 mM EGTA, 10 mM MgAc

Substrate:-

Myelin Basic Protein (MBP) Final concentration: 0.3 mg/ml

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Clone Data Sheet

MST3 [1 - 431]

<u>Protein</u>	MST3 [1 - 431]
<u>Clone number</u>	DU 30889
<u>Species</u>	Human
<u>Accession number</u>	AAH65378
<u>Tags</u>	N-terminal GST
<u>Baculovirus expressed protein</u>	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA VLDIRYGVSR IAYS KDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFGQPLGSPGIPGSTRAAAMAH SPVQSGLPGMQNLKADPEELFTKLEKIGKGSFGEVFKGIDNRTQKVVAI KIIDLEEADEDEIEDIQQEITVLSQCDSFYVTKYYSYLKDTKLWIMEY LGGGSALDLLEPGPLDETQIATILREILKGLDYHSEKKIHRDIKAANV LLSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVIKQ SAYDSK ADIWSLGITAIELARGEPPHSELHPMKVFLIPKNNPPTLEGNYSKPLK EFVEACLNKEPSFRPTAKELLKHKFILRNAKKT SYLTEIDRYKRWKA E QSHDDSSSESDAETDGQASGGSDSGDWIFTIREKDPKNLENGALQPSD LDRNKMKDIPKRPF SQCLSTIISPLFAELKEKSQACGGNLGSIEELRGV IYLAEEACPGISDTMVAQLVQRLQRYSLSGGGTSSH
<u>Native sequence</u>	Amino acids M1 – H431 (end) of human MST3. Residue M243 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.
<u>Protease cleavage</u>	PreScission (<u>LEVLFQGP</u>) residues 221 - 229
<u>Cloning sites</u>	<i>Not</i> I and <i>Not</i> I sites in pFastBAC GST

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Nucleotide sequence of insert

gcggccgcgATGGCTCACTCCCCGGTGCAGTCGGGCCTGCCCGGCATGC
AGAACCTAAAAGCAGACCCAGAAGAGCTTTTTACAAAAGCTAGAGAAAAT
TGGGAAGGGCTCCTTTGGAGAGGTGTTCAAAGGCATTGACAATCGGACT
CAGAAAGTGGTTGCCATAAAGATCATTGATCTGGAAGAAGCTGAAGATG
AGATAGAGGACATTCAACAAGAAATCACAGTGCTGAGTCAGTGTGACAG
TCCATATGTAACCAAATATTATGGATCCTATCTGAAGGATACAAAATTA
TGGATAATAATGGAATATCTTGGTGGAGGCTCCGCACTAGATCTATTAG
AACCTGGCCCATTAGATGAAACCCAGATCGCTACTATATTAAGAGAAAT
ACTGAAAGGACTCGATTATCTCCATTTCGGAGAAGAAAATCCACAGAGAC
ATTAAAGCGGCCAACGTCCTGCTGTCTGAGCATGGCGAGGTGAAGCTGG
CGGACTTTGGCGTGGCTGGCCAGCTGACAGACACCCAGATCAAAAGGAA
CACCTTCGTGGGCACCCCATCTGGATGGCACCCGAGGTCATCAAACAG
TCGGCCTATGACTCGAAGGCAGACATCTGGTCCCTGGGCATAACAGCTA
TTGAACTTGCAAGAGGGGAACACCTCATTCCGAGCTGCACCCCATGAA
AGTTTTATTTCCTCATTCCAAAGAACAACCCACCGACGTTGGAAGGAAAC
TACAGTAAACCCCTCAAGGAGTTTGTGGAGGCCTGTTTGAATAAGGAGC
CGAGCTTTAGACCCACTGCTAAGGAGTTATTGAAGCACAAAGTTTATACT
ACGCAATGCAAAGAAAAGTTCTTACTTGACCGAGCTCATCGACAGGTAC
AAGAGATGGAAGGCCGAGCAGAGCCATGACGACTCGAGCTCCGAGGATT
CCGACGCGGAAACAGATGGCCAAGCCTCGGGGGGCAGTGATTCTGGGGA
CTGGATCTTCACAATCCGAGAAAAAGATCCCAAGAATCTCGAGAATGGA
GCTCTTCAGCCATCGGACTTGGACAGAAATAAGATGAAAGACATCCCAA
AGAGGCCTTTCTCTCAGTGTTTATCTACAATTATTTCTCCTCTGTTTGC
AGAGTTGAAGGAGAAGAGCCAGGCGTGCGGAGGGAAGTTGGGGTCCATT
GAAGAGCTGCGAGGGGTCATCTACCTAGCGGAGGAGGCGTGCCCTGGCA
TCTCCGACACCATGGTGGCCAGCTCGTGCAGCGGCTCCAGAGATACTC
TCTAAGTGGTGGAGGAAGTTTCATCCCACTgagcggccgc