

Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of active MELK [2 - 651]

<u>Enzyme description:-</u>	MELK [2 - 651]
<u>Clone number:-</u>	DU 1199
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	<i>E.coli</i>
<u>Tag:-</u>	N-terminal GST and C-terminal His(6)
<u>Purification method:-</u>	GSH Sepharose followed by Ni ²⁺ -NTA agarose
<u>Expression level:-</u>	0.5 mg/L
<u>Calculated molecular mass:-</u>	102, 092 daltons
<u>Purity:-</u>	90 %
<u>Activation protocol:-</u>	Constitutively active
<u>Enzyme storage buffer:-</u>	50 mM Tris-HCl pH 7.5, 270mM sucrose, 150 mM NaCl, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF
<u>Storage temperature:-</u>	-70 °C
<u>Assay:-</u>	Standard filter binding assay
<u>Assay buffer:-</u>	50 mM Tris-HCl pH 7.5, 0.1 % 2-mercaptoethanol, 0.1 mM EGTA, 10 mM MgAc
<u>Substrate:-</u>	[KKLNRTLSFAEPG] Final concentration: 200 µM
<u>Specific activity range:-</u>	150 – 300 U/mg

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Clone Data Sheet

MELK [2 - 651]

<u>Protein</u>	MELK [2 - 651]
<u>Clone number</u>	DU 1199
<u>Species</u>	Human
<u>Accession number</u>	NM_014791
<u>Tags</u>	N-terminal GST and C-terminal His(6)
<u>Bacterially expressed protein</u>	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPPYYIDGDVKLTQSMAIIRYIADKHNLGGCPKERAESMLEGA VLDIHYGVSRIAYSKDFETLKVDFLSKLPEMLKMFDRLCHKTYLNGDH VTHPDFMLYDALDVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGSKDYDELLKYYELHE TIGTGGFAKVKLACHILTGEVAIKIMDKNTLGSIDLPRIKTEIEALKNL RHQHICQLYHVLETANKIFMVLEYCPGGELFDYIISQDRLSEETRVVF RQIVSAVAYVHSQGYAHSDLKPENLLFDEYHKLKLIDFGLCAPKGNKD YHLQTCCGSLAYAAPELIQGKSYLGSEADVWSMGILLVLMCGFLPFDD DNVMALYKKIMRGKYDVPKWLSPSSILLQQMLQVDPKKRISMKNLLNH PWIMQDYNYPVEWQSKNPFIHLDCCVTLSVHHRNNRQTMEDLISLWQ YDHLTATYLLLAKKARGKPVRLRSSFSCGQASATPFTDIKSNNWSLE DVTASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKS LTPALCRTPANKLNKENVYTPKSAVKNEEYFMFPEPKTPVNKNQHKRE ILTPPNRYTTPSKARNQCLKETPIKIPVNSTGTDKLMTGVISPERRCRS VELDLNQAHMEETPKRKGAKVFGSLERGLDKVITVLTTRSKRKGARDGP RRLKLHYNVTTTRLVNPQOLLNEIMSILPKKHVDVFQKGYTLKCQTQSD FGKVTMQFELEVQCOLQKPDVVGIRRQRLKGDAWVYKRLVEDILSSCKVH HHHHH
<u>Native sequence</u>	Amino acids K2 – V651 (end) of human MELK. Residue K232 of the fusion protein is equivalent to K2 of the native enzyme. The GST tag is located at residues 1 - 220 and the His(6) is located at residues 882 - 887
<u>Protease cleavage</u>	PreScission (<u>LEVLFQGPL</u>) residues 221 - 229
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> 1 site of pGEX 6P-1

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<u>Nucleotide Sequence of insert</u>	GGATCCAAAGATTATGATGAACCTCTCAAATATTATGAATTA CATGAAACTATTGGGACAGGTGGCTTGCAAAGGTCAAACCTT GCCTGCCATATCCTTACTGGAGAGATGGTAGCTATAAAAATC ATGGATAAAAACACACTAGGGAGTGATTGCCCGGATCAAA ACGGAGATTGAGGCCTTGAAGAACCTGAGACATCAGCATATA TGTCAACTCTACCATGTGCTAGAGACAGCCAACAAAATATTC ATGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTGACTAT ATAATTCCCAGGATCGCCTGTCAGAAGAGGAGACCCGGGTT GTCTTCCGTCAGATAGTATCTGCTGTTGCTTATGTGCACAGC CAGGGCTATGCTCACAGGGACCTCAAGCCAGAAAATTGCTG TTTGATGAATATCATAAATTAAAGCTGATTGACTTGGTCTC TGTGCAAAACCCAAAGGGTAACAAGGATTACCATCTACAGACA TGCTGTGGAGTCTGGTTATGCAGCACCTGAGTTAACCAA GGCAAATCATATCTTGGATCAGAGGCAGATGTTGGAGCATG GGCATACTGTTATATGTTCTATGTTGGATTCTACCATTT GATGATGATAATGTAATGGCTTATACAAGAAGATTATGAGA GGAAAATATGATGTTCCAAGTGGCTCTCTCCAGTAGCATT CTGCTTCTTCAACAAATGCTGCAGGTGGACCCAAAGAACGG ATTTCTATGAAAAATCTATTGAACCATCCCTGGATCATGCAA GATTACAACATCCTGTTGAGTGGCAAAGCAAGAACATCCTTT ATTCACCTCGATGATGATTGCGTAACAGAACTTCTGTACAT CACAGAAACAACAGGAAACAATGGAGGATTAAATTCACTG TGGCAGTATGATCACCTCACGGCTACCTATCTCTGTTCTA GCCAAGAAGGCTCGGGAAAACCAGTCGTTAACGGTTCT TCTTCTCCTGTGGACAAGCCAGTGCTACCCATTACAGAC ATCAAGTCAAATAATTGGAGTCTGGAAGATGTGACCGCAAGT GATAAAAATTATGTCGGGGATTAATAGACTATGATTGGTGT GAAGATGATTATCAACAGGTGCTGCTACTCCCCAACATCA CAGTTACCAAGTACTGGACAGAACATCAAATGGGTGGAATCT AAATCATTAACCTCAGCCTTATGCAGAACACCTGCAAATAAA TTAAAGAACAAAGAAAATGTATATACTCCTAAGTCTGCTGTA AAGAATGAAGAGTACTTTATGTTCTGAGCCAAAGACTCCA GTTAATAAGAACCAAGCATAAGAGAGAAATACTCACTACGCCA AATCGTTACACTACACCCTCAAAAGCTAGAAACCAGTGCTG AAAGAAACTCCAATTAAAATACCAGTAAATTCAACAGGAACA GACAAGTTAATGACAGGTGTCATTAGCCCTGAGAGGGCGGTG CGCTCAGTGGATTGGATCTCAACCAAGCACATATGGAGGAG ACTCCAAAAAGAAAGGGAGCCAAAGTGTGTTGGAGCCTTGAA AGGGGGTTGGATAAGGTTATCACTGTGCTCACCAAGGAGCAA AGGAAGGGTTCTGCCAGAGACGGGCCAGAACAGACTAAAGCTT CACTATAATGTGACTACAACTAGATTAGTGAATCCAGATCAA CTGTTGAATGAAATAATGTCTATTCTTCAAAGAACAGCATGTT
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GACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAACACAG
TCAGATTGAAAGTGACAATGCAATTGAATTAGAAGTG
TGCCAGCTTCAAAAACCGATGTGGTGGGTATCAGGAGGCAG
CGGCTTAAGGGCGATGCCTGGGTTACAAAGATTAGTGGAA
GACATCCTATCTAGCTGCAAGGTACACCACCATCACCACCAT
taggcggccgc