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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]

Protein MELK [2 - 651]

Clone number DU 1199

Species Human

Accession number NM_014791

Tags N-terminal GST and C-terminal His(6)

Bacterially expressed protein

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA
VLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS
KYIAWPLQGWQATFGGGDHPPKSDLEVL FQGPLGSKDYDELLKYYELHE
TIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDLPRIKTEIEALKNL
RHQHICQLYHVLETANKIFMVLEYCPGGELFDYIISQDRLSEETR VVF
RQIVSAVAYVHSQGYAHRDLKPENLLFDEYHKLKLI DFGLCAKPKGNKD
YHLQTCCGSLAYAPELIQKSYLGSEADVWSMGILLYVLMCGFLPFDD
DNVMALYKKIMRGKYDVPKWLSPSSILLLQOMLQVDPKKRISMKNLLNH
PWIMQDYNYPVEWQSKNPF IHLDDDCVTELSVHHRNNRQTMEDLISLWQ
YDHLTATYLLLLAKKARGKPVRLRLSSFSCGQASATPFTDIKSNNWSLE
DVTASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKS
LTPALCRTPANKLKNKENVYTPKSAVKNEEYFMFPEPKTPVNKNQHKRE
ILTTPNRYTTPSKARNQCLKETPIKIPVNSTGTDKLMTGVISPERRCRS
VELDLNQAHEETPKRKGAKVFGSLERGLDKVITVLT RSKRKG SARDGP
RRLKLHYNVTTTRLVNPDQLLNEIMSILPKKHVDFVQKGYTLKCQTQSD
FGKVTMQFELEVCQLOKPDVVGIRRQRLKGD AWVYKRLVEDILSSCKVH
HHHHH

Native sequence 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

Protease cleavage PreScission (LEVLFQGPL) residues 221 - 229

Cloning sites *Bam*H1 and *Not*1 site of pGEX 6P-1

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Nucleotide Sequence of insert

GGATCCAAAGATTATGATGAACTTCTCAAATATTATGAATTA
CATGAAACTATTGGGACAGGTGGCTTTGCAAAGGTCAAACCTT
GCCTGCCATATCCTTACTGGAGAGATGGTAGCTATAAAAATC
ATGGATAAAAACACACTAGGGAGTGATTTGCCCCGGATCAA
ACGGAGATTGAGGCCTTGAAGAACCTGAGACATCAGCATATA
TGTCAACTCTACCATGTGCTAGAGACAGCCAACAAAATATTC
ATGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTTGACTAT
ATAATTTCCAGGATCGCCTGTCAGAAGAGGAGACCCGGGTT
GTCTTCCGTCAGATAGTATCTGCTGTTGCTTATGTGCACAGC
CAGGGCTATGCTCACAGGGACCTCAAGCCAGAAAATTTGCTG
TTTGATGAATATCATAAATTAAAGCTGATTGACTTTGGTCTC
TGTGCAAACCCAAGGGTAACAAGGATTACCATCTACAGACA
TGCTGTGGGAGTCTGGCTTATGCAGCACCTGAGTTAATACAA
GGCAAATCATATCTTGGATCAGAGGCAGATGTTTGGAGCATG
GGCATACTGTTATATGTTCTTATGTGTGGATTTCTACCATTT
GATGATGATAATGTAATGGCTTTATACAAGAAGATTATGAGA
GGAAAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATT
CTGCTTCTTCAACAAATGCTGCAGGTGGACCCAAAGAAACGG
ATTTCTATGAAAATCTATTGAACCATCCCTGGATCATGCAA
GATTACAACATCCTGTTGAGTGGCAAAGCAAGAATCCTTTT
ATTCACCTCGATGATGATTGCGTAACAGAACTTTCTGTACAT
CACAGAAACAACAGGCAAACAATGGAGGATTTAATTTCACTG
TGGCAGTATGATCACCTCACGGCTACCTATCTTCTGCTTCTA
GCCAAGAAGGCTCGGGGAAAACCAGTTCGTTTAAAGCTTTCT
TCTTTCTCCTGTGGACAAGCCAGTGCTACCCCATTCACAGAC
ATCAAGTCAAATAATTGGAGTCTGGAAGATGTGACCGCAAGT
GATAAAAATTATGTGGCGGGATTAATAGACTATGATTGGTGT
GAAGATGATTTATCAACAGGTGCTGCTACTCCCCGAACATCA
CAGTTTACCAAGTACTGGACAGAATCAAATGGGGTGGAACTCT
AAATCATTAACCTCAGCCTTATGCAGAACACCTGCAAATAAA
TTAAAGAACAAGAAAATGTATATACTCCTAAGTCTGCTGTA
AAGAATGAAGAGTACTTTATGTTTCCTGAGCCAAAGACTCCA
GTTAATAAGAACCAGCATAAGAGAGAAATACTCACTACGCCA
AATCGTTACTACACCTCAAAGCTAGAAACCAGTGCCTG
AAAGAACTCCAATTAATAACAGTAAATTCAACAGGAACA
GACAAGTTAATGACAGGTGTCATTAGCCCTGAGAGGCGGTGC
CGCTCAGTGAATTGGATCTCAACCAAGCACATATGGAGGAG
ACTCCAAAAGAAAAGGGAGCCAAAGTGTTTGGGAGCCTTGAA
AGGGGGTTGGATAAGGTTATCACTGTGCTCACCAGGAGCAA
AGGAAGGGTTCTGCCAGAGACGGGCCAGAAAGACTAAAGCTT
CACTATAATGTGACTACAACCTAGATTAGTGAATCCAGATCAA
CTGTTGAATGAAATAATGTCTATTCTTCCAAAGAAGCATGTT

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GACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAACACAG
TCAGATTTTGGGAAAGTGACAATGCAATTTGAATTAGAAGTG
TGCCAGCTTCAAAAACCCGATGTGGTGGGTATCAGGAGGCAG
CGGCTTAAGGGCGATGCCTGGGTTTACAAAAGATTAGTGAA
GACATCCTATCTAGCTGCAAGGTACACCATCACCATCACCAT
taggcggccgc