

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of MRCK alpha [1 - 473]

Enzyme description:- MRCK alpha [1 - 473]

Clone number:- DU 62967

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH-Sepharose

Calculated molecular mass:-

Monoisotopic 81, 157.53 daltons

Average Mass 81, 209.98 daltons

[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 5.25

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM 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, 0.1mM EGTA, 10 mM DTT, 10 mM MgAc

Substrate:-

KKRNRTLTV Final concentration: 300 uM

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Clone Data Sheet

MRCK alpha [1 - 473]

<u>Protein</u>	MRCK alpha [1 - 473]
<u>Clone number</u>	DU 62967
<u>Species</u>	Human
<u>Accession number</u>	NM_003607.3
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHYERDEGDKWRNKKFELG LEFPNLPPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAESMLEGA VLDIIRYGVSRRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKS <u>DLEVLFQGPLGSMSGEVRLROLEQFI</u> LDGPAQTNGQCFSVETLLDILICLYDECNNNSPLRREKNILEYLEWAKPF TSKVQMRLLHREDFEILKVIIRGAFGEVAVVVLKNADKVFAMKILNKWE MLKRAETACFREERDVLVNGDNKWITTLHYAFQDDNNLYLVMDYYVGGD LLTLLSKFEDRLPEDMARFYLAEMVIAIDSVHQLHYVHRDIKPDNILMD MNMGHIRLADFGSCLKLMEDGTVQSSVAVGTPDYISPEILOQAMEDGKGRY GPECDWWSLGVCMYEMLYGETPFYAESLVTYKGIMNHKERFQFPAQVT DVSENAKDLIRRLLICSREHRLGQNGIEDFKKHPFFSGIDWDNIRNCEAP YIPEVSSPTDTSNFDVDDDCLKNSETMPPPTHTAFSGHHLPPVGFTYTS SCVLSDRSCLRVTAGPTSLDDLVNVQRTLDNNNATEAYERRIKRLEQEK LELSRKLQESTQTVQALQ
<u>Native sequence</u>	Amino acids M1 – Q473 (end residue is P1719) of human MRCK alpha. Residue M232 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 – 228
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> 1 sites of pGEX6P-1

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Nucleotide
Sequence Of
Insert

ggatccATGTCTGGAGAAGTGCCTTGAGGCAGTTGGAGCAGTTATT
TGGACGGGCCGCTCAGACCAATGGGCAGTGCTTCAGTGTGGAGACATT
ACTGGATATACTCATCTGCCTTATGATGAATGCAATAATTCTCCATTG
AGAAGAGAGAAGAACATTCTCGAATACCTAGAATGGCTAAACCATT
CTTCTAAAGTGAACAAATGCGATTACATAGAGAAGACTTGAAATATT
AAAGGTGATTGGTCGAGGGAGCTTGGGGAGGTTGCTGTAGTAAA
AAAAATGCAGATAAAAGTGTGTTGCCATGAAAATATTGAATAAATGGAAA
TGCTGAAAAGAGCTGAGACAGCATGTTCTGTAAGAAAGGGATGTATT
AGTGAATGGAGACAATAATGGATTACAACCTGCACATGCTTCCAG
GATGACAATAACTTACCTGGTTATGGATTATTATGTTGGTGGGGATT
TGCTTACTCTACTCAGCAAATTGAAGATAGATTGCCTGAAGATATGCC
TAGATTTACTTGGCTGAGATGGTATAGCAATTGACTCAGTCATCAG
CTACATTATGTACACAGAGACATTAACCTGACAATATACTGATGGATA
TGAATGGACATATTGGTTAGCAGATTTGGTTCTGTCTGAAGCTGAT
GGAAGATGGAACGGTCAGTCAGTGGCTGTAGGAACCTCCAGATTAT
ATCTCTCCTGAAATCCTCAAGCCATGGAAGATGGAAAAGGGAGATATG
GACCTGAATGTGACTGGTGGTCTTGGGGTCTGTATGTATGAAATGCT
TTACGGAGAACACCATTATGCAGAATCGCTGGTGGAGACATACGGA
AAAATCATGAACCACAAAGAGAGGTTTCAGTTCCAGCCCCAAGTGA
ATGTGTCTGAAATGCTAAGGATCTTATTGCAAGGCTCATTGTAGCAG
AGAACATCGACTTGGTCAAAATGGAATAGAAGACTTAAGAAACACCCA
TTTTTCAGTGGATTGGATAATATTGGAACACTGTGAAGCACCTT
ATATTCCAGAAGTTAGTAGGCCAACAGATACTGAATTGATGTAGA
TGATGATTGTTAAAAAATTCTGAAACGATGCCAACCAACACATACT
GCATTTCTGCCACCATCTGCCATTGTTGGTTACATATACTAGTA
GCTGTGTACTTCTGATCGGAGCTTTAAGAGTTACGGCTGGTCCCAC
CTCACTGGATCTTGTATGTTAATGTCAGAGGACTCTAGACAACAA
GCAACTGAAGCTTATGAAAGAAGAATTAGCGCCTTGAGCAAGAAA
TTGAACTCAGTAGAAAATTCAAGAGTCAACACAGACTGTCCAAGCTCT
GCAGtgagcggccgc