

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of MKK6 [1 - 334] K82A

<u>Enzyme description:-</u>	MKK6 [1 - 334] K82A
<u>Clone number:-</u>	DU 50032
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	<i>E.coli</i>
<u>Tag:-</u>	N-terminal MBP (maltose binding protein)
<u>Purification method:-</u>	Amylose agarose
<u>Calculated molecular mass:-</u>	
Monoisotopic	83, 038.24 daltons
Average Mass	83, 090.83 daltons
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	5.27
<u>Purity:-</u>	>80 %
<u>Enzyme storage buffer:-</u>	
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	
<u>Storage temperature:-</u>	-70 °C

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Clone Data Sheet

MKK6 [1 - 334] K82A

<u>Protein</u>	MKK6 [1 - 334] K82A
<u>Clone number</u>	DU 50032
<u>Species</u>	Human
<u>Accession number</u>	NM_002758
<u>Tags</u>	N-terminal MBP
<u>Bacterially expressed protein</u>	MMKIEEGKLVIIWINGDKGYNGLAIEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVNDAGAKAGLTLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYYYEELVKDPRIAATMENAQKGEIMPNI PQMSAFWYAVRTAVINAASGRQTVDEALKDAQTNSSSNNNNNNNNNNLGDDDDKVPEFLEVLFGQPLGSPGEFASLEKLAAAMSQSKGKKRNPLKIPKEAFEQPTSSSTPPRDLDISKACISIGNQNFVKKADDLEPIMELGRGAYGVVEKMRHVPSTQIMAVARIRATVNSQEQKRLMDLDISMRTVDCPFTVTFYGFALFREGDVWICMELMDTSLDKFYKQVIDKGQTIPELILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDGFGISGYLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIWSLGITMIELAILRFPYDSWGTPFQQLKVVEEPSQPLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGTDVASFVKLILGD
<u>Native sequence</u>	Amino acids M1 – D334 (end) of human MKK6. Residue M418 of the fusion protein is M1 of the native enzyme. The enzyme has a K82A mutation to produce a kinase dead enzyme. Residue K82 is equivalent to A499 of the fusion protein. The MBP tag is located at residues 1 – 393.
<u>Protease cleavage</u>	PreScission (LEVLFQGP) residues 394 - 401

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Cloning sites

*Not*1 sites of pMEX3Cb

Nucleotide sequence of insert

gcggccgcgATGTCTCAGTCGAAAGGCAAGAAGCGAAACCCTGGCCTT
AAAATTCCAAAAGAAGCATTGTAACAACCTCAGACCAGTTCCACACCA
CCTCGAGATTTAGACTCCAAGGCTTGCATTTCTATTGGAAATCAGAAC
TTTGAGGTGAAGGCAGATGACCTGGAGCCTATAATGGAAGTGGGACGA
GGTGCGTACGGGGTGGTGGAGAAGATGCGGCACGTGCCAGCGGGCAG
ATCATGGCAGTGGCGCGGATCCGAGCCACAGTAAATAGCCAGGAACAG
AAACGGCTACTGATGGATTTGGATATTTCCATGAGGACGGTGGACTGT
CCATTCACCTGTACCTTTTATGGCGCACTGTTTCGGGAGGGTGTGTG
TGGATCTGCATGGAGCTCATGGATACATCACTAGATAAATTCTACAAA
CAAGTTATTGATAAAGGCCAGACAATTCCAGAGGACATCTTAGGGAAA
ATAGCAGTTTCTATTGTAAAAGCATTAGAACATTTACATAGTAAGCTG
TCTGTCATTACAGAGACGTCAAGCCTTCTAATGTACTCATCAATGCT
CTCGGTCAAGTGAAGATGTGCGATTTTGGAAATCAGTGGCTACTTGGTG
GACTCTGTTGCTAAAACAATTGATGCAGGTTGCAAACCATAACATGGCC
CCTGAAAGAATAAACCAGAGCTCAACCAGAAGGGATACAGTGTGAAG
TCTGACATTTGGAGTCTGGGCATCACGATGATTGAGTTGGCCATCCTT
CGATTTCCCTATGATTCATGGGGAACCTCATTTCAGCAGCTCAAACAG
GTGGTAGAGGAGCCATCGCCACAACCTCCCAGCAGACAAGTTCTCTGCA
GAGTTTGTTGACTTTACCTCACAGTGCTTAAAGAAGAATTCCAAAGAA
CGGCCTACATAACCAGAGCTAATGCAACATCCATTTTTTACCCTACAT
GAATCCAAAGGAACAGATGTGGCATCTTTTGTAAGAACTGATTCTTGGA
GACtaagcggccgc