

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of active MLK3 [96 - 386]

<u>Enzyme description:-</u>	MLK3 [96 - 386]
<u>Clone number:-</u>	DU 8313
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	Baculovirus expression vector system
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH Sepharose
<u>Expression level:-</u>	3 mg/L

Calculated molecular mass:-

Monoisotopic 60,759.92 daltons
Average Mass 60,799.30 daltons
[cysteines reduced, methionines have not been oxidised]

<u>Theoretical pI:-</u>	5.74
<u>Purity:-</u>	>80 %
<u>Activation protocol:-</u>	Constitutively active

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

<u>Storage temperature:-</u>	-70 °C
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<u>Assay:-</u>	Standard filter binding assay
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Assay buffer:-

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

Substrate:-

MBP Final concentration: 0.3 mg/ml

<u>Specific activity range:-</u>	To be determined
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Clone Data Sheet

MLK3 [96 - 386]

<u>Protein</u>	MLK3 [96 - 386]
<u>Clone number</u>	DU 8313
<u>Species</u>	Human
<u>Accession number</u>	NM_002419
<u>Tags</u>	N-terminal GST
<u>Baculovirus expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWR NKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGG CPKERAIEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKL PEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPM CLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATF GGGDHPPKSDLEVLFOGPLGSPGIGGGGGIPSNYVSRGGGPP PCEVASFQELRLEEVIIGGGFGKVYRGSWRGELVAVKAARQD PDEDISVTAESVRQEARLFAMLAHPNIIALKAVCLEEPNLCL VMEYAAGGPLSRALAGRRVPPHVLVNWAVQIARGMHYLHCEA LVPVIHRDLKSNNILLLOPIESDDMEHKTALKITDFGLAREWH KTTQMSAAGTYAWMAPEVIKASTFSKGSVDVWSFGVLLWELLT GEVPYRGIDCLAVAYGVAVNKLTLPPIPSTCPEPFAQLMADCW AQDPHRRPDFASILQOLEALEAQVLRMPRDSFHSMQ</p>
<u>Native sequence</u>	<p>Amino acids P96 – Q386 (end P847) of human MLK3. Residue P of the fusion protein is equivalent to P96 of the native enzyme. The GST tag is located at residues 1 – 220.</p>
<u>Protease cleavage</u>	PreScission (<u>LEVLFOGP</u>) residues 221 - 228
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> I site of pFastBac GST

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Nucleotide
Sequence of insert

ggatcccccggtattggaggagggggcggtattCCGTCCAAC TATGTGT
CTCGGGGTGGCGGCCCGCCCCCTGCGAGGTGGCCAGCTTCCAGGAGCT
GCGGCTGGAGGAGGTGATCGGCATTGGAGGCTTTGGCAAGGTGTACAGG
GGCAGCTGGCGAGGTGAGCTGGTGGCTGTGAAGGCAGCTCGCCAGGACC
CCGATGAGGACATCAGTGTGACAGCCGAGAGCGTTCCGCCAGGAGGCCCG
GCTCTTCGCCATGCTGGCACACCCCAACATCATTGCCCTCAAGGCTGTG
TGCCTGGAGGAGCCCAACCTGTGCCTGGTGTGATGGAGTATGCAGCCGGTG
GGCCCCTCAGCCGAGCTCTGGCCGGGCGGCGGTGCCTCCCCATGTGCT
GGTCAACTGGGCTGTGCAGATTGCCCGTGGGATGCACTACCTGCACTGC
GAGGCCCTGGTGCCCGTCATCCACCGTGATCTCAAGTCCAACAACATTT
TGCTGCTGCAGCCCATTGAGAGTGACGACATGGAGCACAAAGACCCTGAA
GATCACCGACTTTGGCCTGGCCCGAGAGTGGCACA AAAACCACACAAATG
AGTGCCGCGGGCACCTACGCCTGGATGGCTCCTGAGGTTATCAAGGCCT
CCACCTTCTCTAAGGGCAGTGACGTCTGGAGTTTTGGGGTGCTGCTGTG
GGA ACTGCTGACCGGGGAGGTGCCATAACCGTGGCATTGACTGCCTTGCT
GTGGCCTATGGCGTAGCTGTTAAACAAGCTCACACTGCCCATCCCATCCA
CCTGCCCCGAGCCCTTCGCACAGCTTATGGCCGACTGCTGGGCGCAGGA
CCCCACCGCAGGCCCGACTTCGCCTCCATCCTGCAGCAGTTGGAGGCG
CTGGAGGCACAGGTCCTACGGGAAATGCCGCGGACTCCTTCCATTCCA
TGCAGtaagcggccgc