

Certificate of Analysis

MAP3K3 (MEKK3), 10 µg

Mitogen-Activated Protein Kinase Kinase Kinase 3, GST-tagged



Part Number: PV3876
Lot Number: 702480A
Immediate Storage: -80°C
Shipping Conditions: dry ice

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Description:

Recombinant human full length protein, GST-tagged, expressed in insect cells. No special measures were taken to activate this kinase.

Specific Activity:

34 nmoles of phosphate transferred to myelin basic protein (MBP) per minute per mg of total protein at 30°C. Activity determined at a final protein concentration of 8.33 µg/mL.

Concentration:

0.21 mg/mL total protein as measured using the Bradford protein assay with BSA as a standard.

Calculated **2,100 nM**.

Aliases:

MEKK3, MAPKKK3

Storage and Handling:

Store at -80°C. At first use, aliquot and store at -80°C to avoid multiple freeze-thaws. If properly stored at -80°C, this product is guaranteed for 6 months from date of purchase.

Storage Buffer:

50 mM Tris (pH 7.5), 150 mM NaCl, 0.5 mM EDTA, 0.02% Triton® X-100, 2 mM DTT and 50% Glycerol.

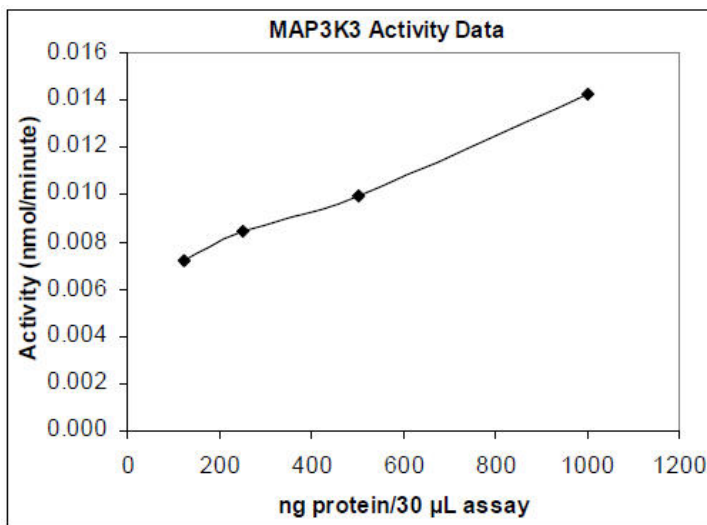
Dilution Buffer*:

20 mM Tris (pH 7.5), 0.02% Triton® X-100, 0.1 mg/mL BSA, 2 mM DTT, 0.5 mM Na₃VO₄ and 10% Glycerol.

* Note: The dilution buffer described above is used for the radiometric assay format only. For high throughput applications such as LanthaScreen®, Adapta® and Z-LYTE® refer to the associated product literature for the recommended buffer.

QUALITY ASSURANCE

MAP3K3 (MEKK3) Activity Graph



Assay Conditions:

MAP3K3 (MEKK3) was pre-diluted in enzyme dilution buffer and assayed in 25 mM Tris (pH 7.5), 10 mM MgCl₂, 0.5 mM EGTA, 0.5 mM Na₃VO₄, 5 mM β-glycerophosphate, 2.5 mM DTT, 0.01% Triton® X-100, 100 µM ATP, 500 µg/mL myelin basic protein (MBP) and trace [³²P]-γ-ATP for 10 minutes at 30°C.

Gel Information for MAP3K3 (MEKK3)

Page Description: The SDS-PAGE and/or Native PAGE were run on 4-20% Tris-Glycine Novex® gels (Catalog #: EC6025BOX).

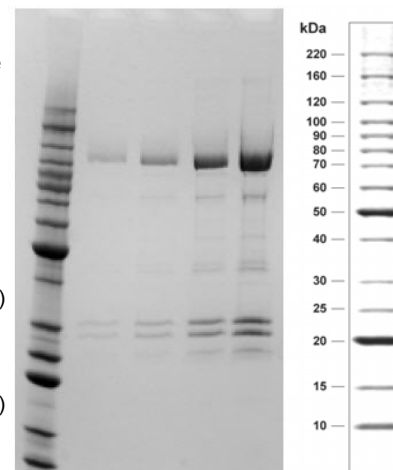
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.5 µg MAP3K3 (MEKK3)

Lane 3: 1 µg MAP3K3 (MEKK3)

Lane 4: 2.5 µg MAP3K3 (MEKK3)

Lane 5: 5 µg MAP3K3 (MEKK3)



Purity:

60% as determined by a Coomassie® blue stained SDS-PAGE gel.

Molecular Weight:

99.8 kDa calculated from the protein sequence(s). Calculated from the protein sequence(s).

Mass Spectrometry:

MAP3K3 (MEKK3) was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified MAP3K3 (MEKK3) identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_002392

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1 MAPILGYWKI KGLVQPTRLL LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID GDVKLTSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL GST TAG
1 MAPILGYWKI KGLVQPTRLL LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID GDVKLTSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL IVGN MAP3K3
1 NP_002392
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101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPOID KYLKSSKYIA
101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPOID KYLKSSKYIA
1
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201 WPLQGWAQTF GGGDHPPKSD LVPR
201 WPLQGWAQTF GGGDHPPKSD LVPRNHQTSL YKKAGSAAAL FNFKKEPFTM DEQEALNSIM NDVALQMNR RHRMPGYETM KNKDTGHSNR QSDVRIKFEH
1 DEQEALNSIM NDVALQMNR RHRMPGYETM KNKDTGHSNR QSDVRIKFEH
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224
301 NGERRIIAFS RPVKYEDVEH KVTTVFQGPL DLHYMNNELS ILLKNQDDL KAIIDILDRSS SMKSLRILL SODRNHNSSS PHSGVSQRVR IKASQSAGDI
52 NGERRIIAFS RPVKYEDVEH KVTTVFQGPL DLHYMNNELS ILLKNQDDL KAIIDILDRSS SMKSLRILL SODRNHNSSS PHSGVSQRVR IKASQSAGDI
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224
401 NTIYQPPEPR SRHLSVSSQN PGRSSPPPGY VPERQHIAR QGSYTSINSE GEFIPETSEQ CMLDPLSSAE NSLSGSCQSL DRSDSPSFR KSRMSRAQSF
152 NTIYQPPEPR SRHLSVSSQN PGRSSPPPGY VPERQHIAR QGSYTSINSE GEFIPETSEQ CMLDPLSSAE NSLSGSCQSL DRSDSPSFR KSRMSRAQSF
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224
501 PDNRQEYSR ETQLYDKGVK GGTYPYRYHV SVHHKDYSYG RRTFPRIRRH QGNLFTLVPS SRSLSTNGEN MGLAVQYLDP RGRLSADSE NALSQERNV
252 PDNRQEYSR ETQLYDKGVK GGTYPYRYHV SVHHKDYSYG RRTFPRIRRH QGNLFTLVPS SRSLSTNGEN MGLAVQYLDP RGRLSADSE NALSQERNV
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224
601 PTKSPSAPIN WRRGKLLGQG AFGRVLYCYD VDTGRELASK QVQFDPDSPE TSKEVSALEC EIQLLKNLQH ERIVQYGGCL RDRAEKLTI FMEYMPGGSV
352 PTKSPSAPIN WRRGKLLGQG AFGRVLYCYD VDTGRELASK QVQFDPDSPE TSKEVSALEC EIQLLKNLQH ERIVQYGGCL RDRAEKLTI FMEYMPGGSV
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224
701 KDQLKAYGAL TESVTRKYTR QILEGMSYLH SNMIVHRDIK GANILRDSAG NVKLGDFGAS KRLQITICMSG TGMRSVTGTP YWMSPEVISG EGYGRKADVW
452 KDQLKAYGAL TESVTRKYTR QILEGMSYLH SNMIVHRDIK GANILRDSAG NVKLGDFGAS KRLQITICMSG TGMRSVTGTP YWMSPEVISG EGYGRKADVW
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224
801 SLGCTVVEML TEKPPWAEYE AMAAIFKIAT QPTNPQLPSH ISEHGRDFLR RIFVEARQRP SAEELLTHHF AQLMY
552 SLGCTVVEML TEKPPWAEYE AMAAIFKIAT QPTNPQLPSH ISEHGRDFLR RIFVEARQRP SAEELLTHHF AQLMY

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* highlighted residues denote differences from the reference protein sequence(s).



Marlene Johnson, Manager, QA/QC

Date: 24/Feb/2012

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