Certificate of Analysis
MAP3K14 (NIK), 10 µg

Mitogen-Activated Protein Kinase Kinase Kinase 14, GST-tagged

Part Number: PV4902
Lot Number: 1759171B
Immediate Storage: -80°C
Shipping Conditions: dry ice

5791 Van Allen Way
Carlsbad, CA 92008
Phone: 760.603.7200
Fax: 760.602.6500
www.lifetechnologies.com

Description:

Recombinant human, amino acids 318-947, GST-tagged, expressed in insect cells. No special measures were taken to activate this kinase.

Specific Activity:

6 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 4.17 µg/mL.

Concentration:

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

Calculated **2,170 nM**.

Aliases:

NIK, HSNIK, FTDCR1B

Storage and Handling:

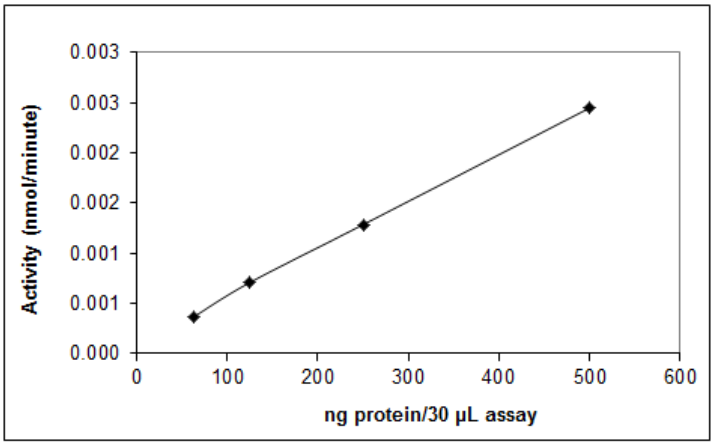
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 ug, 10ug and 20ug sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 20 µL are not recommended. **Please never store a kinase diluted.** 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.

QUALITY ASSURANCE

MAP3K14 (NIK) Activity Graph



Gel Information for MAP3K14 (NIK)

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

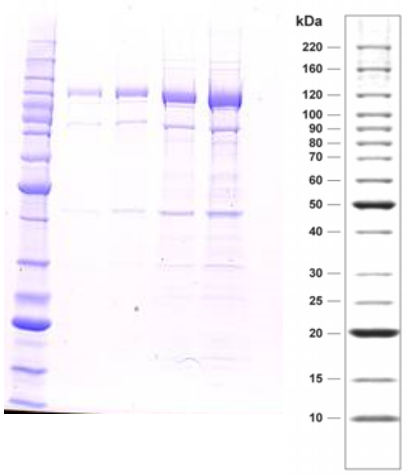
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.5 µg MAP3K14 (NIK)

Lane 3: 1.0 µg MAP3K14 (NIK)

Lane 4: 2.5 µg MAP3K14 (NIK)

Lane 5: 5.0 µg MAP3K14 (NIK)



Dilution Buffer:

20 mM Tris (pH 7.5), 0.02% Triton® X−100, 0.1 mg/mL BSA, 5 mM β−glycerophosphate, 2 mM DTT, 1 mM Na_3VO_4 and 10% Glycerol.

Assay Conditions:

MAP3K14 (NIK) was pre-diluted in enzyme dilution buffer and assayed in 20 mM Tris (pH 7.5), 10 mM $MgCl_2$, 1 mM EGTA, 1 mM Na_3VO_4, 5 mM β−glycerophosphate, 2 mM DTT, 0.02% Triton® X-100, 100 µM ATP, 830 µg/mL myelin basic protein (MBP) and trace [^{32}P]-γ-ATP for 10 minutes at 30°C.

Purity:

55% as determined by a Coomassie® blue stained SDS-PAGE gel.

Molecular Weight:

96.9 kDa. Calculated from the protein sequence(s).

Mass Spectrometry:

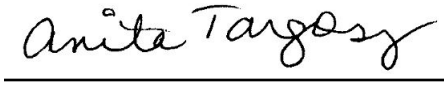
MAP3K14 (NIK) was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified MAP3K14 (NIK) identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_003945.2

```
  1 MAPILGYWKI KGLVQPTRLL LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL GST TAG
  1 MAPILGYWKI KGLVQPTRLL LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL IVGN MAP3K14
318 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- NP_003945.2

101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA
101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA
318 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------

201 WPLQGWQATF GGGDHPPKSD LVPR
201 WPLQGWQATF GGGDHPPKSD LVPRHNQTSL YKKAGTMLEP SCLSRGAHEK FSVEEYLVHA LQGSVSSGQA HSLTSLAKTW AARGSRSREP SPKTEDNEGV
318 ---------- ---------- ---------- -------LEP SCLSRGAHEK FSVEEYLVHA LQGSVSSGQA HSLTSLAKTW AARGSRSREP SPKTEDNEGV

224
301 LLTEKLKPVD YEYREEVHWA THQLRLGRGS FGEVHRMEDK QTGFQCAVKK VRLEVFRAEE LMACAGLTSP RIVPLYGAVR EGPWVNIFME LLEGGSLGQL
381 LLTEKLKPVD YEYREEVHWA THQLRLGRGS FGEVHRMEDK QTGFQCAVKK VRLEVFRAEE LMACAGLTSP RIVPLYGAVR EGPWVNIFME LLEGGSLGQL

224
401 VKEQGCLPED RALYYLGQAL EGLEYLHSRR ILHGDVKADN VLLSSDGSHA ALCDFGHAVC LQPDGLGKSL LTGDYIPGTE THMAPEVVLG RSCDAKVDVW
481 VKEQGCLPED RALYYLGQAL EGLEYLHSRR ILHGDVKADN VLLSSDGSHA ALCDFGHAVC LQPDGLGKSL LTGDYIPGTE THMAPEVVLG RSCDAKVDVW

224
501 SSCCMMLHML NGCHPWTQFF RGPLCLKIAS EPPPVREIPP SCAPLTAQAI QEGLRKEPIH RVSAAELGGK VNRALQQVGG LKSPWRGEYK EPRHPPPNQA
581 SSCCMMLHML NGCHPWTQFF RGPLCLKIAS EPPPVREIPP SCAPLTAQAI QEGLRKEPIH RVSAAELGGK VNRALQQVGG LKSPWRGEYK EPRHPPPNQA

224
601 NYHQTLHAQP RELSPRAPGP RPAEETTGRA PKLQPPLPPE PPEPNKSPPL TLSKEESGMW EPLPLSSLEP APARNPSSPE RKATVPEQEL QQLEIELFLN
681 NYHQTLHAQP RELSPRAPGP RPAEETTGRA PKLQPPLPPE PPEPNKSPPL TLSKEESGMW EPLPLSSLEP APARNPSSPE RKATVPEQEL QQLEIELFLN

224
701 SLSQPFSLEE QEQILSCLSI DSLSLSDDSE KNPSKASQSS RDTLSSGVHS WSSQAEARSS SWNMVLARGR PTDTPSYFNG VKVQIQSLNG EHLHIREFHR
781 SLSQPFSLEE QEQILSCLSI DSLSLSDDSE KNPSKASQSS RDTLSSGVHS WSSQAEARSS SWNMVLARGR PTDTPSYFNG VKVQIQSLNG EHLHIREFHR

224
801 VKVGDIATGI SSQIPAAAFS LVTKDGQPVR YDMEVPDSGI DLQCTLAPDG SFAWSWRVKH GQLENRP
881 VKVGDIATGI SSQIPAAAFS LVTKDGQPVR YDMEVPDSGI DLQCTLAPDG SFAWSWRVKH GQLENRP
```

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



Anita Targosz Date: 02/Dec/2015