Certificate of Analysis
DAPK3 (ZIPK), 100 µg

Death-Associated Protein Kinase 3, GST-tagged

Part Number: PR7001B
Lot Number: 1083962B
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.

Manufacturing:

Manufactured under ISO 9001 certification at Life Technologies in Madison, WI, USA.

Specific Activity:

697 nmoles of phosphate transferred to ZIPtide peptide substrate (KKLNRTLSFAEPG) per minute per mg of total protein at 30°C. Activity determined at a final protein concentration of 1.67 µg/mL.

Concentration:

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

Calculated **4,380 nM**.

Aliases:

ZIP, ZIPK

Storage and Handling:

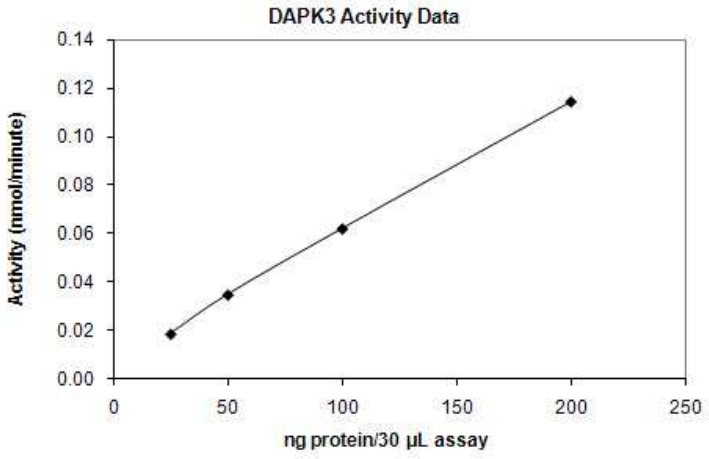
For maximum recovery please spin prior to use. Aliquots of the 5 ug, 10ug and 20ug sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 20 µL are not recommended. **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

DAPK3 (ZIPK) Activity Graph



Gel Information for DAPK3 (ZIPK)

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

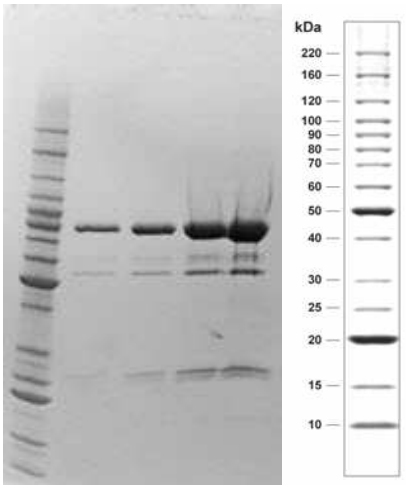
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 1 µg DAPK3 (ZIPK)

Lane 3: 2 µg DAPK3 (ZIPK)

Lane 4: 5 µg DAPK3 (ZIPK)

Lane 5: 10 µg DAPK3 (ZIPK)



Dilution Buffer:

20 mM Tris (pH 7.5), 0.02% Triton® X−100, 0.1 mg/mL BSA, 2 mM DTT, 0.5 mM Na_3VO_4 and 10% Glycerol.

Assay Conditions:

DAPK3 (ZIPK) was pre-diluted in enzyme dilution buffer and assayed in 12.5 mM Tris (pH 7.5), 10 mM $MgCl_2$, 1 mM EGTA, 0.5 mM Na_3VO_4, 5 mM β−glycerophosphate, 2.5 mM DTT, 0.01% Triton® X-100, 200 µM ATP, 670 µg/mL ZIPtide peptide substrate (KKLNRTLSFAEPG) and trace [^{32}P]-γ-ATP for 10 minutes at 30°C.

Purity:

80% as determined by a Coomassie® blue stained SDS-PAGE gel.

Molecular Weight:

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

Mass Spectrometry:

DAPK3 (ZIPK) was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified DAPK3 (ZIPK) identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_001339

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   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 DAPK3
   1 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- NP_001339

 101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA
 101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA
   1 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------

 201 WPLQGWQATF GGGDHPPKSD LVPR
 201 WPLQGWQATF GGGDHPPKSD LVPRHNQTSL YKKAGTMSTF RQEDVEDHYE MGEELGSGQF AIVRKCRQKG TGKEYAAKFI KKRRLSSSRR GVSREEIERE
   1 ---------- ---------- ---------- ------MSTF RQEDVEDHYE MGEELGSGQF AIVRKCRQKG TGKEYAAKFI KKRRLSSSRR GVSREEIERE

 224
 301 VNILREIRHP NIITLHDIFE NKTDVVLILE LVSGGELFDF LAEKESLTED EATQFLKQIL DGVHYLHSKR IAHFDLKPEN IMLLDKNVPN PRIKLIDFGI
  65 VNILREIRHP NIITLHDIFE NKTDVVLILE LVSGGELFDF LAEKESLTED EATQFLKQIL DGVHYLHSKR IAHFDLKPEN IMLLDKNVPN PRIKLIDFGI

 224
 401 AHKIEAGNEF KNIFGTPEFV APEIVNYEPL GLEADMWSIG VITYILLSGA SPFLGETKQE TLTNISAVNY DFDEEYFSNT SELAKDFIRR LLVKDPKRRM
 165 AHKIEAGNEF KNIFGTPEFV APEIVNYEPL GLEADMWSIG VITYILLSGA SPFLGETKQE TLTNISAVNY DFDEEYFSNT SELAKDFIRR LLVKDPKRRM

 224
 501 TIAQSLEHSW IKAIRRRNVR GEDSGRKPER RRLKTTRLKE YTIKSHSSLP PNNSYADFER FSKVLEEAAA AEEGLRELQR SRRLCHEDVE ALAAIYEEKE
 265 TIAQSLEHSW IKAIRRRNVR GEDSGRKPER RRLKTTRLKE YTIKSHSSLP PNNSYADFER FSKVLEEAAA AEEGLRELQR SRRLCHEDVE ALAAIYEEKE

 224
 601 AWYREESDSL GQDLRRLRQE LLKTEALKRQ AQEEAKGALL GTSGLKRRFS RLENRYEALA KQVASEMRFV QDLVRALEQE KLQGVECGLR.
 365 AWYREESDSL GQDLRRLRQE LLKTEALKRQ AQEEAKGALL GTSGLKRRFS RLENRYEALA KQVASEMRFV QDLVRALEQE KLQGVECGLR
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* highlighted residues denote differences from the reference protein sequence(s).

Becky. Baker, QA Engineer II Date: 03/May/2013