Certificate of Analysis
PIK3C2B (PI3K-C2 beta), 100 µg

Phosphoinositide-3-Kinase, Class 2, Beta Polypeptide, GST-tagged

Part Number: PR9006A
Lot Number: 2874064D
Immediate Storage: -80°C
Shipping Conditions: dry ice

5781 Van Allen Way
Carlsbad, CA 92008
Phone: 760.603.7200
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Description:

Recombinant human (amino acids 155-1383), GST-tagged, expressed in insect cells. No special measures were taken to activate this kinase.

Specific Activity:

0.90 nmoles of ADP formed per minute per mg of total protein using an ADP accumulation assay. An ADP/ATP standard curve is used to calculate percent conversion of ATP to ADP. PIK3C2B (PI3K-C2 beta) activity determined at a final protein concentration of 10000 ng/mL.

Concentration:

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

Calculated **3,760 nM**.

Aliases:

C2-PI3K, PI3K-C2beta, DKFZp686G16234

Storage and Handling:

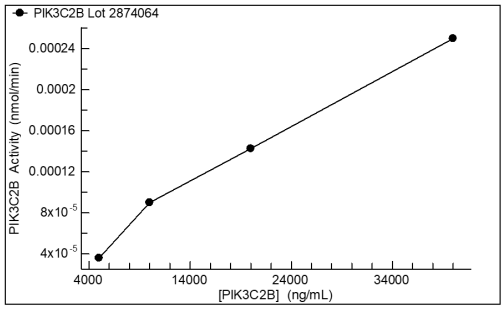
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 ug, 10ug and 20ug sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below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

PIK3C2B (PI3K-C2 beta) Activity Graph



Assay Buffer:

50 mM HEPES (pH 7.5), 100 mM NaCl, 0.03% CHAPS, 1 mM EGTA, and 3 mM $MgCl_2$ and 2 mM DTT. Prepared from 5X Kinase Buffer R (PV5101) plus DTT.

Assay Conditions:

PIK3C2B (PI3K-C2 beta) was diluted in assay buffer and the activity determined in a 10 µL ADP accumulation assay with 10 µM ATP and 100 µM PI Substrate at room temperature for 1 hour.

Gel Information for PIK3C2B (PI3K-C2 beta)

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

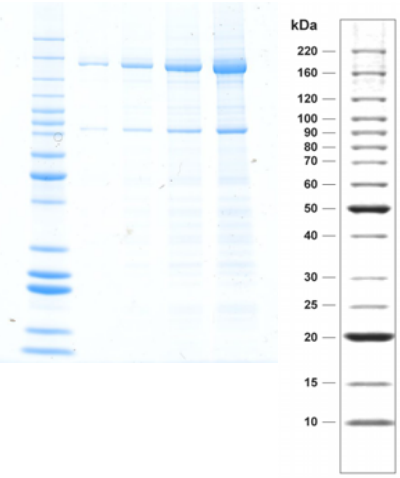
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.5 µg PIK3C2B (PI3K-C2 beta)

Lane 3: 1.0 µg PIK3C2B (PI3K-C2 beta)

Lane 4: 2.5 µg PIK3C2B (PI3K-C2 beta)

Lane 5: 5.0 µg PIK3C2B (PI3K-C2 beta)



Purity:

45% as determined by a SDS-PAGE gel stained with SimplyBlue™ SafeStain.

Molecular Weight:

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

Mass Spectrometry:

PIK3C2B (PI3K-C2 beta) was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified PIK3C2B (PI3K-C2 beta) identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_002637.2

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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 PIK3C2B
 155 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- NP_002637.2

 101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA
 101 DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA
 155 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------

 201 WPLQGWQATF GGGDHPPKSD LVPR
 201 WPLQGWQATF GGGDHPPKSD LVPRHNQTSL YKKAGSAAAP FTSPPPLPPR ASIWDTPPLP PRKGSPSSSK ISQPSDINTF SLVEQLPGKL LEHRILEEEE
 155 ---------- ---------- ---------- ---------- --SPPPLPPR ASIWDTPPLP PRKGSPSSSK ISQPSDINTF SLVEQLPGKL LEHRILEEEE

 224
 301 VLGGGGQGRL LGSVDYDGIN DAITRLNLKS TYDAEMLRDA TRGWKEGRGP LDFSKDTSGK PVARSKTMPP QVPPRTYASR YGNRKNATPG KNRRISAAPV
 213 VLGGGGQGRL LGSVDYDGIN DAITRLNLKS TYDAEMLRDA TRGWKEGRGP LDFSKDTSGK PVARSKTMPP QVPPRTYASR YGNRKNATPG KNRRISAAPV

 224
 401 GSRPHTVANG HELFEVSEER DEEVAAFCHM LDILRSGSDI QDYFLTGYVW SAVTPSPEHL GDEVNLKVTV LCDRLQEALT FTCNCSSTVD LLIYQTLCYT
 313 GSRPHTVANG HELFEVSEER DEEVAAFCHM LDILRSGSDI QDYFLTGYVW SAVTPSPEHL GDEVNLKVTV LCDRLQEALT FTCNCSSTVD LLIYQTLCYT

 224
 501 HDDLRNVDVG DFVLKPCGLE EFLQNKHALG SHEYIQYCRK FDIDIRLQLM EQKVVRSDLA RTVNDDQSPS TLNYLVHLQE RPVKQTISRQ ALSLLFDTYH
 413 HDDLRNVDVG DFVLKPCGLE EFLQNKHALG SHEYIQYCRK FDIDIRLQLM EQKVVRSDLA RTVNDDQSPS TLNYLVHLQE RPVKQTISRQ ALSLLFDTYH

 224
 601 NEVDAFLLAD GDFPLKADRV VQSVKAICNA LAAVETPEIT SALNQLPPCP SRMQPKIQKD PSVLAVRENR EKVVEALTAA ILDLVELYCN TFNADFQTAV
 513 NEVDAFLLAD GDFPLKADRV VQSVKAICNA LAAVETPEIT SALNQLPPCP SRMQPKIQKD PSVLAVRENR EKVVEALTAA ILDLVELYCN TFNADFQTAV

 224
 701 PGSRKHDLVQ EACHFARSLA FTVYATHRIP IIWATSYEDF YLSCSLSHGG KELCSPLQTR RAHFSKYLFH LIVWDQQICF PVQVNRLPRE TLLCATLYAL
 613 PGSRKHDLVQ EACHFARSLA FTVYATHRIP IIWATSYEDF YLSCSLSHGG KELCSPLQTR RAHFSKYLFH LIVWDQQICF PVQVNRLPRE TLLCATLYAL

 224
 801 PIPPPGSSSE ANKQRRVPEA LGWVTTPLFN FRQVLTCGRK LLGLWPATQE NPSARWSAPN FHQPDSVILQ IDFPTSAFDI KFTSPPGDKF SPRYEFGSLR
 713 PIPPPGSSSE ANKQRRVPEA LGWVTTPLFN FRQVLTCGRK LLGLWPATQE NPSARWSAPN FHQPDSVILQ IDFPTSAFDI KFTSPPGDKF SPRYEFGSLR

 224
 901 EEDQRKLKDI MQKESLYWLT DADKKRLWEK RYYCHSEVSS LPLVLASAPS WEWACLPDIY VLLKQWTHMN HQDALGLLHA TFPDQEVRRM AVQWIGSLSD
 813 EEDQRKLKDI MQKESLYWLT DADKKRLWEK RYYCHSEVSS LPLVLASAPS WEWACLPDIY VLLKQWTHMN HQDALGLLHA TFPDQEVRRM AVQWIGSLSD

 224
1001 AELLDYLPQL VQALKYECYL DSPLVRFLLK RAVSDLRVTH YFFWLLKDGL KDSQFSIRYQ YLLAALLCCC GKGLREEFNR QCWLVNALAK LAQQVREAAP
 913 AELLDYLPQL VQALKYECYL DSPLVRFLLK RAVSDLRVTH YFFWLLKDGL KDSQFSIRYQ YLLAALLCCC GKGLREEFNR QCWLVNALAK LAQQVREAAP

 224
1101 SARQGILRTG LEEVKQFFAL NGSCRLPLSP SLLVKGIVPR DCSYFNSNAV PLKLSFQNVD PLGENIRVIF KCGDDLRQDM LTLQMIRIMS KIWVQEGLDM
1013 SARQGILRTG LEEVKQFFAL NGSCRLPLSP SLLVKGIVPR DCSYFNSNAV PLKLSFQNVD PLGENIRVIF KCGDDLRQDM LTLQMIRIMS KIWVQEGLDM

 224
1201 RMVIFRCFST GRGRGMVEMI PNAETLRKIQ VEHGVTGSFK DRPLADWLQK HNPGEDEYEK AVENFIYSCA GCCVATYVLG ICDRHNDNIM LKTTGHMFHI
1113 RMVIFRCFST GRGRGMVEMI PNAETLRKIQ VEHGVTGSFK DRPLADWLQK HNPGEDEYEK AVENFIYSCA GCCVATYVLG ICDRHNDNIM LKTTGHMFHI

 224
1301 DFGRFLGHAQ MFGNIKRDRA PFVFTSDMAY VINGGDKPSS RFHDFVDLCC QAYNLIRKHT HLFLNLLGLM LSCGIPELSD LEDLKYVYDA LRPQDTEANA
1213 DFGRFLGHAQ MFGNIKRDRA PFVFTSDMAY VINGGDKPSS RFHDFVDLCC QAYNLIRKHT HLFLNLLGLM LSCGIPELSD LEDLKYVYDA LRPQDTEANA

 224
1401 TTYFTRLIES SLGSVATKLN FFIHNLAQMK FTGSDDRLTL SFASRTHTLK SSGRISDVFL CRHEKIFHPN K
1313 TTYFTRLIES SLGSVATKLN FFIHNLAQMK FTGSDDRLTL SFASRTHTLK SSGRISDVFL CRHEKIFHPN K
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* highlighted residues denote differences from the reference protein sequence(s).

Chevohn Joseph, Director, Quality Date: 25/Mar/2024